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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.

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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/340,376, filed December 14, 2001; Attorney Docket Number 018501-006400US, filed February 8, 2002; USSN 60/347,211, filed January 8, 2002; USSN 60/334,393, filed November 29, 2001; USSN 60/335,394, filed November 15, 2001; USSN 60/347,349, filed January 10, 2002; USSN 60/368,809, filed March 29, 2002; USSN 60/409,450, filed September 9, 2002; USSN 60/359,077, filed February 20, 2002; USSN 60/386,614, filed June 5, 2002; USSN 60/356,714, filed February 13, 2002; USSN 60/397,775 filed July 22, 2002; USSN 60/332,464, filed November 21, 2001; USSN 60/397,845, filed July 22, 2002; USSN 60/370,110, filed April 4, 2002; USSN 60/396,839, filed July 16, 2002; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes. The application also incorporates by reference PCT/US02/29560; PCT/US02/02242; and PCT/US02/17594.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer and other diseases; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of these conditions. The invention further relates to methods for identifying and using agents and/or targets that modulate these conditions.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is in Japan.

Cancers share the charactaristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over

70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis, prognosis, and treatment of cancer patients.

Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, e.g., reproductive organs, especially those absent in one sex. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell.

In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-80; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising at sequence at least 80% identical to a sequence as described in Tables 2A-80, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-80; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression

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of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini

(ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznek (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwe, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic

Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901; Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 2B-76B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in diseased samples (see Tables 1-3), particularly sequences involved in angiogenesis, arthritis, prostate cancer, breast cancer, colorectal cancer, cervical cancer, bladder cancer, head and neck cancer, esophageal cancer, lung cancer, ovarian cancer, pancreatic cancer, renal cancer, stomach cancer, skin cancer, testicular cancer, uterine cancer, glioblastoma, Ewing sarcoma, soft tissue sarcoma, and lung fibrosis. Tables 2A-80 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-80; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-80 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is

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typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is about 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from about 20 to 600, usually about 50 to 200, more usually about 100 to 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-

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scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its

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native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain somebasic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts,

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et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β-sheet and α-helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkahge, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein;

Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively

insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I, electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

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radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; chemoattracting moieties, immune modulators (micA/B), or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is

achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid

sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to

8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for

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inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 2A-80.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'$_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'$_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'$_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in

Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, effector function, chemoattractant, immune modulator, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis

and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Maliganant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based

upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases,

e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1-3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

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The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guuide to the Analysis of Genes and Proteins Wiley; Mount (2001)

Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention

provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute

the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may

have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated

molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g, secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g., moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-80, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

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particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, supra; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlyation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

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be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threone is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

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amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 2A-80 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, target a drug loaded liposome, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells. See, e.g., USSN 09/544,494.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce

deleterious side effects that may be associated with the untargeted therapeutic moiety. Antibody fragments may be used to target toxin loaded liposomes.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μM, preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Selectivity of binding to the specific target and not to related sequences is often also important.

Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Pätent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

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compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

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vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics, e.g., toxin loaded liposomes, to the treated cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of cancer cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^{3}H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^{3}H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^{3}H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Insti. 37:167-175; Eagle, et al.(1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

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Polynucleotide modulators of cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al.(1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

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administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g.,Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294,; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are availablel for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A and 3A, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

blood vessels/angiogenesis: hemangiomas, lymphangiomas, angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, lymphadenitis, lymphangitis, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented villonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids

bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma, squamous cell carcinoma

bone: Ewing sarcoma, sarcomas arising from skeletal and extraskeletal connective tissues, including the peripheral nervous system (e.g. chondrosarcoma, osteosarcoma)

brain: glioblastoma, oligodendroglioma, anablastic astrocytoma, meningioma, medulablastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pineocytoma, neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neurocepithelioma, neuroma, ganglioneuroma

breast: ductal carcinoma in situ, lobular carcinoma in situ

cervix: cancer of the cervix, vagina, or vulva

colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leimyo sarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)

esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastrodigestive carcinomas (e.g., cancers of the stomach, colon, or rectum)

fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing

head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus

kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomyolipoma, oncocytoma

leukocytes: acute lymphoblastic leukemia/lymphoma, chronic lymphocytic leukemia, follicular lymphoma, large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, mantle cell lymphoma, lymphoplasmacytic lymphoma, peripheral T-cell lymphoma, adult T-cell leukemia/lymphoma, Hodgkin disease, acute myelogenous leukemia, chronic myelogenous leukemia, thymic hyperplasia, hairy cell leukemia, malignant transformation, inappropriate activation or abnormalities of leukocytes (e.g., immature, precursor B (pre-B) or precursor T (pre-T) lymphocytes, monocytes, neutrophils, eosinophils, basophils, dendritic cells, lymphoblasts), arthritis, inflammation, leukocytosis, lymphadenitis, lymphangitis, bacteremia, chronic nonspecific lymphadenitis, psoriasis, wound healing

liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct

lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer

ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryomal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosal stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma

pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes melitis, chronic pancreatitis

prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis

skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder

soft tissue: soft tissue tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrohistiocytic sarcoma) smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma) tumors of the blood and lymph vessels (e.g., angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g., neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, extraskeletal Ewing's sarcoma, schwannoma, neuroma, ganglioneuroma), paraganglioma, extraskeletal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma), pluripotential mesenchymal tumors, epitheliod sarcomas, rhabdoid tumors, desmoplastic small cell tumors, alveolar sarcoma

stomach: adenocarcinoma, squamous cell carcinoma, adenoacanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas

testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)

uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed mullerian tumors, adenosarcoma)

Tables 2B-72B, 76B, and 79B list accession numbers for Pkeys lacking UnigeneID's for Tables 2A-72A, 76A, and 79A, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 2C-72C, 76C, and 79C list genomic positioning for Pkeys lacking Unigene ID's and accession numbers in Tables 2A-72A, 76A, and 79A, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Table 2A, Disease Indications and Preferred Utilities for Selected Genes

Table 2A provides preferred disease indications and preferred utilities for about 413 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number
UnigeneID:	Unigene ID number

Unigene Title: Unigene gene title
Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigeneID; Unigene Title; Disease; Utility

102892; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk; mAb+diag+s.m.
104865; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL
104978; AI199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, lung, pros, blad, stom; CTL
109424; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb+s.m.
110765; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
110906; AA035211; Hs.17404; SOX7 SRY (sex determining regi; angio, blad; CTL
115522; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; GTL
116176; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL
118695; AK000465; Hs.50081; KIAA1199 protein; colon, lung; diag
123049; BE047680; Hs.211869; dickkopf (Xenopus laevis) homo; EWS; mAb+diag
131486; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
133370; AF245505; Hs.72157; Adlican; breast, lung, panc; diag
310016; AW449612; Hs.152475; ESTs; colon; CTL
322303; AI357412; Hs.157601; ESTs; colon, pros, fibro, breast; CTL+diag
400289; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, cerv, ovar, headnk, esoph; mAb+diag+s.m.
400297; AI127076; Hs.288381; hypothetical protein DKFZp564O; breast, blad, colon, pros; mAb
400303; AA242758; Hs.79136; LIV-1 protein, estrogen regula; breast, ovar, pros, stom, uter, blad, lung, headnk; mAb
400843; ; ; NM_003105*:Homo sapiens sortil; blad; s.m.
402075; ; ; ENSP00000251056*:Plasma membra; blad, lung, headnk, cerv, mela, esoph; mAb+diag
402901; ; ; NM_025206*:Homo sapiens hypoth; blad ; CTL
404287; ; ; FGENESH predicted novel CUB-do; panc, lung, colon, uter, esoph; mAb+s.m.
404682; ; ; ortholog of mouse polydomain p; panc; diag
404875; ; ; NM_022819*:Homo sapiens phosph; blad; CTL+s.m.
404977; ; ; Insulin-like growth factor 2 (; blad, ovar, sarc; mAb+diag
405033; ; ; C1002652*:gi|5443271sp|Q04799|; blad; s.m.
406400; ; ; kallikrein 8 (neuropsin/ovasin; ovar, uter; diag
406964; M21305; ; FGENES predicted novel secrete; angio, blad, fibro, sarc; diag
407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299; glio, blad; CTL
407792; AI077715; Hs.39384; putative secreted ligand homol; ovar, uter, cerv, panc; mAb+diag
407811; AW190902; Hs.40098; cysteine knot superfamily 1, B; blad, panc, stom, uter, lung, esoph; diag
407836; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL
407975; X89426; Hs.41716; endothelial cell-specific mole; angio, renal; diag
408243; Y00787; Hs.624; interleukin 8; blad, stom, headnk, cerv, lung, angio, esoph, panc; diag
408367; AK001178; Hs.44424; Homo sapiens orphan neurotrans; mela; mAb+s.m.
408369; R38438; Hs.118747; SLC15A2 Solute carrier family ; pros, lung, fibro, uter, glio, cerv, ovar; mAb
408380; AF123050; Hs.44532; diubiquitin; lung, blad, headnk, panc, stom, fibro, esoph, mela; CTL
408482; NM_000676; Hs.45743; adenosine A2b receptor; lung, esoph, headnk, colon; mAb+s.m.
408562; AI436323; Hs.31141; roundabout (axon guidance rece; uter, fibro, sarc; mAb+s.m.
408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, ; lung; mAb+s.m.
408908; BE296227; Hs.250822; serine/threonine kinase 15; blad, lung, headnk, stom,colon; s.m.
409041; AB033025; Hs.50081; Hypothetical protein, XP_05186; uter, ovar, lung, colon, stom, headnk, breast, panc; CTL+diag
409079; W87707; Hs.82065; interleukin 6 signal transduce; breast, pros; mAb+s.m.
409103; AF251237; Hs.112208; XAGE-1 protein; lung; CTL
409178; BE393948; Hs.50915; kallikrein 5; ovar, breast, mela; diag
409220; BE243323; Hs.51233; tumor necrosis factor receptor; angio, renal, colon, stom; mAb+s.m.
409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100k; lung, headnk, panc, stom, cerv, esoph, blad; diag
409632; W74001; Hs.55279; serine (or cysteine) proteinas; lung, blad, headnk; diag
409663; AI743750; Hs.98306; KIAA1862 protein; renal; CTL
409757; NM_001898; Hs.123114; cystatin SN; panc, stom, lung, blad; diag
409889; AW630041; Hs.56937; suppression of tumorigenicity ; colon, ovar, pros; mAb+s.m.
409893; AW247090; Hs.57101; minichromosome maintenance def; lung, cerv, blad, test, esoph; CTL+s.m.
409956; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, panc, ovar, colon, headnk, lung, blad, esoph; diag
410001; AB041036; Hs.57771; kallikrein 11; ovar, pros, uter, cerv, lung ; diag
410055; AJ250839; Hs.58241; gene for serine/threonine prot; renal; s.m.
410153; BE311926; Hs.15830; hypothetical protein FLJ12691; renal,blad; CTL
410274; AA381807; Hs.336402; hypoxia-inducible protein 2; lung, renal; CTL
410309; BE043077; Hs.278153; alpha-2,8-sialyltransferase II; panc; s.m.
410407; X66839; Hs.63287; carbonic anhydrase IX; renal, lung, colon, stom, ovar, uter, blad, sarc; mAb+s.m.
410418; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
411274; NM_002776; Hs.69423; kallikrein 10; colon, ovar, uter, cerv, headk, panc; diag
411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA13; renal; mAb+s.m.
411773; NM_006799; Hs.72026; protease, serine, 21 (testisin; ovar; diag
411975; AI916058; Hs.144583; 3'UTR of: dead ringer (Drosoph; test, colon; CTL
412078; X69699; Hs.73149; paired box gene 8; ovar; CTL
412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, headnk, breast, ovar, panc, angio, test, mela; s.m.
412314; AA825247; Hs.356084; G protein-coupled receptor 27 ; ovar, uter, test; mAb+s.m.
412609; Z48804; Hs.74124; ocular albinism 1 (Nettleship-; mela; s.m.
412628; AI972402; Hs.306051; hypothetical protein MGC2648; pros; diag
412709; AL022327; Hs.74518; KIAA0027 protein; glio, sarc; mAb+s.m.
412719; AW016610; Hs.816; ESTs; lung, headnk, blad, glio, cerv, sarc; s.m.
412959; D87458; Hs.75090; KIAA0282 protein; glio; CTL+s.m.
413048; M93221; Hs.75182; mannose receptor, C type 1; fibro, panc; mAb

413063; AL035737; Hs.75184; chitinase 3-like 1 (cartilage ; glio, ovar, blad, lung ; diag
413278; BE563085; Hs.833; interferon-stimulated protein,; panc, lung, blad, breast, cerv, ovar, headnk, esoph, mela; CTL+s.m.
413324; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxyg; blad, lung, mela, fibro, uter, sarc; s.m.
413554; AA319146; Hs.75426; secretogranin II (chromogranin; panc, glio; diag
413719; BE439580; Hs.75498; small inducible cytokine subfa; leuk, panc, lung, headnk, cerv, colon, uter, stom, esoph; diag
414555; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; s.m.
414577; AI056548; Hs.378938; hypothetical protein FLJ20992 ; angio; CTL+diag
414774; X02419; Hs.77274; plasminogen activator, urokina; lung, blad, headnk, panc, stom, ovar, esoph; diag
414812; X72755; Hs.77367; monokine induced by gamma inte; breast, blad, lung, fibro, panc, colon, headnk, cerv, stom, renal, ovar, test, mela, esoph; diag
414883; AA926960; Hs.348669; CDC28 protein kinase 1; lung, ovar, stom, colon, cerv, headnk, test; s.m.
414907; X90725; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.
414991; C17898; ; Homo sapiens up-regulated by B; fibro, lung; mAb+diag
415138; C18356; Hs.295944; tissue factor pathway inhibito; angio, panc, stom, lung, uter; CTL+diag
415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb+s.m.
415668; AW957684; Hs.306814; Homo sapiens lysyl oxidase-lik; mela; diag
415669; NM_005025; Hs.78589; serine (or cysteine) proteinas; lung; mAb+diag+s.m.
415817; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, cerv, mela, esoph, fibro; mAb+s.m.
415929; AA724373; Hs.304950; Homo sapiens mucolipin-3 (MCOL; mela; mAb
416091; AF295370; Hs.283082; defensin, beta 3; headnk, esoph, mela; CTL+diag
416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient; lung, headnk, colon, uter, stom; CTL+s.m.
416250; AA581386; Hs.73452; Kremen 2; esoph, lung, cerv, ovar; mAb+s.m.
416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); ovar, uter; diag
416636; N32536; Hs.42645; solute carrier family 16 (mono; breast, panc, uter, mela; mAb+s.m.
416658; U03272; Hs.79432; fibrillin 2 (congenital contra; lung, ovar, uter, blad, angio, test, sarc; diag
416836; D54745; Hs.80247; cholecystokinin; pros, EWS, glio ; diag
416857; AA188775; Hs.292453; FGENESH predicted TM containin; glio; mAb+s.m.
416965; N26223; Hs.160436; MDAC1; fibro, ovar, uter; mAb
417034; NM_006183; Hs.80962; neurotensin; lung, headnk, cerv; diag
417079; U65590; Hs.81134; interleukin 1 receptor antagon; blad, lung, headnk, cerv, esoph; diag
417166; AA431323; Hs.42146; Paired box protein Pax-3; mela, sarc; CTL
417389; BE260964; Hs.82045; midkine (neurite growth-promot; ovar, lung, blad, uter, cerv, panc, stom, mela, test, colon, sarc; mAb+diag
417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyc; panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal; mAb
417771; AA804698; Hs.82547; retinoic acid receptor respond; blad, cerv, panc, pros, ovar; mAb
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; lung, panc, breast, ovar, headnk, stom, sarc; CTL
417931; W95642; Hs.82961; trefoil factor 3 (intestinal); ovar, panc, stom, colon, uter, pros; diag
417933; X02308; Hs.82962; thymidylate synthetase; blad, lung, angio, colon, panc, esoph; s.m.
418007; M13509; Hs.83169; matrix metalloproteinase 1 (in; lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mela; mAb+diag+s.m.
418030; BE207573; Hs.83321; neuromedin B; glio, panc; diag
418064; BE387287; Hs.83384; S100 calcium-binding protein, ; mela; diag
418281; U09550; Hs.1154; oviductal glycoprotein 1, 120k; uter, ovar; CTL+diag
418478; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk, panc, cerv, mela, sarc; s.m.
418506; AA084248; Hs.372651; Unknown protein for MGC:29643 ; angio, ovar, glio, uter, lung, blad, panc, mela, sarc; mAb+diag
418526; BE019020; Hs.85838; solute carrier family 16 (mono; lung, blad, renal, panc, stom, colon, ovar; mAb+s.m.
418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via d; esoph, headnk; s.m.
418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-; lung, blad, stom, ovar, panc, esoph, cerv, sarc; CTL
418738; AW388633; Hs.6682; solute carrier family 7, (cati; angio, lung, ovar, blad, colon, stom, panc, uter, leuk; mAb+s.m.
418830; BE513731; Hs.348874; hypothetical protein MGC4816; lung; CTL
418867; D31771; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
418870; AF147204; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad, renal; mAb+s.m.
419080; AW150835; Hs.18878; hypothetical protein FLJ21620; renal, lower uter, lung; CTL
419121; AA374372; Hs.89626; parathyroid hormone-like hormo; lung, esoph, headnk, blad; diag
419171; NM_002846; Hs.89655; protein tyrosine phosphatase, ; lung; mAb+s.m.
419172; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio, renal; mAb+s.m.
419183; U60669; Hs.89663; cytochrome P450, subfamily XXI; blad, lung, headnk, panc; CTL+s.m.
419216; AU076718; Hs.164021; small inducible cytokine subfa; panc, lung, stom, cerv, pros, headnk, esoph; diag
419235; AW470411; Hs.288433; neurotrimin; panc, fibro, headnk, lung; mAb+diag
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ovar, pros, lung, breast, uter, test, panc, stom, sarc; mAb+s.m.
419508; AW997938; Hs.90786; ATP-binding cassette, sub-fami; glio, omuc, stom, lung, panc, colon, renal, uter; mAb+s.m.
419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); lung, fibro, test; mAb+diag
419704; AA429104; Hs.45057; ESTs; glio; CTL+s.m.
419723; AL120193; Hs.339810; longevity assurance (LAG1, S. ; glio; mAb+diag
419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; blad, lung, colon, ovar, test, esoph, mela, sarc; CTL+s.m.
419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA; fibro, stom, blad, esoph, uter; diag
420159; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 fi; blad, stom; mAb
420162; BE378432; Hs.95577; cyclin-dependent kinase 4; lung, mela, sarc; s.m.
420370; Y13645; Hs.97234; uroplakin 2; blad; mAb
420440; NM_002407; Hs.97644; mammaglobin 2; ovar, uter, cerv; diag
420602; AF060877; Hs.99236; regulator of G-protein signall; headnk, glio, cerv, mela; CTL+s.m.
420610; AI683183; Hs.99348; distal-less homeo box 5; uter, endo, lung; CTL
420737; L08096; Hs.99899; CD70 ; tumor necrosis factor ; renal; mAb+s.m.
420876; AA918425; Hs.177744; FGENES predicted novel protein; panc, blad; s.m.
421066; AU076725; Hs.101408; branched chain aminotransferas; blad, lung; CTL+s.m.
421110; AJ250717; Hs.1355; cathepsin E; blad, panc, stom, lung, fibro, ovar, esoph; sm+diag
421340; F07783; Hs.1369; decay accelerating factor for ; angio, panc, stom; diag
421379; Y15221; Hs.103982; small inducible cytokine subfa; breast, panc, headnk, lung, stom, blad, cerv, colon, leuk, fibro, test, mela, esoph; diag
421471; U90545; Hs.327179; solute carrier family 17 (sodi; renal; mAb+s.m.
421474; U76362; Hs.104637; solute carrier family 1 (gluta; lung; mAb+s.m.
421524; AA312082; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
421552; AF026692; Hs.105700; secreted frizzled-related prot; breast, ovar, panc, cerv, uter, pros, lung, stom, headnk; diag
421563; NM_006433; Hs.105806; granulysin; fibro; diag
421574; AJ000152; Hs.105924; defensin, beta 2; headnk, lung; CTL+diag
421582; AI910275; Hs.350470; trefoil factor 1 (breast cance; breast, panc, lung, omuc; diag

421659; NM_014459; Hs.106511; protocadherin 17; fibro; mAb
421753; BE314828; Hs.107911; ATP-binding cassette, sub-fami; lung; mAb+s.m.
421817; AF146074; Hs.108660; ATP-binding cassette, sub-fami; lung, cerv, headnk, blad; mAb+s.m.
421829; AB018330; Hs.108708; calcium/calmodulin-dependent p; pros; s.m.
422048; NM_012445; Hs.288126; spondin 2, extracellular matri; panc, pros, sarc; diag
422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, ; pros; s.m.
422109; S73265; Hs.1473; gastrin-releasing peptide; panc, lung, colon, fibro; diag
422158; L10343; Hs.112341; protease inhibitor 3, skin-der; headnk, blad, lung, cerv, stom, esoph; diag
422192; AA305159; Hs.113019; fis485; mela; s.m.
422260; AA315993; Hs.105484; regenerating gene type IV; colon, omuc, stom, panc; mAb+diag
422282; AF019225; Hs.114309; apolipoprotein L; blad, lung, headnk, renal; diag
422283; AW411307; Hs.114311; CDC45 (cell division cycle 45,; lung, blad, test, cerv, headnk, esoph; s.m.
422330; D30783; Hs.115263; epiregulin; panc, colon, blad; mAb+diag
422397; AJ223366; Hs.116051; MYEOV Myeloma overexpressed ge; panc, stom, colon, esoph, renal, blad; CTL+s.m.
422424; AI186431; Hs.296638; prostate differentiation facto; blad, panc, pros, angio, colon, stom, lung, mela; diag
422578; AF239666; Hs.1545; caudal type homeo box transcri; colon; CTL
422627; BE336857; Hs.118787; transforming growth factor, be; colon, renal, sarc; mAb+diag
422765; AW409701; Hs.1578; baculoviral IAP repeat-contain; lung, blad; s.m.
422809; AK001379; Hs.121028; hypothetical protein FLJ10549; blad, cer, lung, uter, anglo, stom, test; s.m.
422867; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar, pros, panc, lung, colon, uter, sarc; diag
422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell ; ovar, blad, panc, lung, headnk, colon,stom; CTL+s.m.
423161; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, blad; mAb+s.m.
423184; NM_004428; Hs.1624; ephrin-A1; pros, panc, renal,colon; mAb+s.m.
423242; AL039402; Hs.125783; DEME-6 protein; breast, renal, ovar, pros, colon; CTL
423508; AW604297; Hs.129711; hepatitis A virus cellular rec; renal, colon; mAb
423583; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
423634; AW959908; Hs.1690; heparin-binding growth factor ; lung, blad, headnk, panc; diag
423673; BE003054; Hs.1695; matrix metalloproteinase 12 (m; blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test; mAb+diag+s.m.
423936; U77629; Hs.135639; achaete-scute complex (Drosoph; colon, stom, ovar; CTL
423961; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc, headnk, ovar, mela, sarc; mAb+diag
424008; R02740; Hs.137555; putative chemokine receptor; G; blad, headnk, stom, cerv, esoph; mAb+s.m.
424046; AF027866; Hs.138202; serine (or cysteine) proteinas; headnk, lung, cerv; diag
424321; W74048; Hs.1765; lymphocyte-specific protein ty; mela, fibro; s.m.
424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); lung, colon, test; s.m.
424411; NM_005209; Hs.146549; crystallin, beta A2; panc, sarc; s.m.
424502; AF242388; Hs.149585; lengsin; lung; s.m.
424503; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros,anglo, blad, lung; mAb+s.m.
424620; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
424687; J05070; Hs.151738; matrix metalloproteinase 9 (ge; headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela, sarc; diag
424735; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.
424825; AF207069; Hs.153357; procollagen-lysine, 2-oxogluta; mela; CTL+s.m.
424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a); ovar, blad, lung, headnk, panc, stom; s.m.
424917; AI636208; Hs.96901; hypothetical protein FLJ23049; fibro, uter, ovar; CTL
424943; AU077260; Hs.153924; death-associated protein kinas; fibro; s.m.
425009; X58288; Hs.154151; protein tyrosine phosphatase, ; renal, fibro; mAb+s.m.
425071; NM_013989; Hs.154424; deiodinase, iodothyronine, typ; pros, colon, stom, uter, cerv, headnk, esoph, panc; diag
425115; R44664; Hs.123956; downstream of: G protein-coup; glio; mAb+s.m.
425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph, sarc; mAb+diag+s.m.
425263; NM_001197; Hs.155419; BCL2-interacting killer (apopt; pros; s.m.
425322; U63630; Hs.155637; protein kinase, DNA-activated,; lung, headnk; s.m.
425535; AB007937; Hs.158287; syndecan 3; mela, glio; mAb+s.m.
425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, headnk, cerv, esoph, blad; mAb
425721; AC002115; Hs.159309; uroplakin 1A; blad; mAb
425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homo; endo, uter, colon; CTL+diag
425734; AF056209; Hs.159396; peptidylglycine alpha-amidatin; lung; s.m.
425776; U25128; Hs.159499; parathyroid hormone receptor 2; ovar, uter, lung; mAb+diag
425842; AI587490; Hs.159623; NK-2 (Drosophila) homolog B; panc, glio; s.m.
425852; AK001504; Hs.159651; death receptor 6, TNF superfam; blad, lung, headnk; mAb+s.m.
425883; AL137708; Hs.161031; Homo sapiens mRNA; cDNA DKFZp4; blad, panc; mAb
425998; AU076629; Hs.165950; fibroblast growth factor recep; renal; mAb+s.m.
426028; NM_001110; Hs.172028; a disintegrin and metalloprote; blad; mAb+diag
426215; AW963419; Hs.155223; stanniocalcin 2; breast, lung, renal, colon, ovar, uter; mAb+diag
426227; U67058; Hs.154299; Human proteinase activated rec; panc, lung, colon, esoph, stom; mAb+s.m.
426322; J05068; Hs.2012; transcobalamin I (vitamin B12 ; panc, blad, stom; diag
426344; H41821; Hs.322469; transcriptional activator of t; glio; CTL+s.m.
426427; M86699; Hs.169840; TTK protein kinase; ovar, lung, headnk, cerv, colon, uter, stom, test; CTL+s.m.
426451; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; blad, breast; s.m.
426514; BE616633; Hs.170195; bone morphogenetic protein 7 (; ovar, colon, blad, lung, cerv; mAb+diag
426600; NM_003378; Hs.171014; VGF nerve growth factor induci; mela, sarc; diag
426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor i; lung, esoph, pros, uter, panc, colon, ovar, headnk; mAb+s.m.
426812; AF105365; Hs.172613; solute carrier family 12 (pota; renal; mAb+s.m.
426890; AA393167; Hs.41294; ESTs; renal, colon, ovar, uter, stom; CTL
427239; BE270447; Hs.356512; ubiquitin carrier protein; lung, blad, test, mela, sarc; CTL+s.m.
427335; AA448542; Hs.278444; G antigen 7B; lung, headnk, blad, mela, esoph, sarc; CTL
427343; AI880044; Hs.176977; protein kinase C binding prote; glio; CTL+s.m.
427722; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, stom, panc; CTL
427747; AW411425; Hs.180655; serine/threonine kinase 12; blad, lung, ovar, stom, test, esoph, sarc; s.m.
427923; AW274357; Hs.301406; FGENESH predicted 11 TM protei; mela; mAb
427969; NM_001963; Hs.2230; epidermal growth factor (beta-; panc; mAb+diag
428093; AW594506; Hs.104830; ESTs; ovar, panc; CTL
428179; AI127772; Hs.380877; serum/glucocorticoid regulated; breast; s.m.
428187; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter, colon, stom; mAb+s.m.
428242; H55709; Hs.2250; leukemia inhibitory factor (ch; ovar, panc, leuk, lung; diag

428296; NM_003058; Hs.183572; solute carrier family 22 (orga; renal; mAb+s.m.
428330; L22524; Hs.2256; matrix metalloproteinase 7 (ma; uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela; mAb+diag+s.m.
428368; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk, stom, esoph, colon; diag
428392; H10233; Hs.2265; secretory granule, neuroendocr; panc; diag
428450; NM_014791; Hs.184339; KIAA0175 gene product; ovar, cerv, panc, lung, blad, mela; s.m.
428479; Y00272; Hs.334562; cell division cycle 2, G1 to S; lung, blad, colon, uter, ovar; s.m.
428484; AF104032; Hs.184601; solute carrier family 7 (catio; lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela; mAb+s.m.
428486; AW583497; Hs.184604; pancreatic polypeptide; panc; diag
428505; AL035461; Hs.2281; chromogranin B (secretogranin ; panc, lung; diag
428513; BE220806; Hs.184697; plexin C1; mela, panc, breast stom, headnk; mAb
428579; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosoph; blad, ovar, pros, lung, stom, test; CTL+s.m.
428698; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, panc, stom, headnk, ovar, EWS; mAb
428748; AW593206; Hs.98785; Ksp37 protein; lung, sarc; diag
428758; AA433988; Hs.98502; CA125 antigen; mucin 16; ovar, cerv, lung, panc, stom, renal; diag
428778; AK000530; Hs.193326; fibroblast growth factor recep; ovar; mAb+s.m.
428953; AA306610; Hs.348183; tumor necrosis factor receptor; cerv, panc, colon, stom, headnk, renal; mAb+diag
428969; AF120274; Hs.194689; artemin; lung, cerv; diag
428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG; stom, panc, colon, ovar, fibro; mAb+s.m.
429149; AW193360; Hs.197962; Homolog of mouse ADP-ribosylat; glio; mAb+s.m.
429211; AF052693; Hs.198249; gap junction protein, beta 5 (; lung, blad, headnk, cerv, esoph, stom, mela; mAb+s.m.
429263; AA019004; Hs.198396; ATP-binding cassette, sub-fami; lung; mAb+s.m.
429276; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad, glio; mAb+s.m.
429353; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros ; mAb+s.m.
429547; AW009166; Hs.99376; FGENESH predicted novel secret; panc, headnk, lung, ovar; diag
429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung, fibro; mAb+diag
429903; AL134197; Hs.93597; cyclin-dependent kinase 5, reg; lung, mela; s.m.
429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin; leio; mAb+s.m.
430147; R60704; Hs.234434; hairy/enhancer-of-split relate; glio; s.m.
430178; AW449612; Hs.152475; 3'UTR of: achaete-scute comple; colon, stom, ovar; CTL
430377; NM_001922; Hs.301865; dopachrome tautomerase (dopach; mela; CTL
430413; AW842182; Hs.241392; small inducible cytokine A5 (R; fibro, esoph, mela; diag
430486; BE062109; Hs.241551; chloride channel, calcium acti; lung, blad, headnk, cerv, esoph; mAb+s.m.
430822; AJ005371; Hs.248017; glyceraldehyde-3-phosphate deh; mela, sarc; s.m.
431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey; ovar, uter; diag
431462; AW583672; Hs.256311; granin-like neuroendocrine pep; panc, lung, glio, test; diag
431515; NM_012152; Hs.258583; EDG-7 (endothelial differenti; ovar, pros, lung, blad; mAb+s.m.
431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetas; esoph, cerv; CTL+s.m.
431629; AU077025; Hs.265827; interferon, alpha-inducible pr; panc, uter, cerv, stom, esoph, mela; mAb+diag
431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD4; ovar, panc, blad, headnk, mela, renal; mAb+s.m.
431745; AW972448; Hs.163425; Novel FGENESH predicted cadher; fibro, ovar, uter; mAb
431840; AA534908; Hs.2860; POU domain, class 5, transcrip; test, renal, blad; CTL
431846; BE019924; Hs.271580; uroplakin 1B; lung, blad, headnk, uter, cerv, stom, ovar; mAb+diag
431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela; mAb+diag
432101; AI918950; Hs.123642; EphA3; pros, panc, EWS sarc; s.m.
432179; X75208; Hs.2913; EphB3; ovar, colon; mAb+s.m.
432196; AW300888; Hs.273230; hypothetical protein FLJ10830; renal; CTL
432201; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, ovar, stom, panc, uter, cerv, lung ; mAb+diag+s.m.
432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis; renal; CTL
432596; AJ224741; Hs.278461; matrilin 3; panc, breast, sarc; diag
432606; NM_002104; Hs.3066; granzyme K (serine protease, g; renal, breast, lung, stom, hepC, fibro, leuk; CTL
432829; W60377; Hs.57772; ESTs; blad; CTL+s.m.
432874; W94322; Hs.279651; melanoma inhibitory activity; panc, stom, mela, sarc; diag
432990; AL036071; Hs.279899; tumor necrosis factor receptor; pros, renal; mAb+s.m.
433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; colon, breast, lung, blad, cerv, uter, test, mela; s.m.
433447; U29195; Hs.3281; neuronal pentraxin II; mela, esoph, colon, renal; diag
433848; AF095719; Hs.93764; carboxypeptidase A4; headnk, esoph, lung; s.m.
433867; AK000596; Hs.3618; hippocalcin-like 1; renal; CTL
434206; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung, stom; CTL+s.m.
434276; AF123659; Hs.93605; leucine zipper, putative tumor; mela; s.m.
434293; NM_004445; Hs.3796; EphB6; blad, pros; s.m.
435013; H91923; Hs.110024; NM_020142:Homo sapiens NADH:ub; renal, lung, sarc; CTL
435472; AW972330; Hs.283022; triggering receptor expressed ; glio; mAb
435505; AF200492; Hs.211238; interleukin-1 homolog 1; lung, headnk; diag
436456; AW292677; Hs.248122; melanin-concentrating hormone ; mela, glio; mAb+s.m.
436480; AJ271643; Hs.87469; putative acid-sensing ion chan; glio; mAb+s.m.
436481; AA379597; Hs.5199; HSPC150 protein similar to ubi; lung, blad, colon, ovar, uter, headnk, test; s.m.
436576; AI458213; Hs.77542; ESTs; renal, panc, headnk, lung; mAb+s.m.
436608; AA628980; Hs.192371; down syndrome critical region ; blad, lung, sarc; CTL+s.m.
436695; AF037335; Hs.5338; carbonic anhydrase XII; breast, renal, ovar, glio; mAb+s.m.
436961; AW375974; Hs.156704; ESTs; lung, panc, renal, uter, colon ; CTL
436982; AB018305; Hs.5378; spondin 1, (f-spondin) extrace; ovar, fibro; diag
437016; AU076916; Hs.5398; guanine monphosphate synthetas; lung, blad, cerv, esoph, colon, headnk; s.m.
437044; AL035864; Hs.69517; differentially expressed in Fa; headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph; CTL
437789; AI581344; Hs.127812; ESTs, Weakly similar to T17330; lung; CTL
437852; BE001836; Hs.256897; putative GPCR; blad, lung; mAb+s.m.
438380; T06430; Hs.6194; chondroitin sulfate proteoglyc; glio, mela; diag
438549; BE386801; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag
439018; AW300887; Hs.26638; membrane-spanning 4-domains, s; uter, stom, pros, fibro; mAb
439223; AW238299; Hs.250618; UL16 binding protein 2; lung, headnk, cerv, esoph, leuk, blad, colon; mAb
439477; W69813; Hs.58042; ESTs, Moderately similar to GF; lung; mAb+s.m.
439569; AW602166; Hs.222399; CEGP1 protein; breast, pros, blad; diag
439606; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv, esoph; mAb+s.m.

439738; BE246502; Hs.9598; sema domain, immunoglobulin do; blad, lung, cerv, renal; mAb+s.m.
439979; AW600291; Hs.6823; hypothetical protein FLJ10430; renal, cerv, pros, headnk, colon, test, sarc; mAb
440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containin; blad, ovar, lung, headnk, test; s.m.
440065; W03476; Hs.266331; Homo sapiens Fc receptor homol; mela; diag
440304; BE159984; Hs.125395; hepatitis A virus cellular rec; renal, colon, blad; mAb+s.m.
440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin; glio, ovar, uter, renal, hepC; mAb+diag
440672; AF083811; Hs.7345; MAD1 (mitotic arrest deficient; mela; s.m.
441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog ; lung, blad, headnk, test, mela, esoph; s.m.
442117; AW664964; Hs.128899; ESTs; hypothetical protein for; breast, lung, blad, panc, headnk, stom, ovar, pros, sarc; mAb+s.m.
442133; AW874138; Hs.129017; ESTs; type Ia transmembrane p; ovar, uter; mAb
442275; AW449467; Hs.54795; Homo sapiens secretoglobin, fa; fibro; diag
442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; fibro, ovar, uter; CTL
443105; X96753; Hs.9004; chondroitin sulfate proteoglyc; mela; mAb+diag
443247; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL
443324; R44013; Hs.164225; ESTs; fibro; mAb+diag
443426; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad, stom, test, mela, sarc; CTL
443595; AF169312; Hs.9613; PPAR(gamma) angiopoietin relat; renal; diag
443646; AI085198; Hs.164226; Thrombospondin 1; angio, panc, uter; diag
443859; NM_013409; Hs.9914; follistatin; lung, cerv, headnk, blad, esoph; diag
443987; AW163123; Hs.10071; seven transmembrane protein TM; renal; mAb+s.m.
444006; BE395085; Hs.334762; type I transmembrane protein F; panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv; mAb
444090; S69115; Hs.10306; natural killer cell group 7 se; fibro, renal, mela; diag
444371; BE540274; Hs.239; forkhead box M1; lung, headnk, blad, glio, test, mela; s.m.
444381; BE387335; Hs.283713; hypothetical protein BC014245; breast, colon, blad, lung, panc, headnk, ovar, stom, uter, renal, angio, test, mela, esoph, sarc; CTL+diag
444488; AW192879; Hs.355660; ancient conserved domain prote; renal; mAb+s.m.
444527; NM_005408; Hs.11383; small inducible cytokine subfa; fibro, esoph; diag
444781; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk, cerv; mAb+diag
444783; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph; CTL+s.m.
445417; AK001058; Hs.12630; a disintegrin-like and metallo; panc, headnk, stom, lung, esoph, sarc, colon; diag
445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv, sarc; mAb+diag
445891; AW391342; Hs.199460; DPCR1 protein; stom, panc, esoph, omuc, esoph; mAb
445895; D29954; Hs.13421; KIAA0056 protein; pros; CTL
446051; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
446163; AA026880; Hs.25252; prolactin receptor; breast, cerv, uter; mAb+s.m.
446341; AL040763; Hs.310735; FGENESH prediction similar to ; mela; mAb+s.m.
446619; AU076643; Hs.313; secreted phosphoprotein 1 (ost; ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter, sarc; diag
446650; AB016625; Hs.15813; solute carrier family 22 (orga; renal; mAb+s.m.
446921; AB012113; Hs.16530; small inducible cytokine subfa; breast, panc, headnk, lung, fibro, mela; diag
447033; AI357412; Hs.157601; Predicted gene: Eos cloned; se; colon, pros, fibro, breast, ovar, lung, panc, sarc; CTL+diag
447072; D61594; Hs.17279; tyrosylprotein sulfotransferas; glio, panc; CTL+s.m.
447131; NM_004585; Hs.17466; retinoic acid receptor respond; renal, breast, stom, lung, mela, ovar; mAb+s.m.
447208; BE315291; Hs.237971; hypothetical protein MGC5627; esoph, stom, colon; CTL+diag
447269; NM_004861; Hs.17958; cerebroside (3'-phosphoadenyly; renal; CTL
447342; AI199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, blad, pros, lung, stom, ovar; CTL
447400; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
447674; BE270640; Hs.19192; cyclin-dependent kinase 2; mela; s.m.
448243; AW369771; Hs.367688; integrin, beta 8; ovar, uter, lung, stom, headnk, glio, panc ; mAb+s.m.
448610; NM_006157; Hs.21602; nel (chicken)-like 1; mela, sarc; diag
448733; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung, renal; mAb+s.m.
448844; AI581519; Hs.177164; FGENESH predicted novel cell s; panc, lung, stom, omuc; mAb+s.m.
449032; AA045573; Hs.22900; nuclear factor (erythroid-deri; colon, test, stom; CTL+s.m.
449048; Z45051; Hs.22920; similar to S68401 (cattle) glu; panc, ovar, uter, glio, headnk, lung, sarc; mAb
449444; AW818436; Hs.351306; solute carrier family 16 (mono; renal, panc; mAb+s.m.
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor; lung, panc, renal, stom, hepC, fibro, leuk, mela; mAb+s.m.
449720; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL
449722; BE280074; Hs.23960; cyclin B1; headnk, blad, lung, panc, angio, test, mela, esoph; s.m.
450001; NM_001044; Hs.406; solute carrier family 6 (neuro; renal; mAb+s.m.
450375; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc, lung, esoph, colon, sarc; mAb+diag+s.m.
450531; AW301032; Hs.203800; (BC017500) Similar to hypothet; colon; CTL
450701; H39950; Hs.288467; hypothetical protein XP_098151; lung, headnk, panc, breast, stom, ovar, esoph, colon, sarc; mAb+diag
450726; AW204600; Hs.355462; HUMPSPBA Human pulmonary surfa; fibro, lung; s.m.
450931; N25156; Hs.25648; tumor necrosis factor receptor; lung, renal; mAb+s.m.
450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; blad, lung, ovar, panc; diag
451310; AW250651; Hs.26213; Human DNA sequence from clone ; colon, panc; CTL
451527; AF022813; Hs.26518; transmembrane 4 superfamily me; renal; mAb
451537; R56631; Hs.26550; retinoid X receptor, gamma; mela; CTL+s.m.
451668; Z43948; Hs.326444; cartilage acidic protein 1; blad, ovar, lung; mAb+diag
451939; U80456; Hs.27311; single-minded (Drosophila) hom; pros; CTL
451979; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
451988; AF263928; Hs.27410; papillomavirus regulatory fact; renal; CTL
452017; AF109302; Hs.27495; prostate cancer associated pro; pros; s.m.
452097; AB002364; Hs.27916; a disintegrin-like and metallo; ovar; mAb+s.m.+diag
452190; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast, stom, panc; mAb
452194; AI694413; Hs.373599; olfactory receptor, family 2, ; stom, panc, renal, colon, mela, fibro; mAb+s.m.
452203; X57522; Hs.352018; transporter 1, ATP-binding cas; cerv, esoph, blad, stom, mela, renal; mAb+s.m.
452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast, headnk, panc, stom, lung, esoph, fibro; diag
452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-i; blad, breast, panc, headnk,stom, lung, leuk, renal, esoph; diag
452431; U88879; Hs.29499; toll-like receptor 3; renal, hepC; mAb
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung, headnk, ovar, stom, uter, panc; mAb
452838; U65011; Hs.30743; preferentially expressed antig; lung, ovar, breast, mela, test, esoph, renal, sarc; CTL
452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; headnk, breast, colon, leuk, lung, blad, esoph, stom, sarc; mAb+diag
453195; BE241876; Hs.32352; hypothetical protein DKFZp434K; renal; CTL
453496; AA442103; Hs.33084; solute carrier family 2 (facil; renal, pros; mAb+s.m.

453837; AL136387; Hs.256126; baculoviral IAP repeat-contain; renal, mela, sarc; s.m.
453968; AA847843; Hs.62711; High mobility group (nonhistor; lung, uter, blad, test; CTL+s.m.
456546; AI690321; Hs.203845; KCNK15 potassium channel, subf; ovar ; mAb+s.m.
456662; NM_002448; Hs.1494; msh (Drosophila) homeo box hom; uter, ovar ; CTL
457133; M54968; Hs.351221; v-kl-ras2 Kirsten rat sarcoma ; panc; s.m.
457489; AI693815; Hs.127179; cryptic gene; panc, pros, lung; diag
457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein ; lung, cerv, headnk; mAb+diag
458079; AI796870; Hs.381220; Homo sapiens similar to RIKEN ; mela, fibro, sarc; mAb
458627; AW088642; Hs.97984; SRY (sex determining region Y); ovar, uter, test; CTL

TABLE 2B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

TABLE 2C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
402901	8894222	Minus	175426-175667
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 3A. Disease Indications and Preferred Utilities for Selected Genes

Table 3A provides preferred disease indications and preferred utilities for about 2709 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number
UnigeneID: Unigene ID number
Unigene Title: Unigene gene title
Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), anglo (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigeneID; Unigene Title; Disease; Utility

100125; R02740; Hs.137555; putative chemokine receptor; G; blad; mAb+s.m.
100131; D12485; Hs.11951; ectonucleotide pyrophosphatase; breast; mAb
100147; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc; mAb+diag
100241; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; blad; mAb
100299; D49493; Hs.2171; growth differentiation factor ; EWS; diag
100335; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
100365; AI878927; Hs.79284; mesoderm specific transcript (; colon, pros; diag
100372; NM_014791; Hs.184339; KIAA0175 gene product; ovar, lung, cerv, panc; s.m.
100405; AW291587; Hs.82733; nidogen 2; anglo; diag
100420; D86983; Hs.118893; Melanoma associated gene; breast, pros, lung, colon, anglo, leuk; diag
100448; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G; breast; mAb+s.m.
100452; D87742; Hs.241552; KIAA0268 protein; pros; diag
100559; NM_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung; CTL+s.m.
100654; A03758; Hs.184411; NM_000477*:Homo sapiens albumi; pros; diag
100655; A03758; Hs.184411; Emplrically selected from AFFX; pros; diag
100668; L05424; Hs.169610; CD44 antigen (homing function ; lung, breast; mAb
100824; AI393237; Hs.193989; runt-related transcription fac; ovar; CTL+s.m.
100930; J04129; Hs.82269; progestagen-associated endomet; lung; diag
101063; D54745; Hs.80247; cholecystokinin; pros, EWS; diag
101097; BE245301; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad; mAb+s.m.
101104; AW862258; Hs.169266; neuropeptide Y receptor Y1; breast, EWS; mAb
101192; BE247295; Hs.78452; solute carrier family 20 (phos; anglo; mAb+s.m.
101193; L20861; Hs.152213; wingless-type MMTV integration; blad, lung; diag
101249; L18964; Hs.1904; protein kinase C, iota; ovar; s.m.

101261; D30857; Hs.82353; protein C receptor, endothelia; angio; mAb+s.m.
101389; AW951430; Hs.78888; diazepam binding inhibitor (GA; pros; mAb+s.m.
101431; BE185289; Hs.1076; small proline-rich protein 1B ; lung, blad; diag
101447; M21305; ; gb:Human alpha satellite and s; angio, blad; diag
101461; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; diag
101485; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, ovar; mAb
101506; J02931; Hs.62192; coagulation factor III (thromb; pros; mAb
101526; NM_002197; Hs.220529; aconitase 1, soluble; lung, colon, headnk, panc; mAb
101543; M31166; Hs.2050; pentaxin-related gene, rapidly; angio, ovar; diag
101545; BE246154; Hs.154210; endothelial differentiation, s; angio; mAb+s.m.
101560; AW958272; Hs.347326; intercellular adhesion molecul; angio; mAb
101626; M57399; Hs.44; pleiotrophin (heparin binding ; lung; diag
101649; AW959908; Hs.1690; heparin-binding growth factor ; lung, blad; diag
101714; M68874; Hs.211587; phospholipase A2, group IVA (c; angio; s.m.
101724; L11690; Hs.198689; bullous pemphigoid antigen 1 (; breast, pros, blad, lung; mAb+CTL
101741; NM_003199; Hs.326198; transcription factor 4; angio; CTL+s.m.
101748; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, blad, headnk, cerv; mAb
101759; M80244; Hs.184601; solute carrier family 7 (catio; lung, glio, blad, headnk; mAb+s.m.
101791; M83822; Hs.62354; cell division cycle 4-like; pros; s.m.
101804; M86699; Hs.169840; TTK protein kinase; ovar, lung, blad, cerv; CTL+s.m.
101806; AA586894; Hs.112408; S100 calcium-binding protein A; lung, breast, blad; diag
101809; M86849; Hs.323733; gap junction protein, beta 2, ; colon, blad, lung, panc, headnk; mAb
101839; AA446644; Hs.692; GA733-2 antigen; epithelial gl; ovar, pros; mAb
101845; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, cerv; mAb+s.m.
101851; BE260964; Hs.82045; midkine (neurite growth-promot; lung, blad, ovar, breast, panc; mAb+diag
102009; BE245149; Hs.82643; protein tyrosine kinase 9; ovar; s.m.
102012; BE259035; Hs.118400; singed (Drosophila)-like (sea ; angio; diag
102024; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
102048; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
102076; BE299197; Hs.179665; cyclin-dependent kinase inhibi; pros; CTL+s.m.
102125; NM_006456; Hs.288215; sialyltransferase; breast, lung, ovar; s.m.
102136; AA300576; Hs.85769; acidic 82 kDa protein mRNA; ovar; diag
102151; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
102154; U17760; Hs.75517; laminin, beta 3 (nicein (125kD; lung, blad, headnk; diag
102178; AW178761; Hs.227948; serine (or cysteine) proteinas; blad; mAb+diag
102187; U20325; Hs.1707; cocaine- and amphetamine-regul; breast; diag
102193; AL036335; Hs.313; secreted phosphoprotein 1 (ost; ovar, lung, fibro; diag
102200; AA232362; Hs.317432; branched chain aminotransferas; ovar; s.m.
102208; U22961; Hs.184411; gb:Human mRNA clone with simil; pros; diag
102211; BE314524; Hs.78776; putative transmembrane protein; breast, blad; mAb
102283; AW161552; Hs.83381; guanine nucleotide binding pro; angio; CTL+s.m.
102297; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
102304; AF015224; Hs.46452; mammaglobin 1; breast; diag
102305; AL043202; Hs.90073; chromosome segregation 1 (yeas; ovar, lung, blad ; diag
102348; U37519; Hs.87539; aldehyde dehydrogenase 3 famil; lung, blad; s.m.
102380; U40434; Hs.155981; mesothelin; ovar; diag
102394; NM_003816; Hs.2442; a disintegrin and metalloprote; panc; s.m.
102455; U48705; Hs.75562; discoidin domain receptor fami; breast; mAb
102457; NM_001394; Hs.2359; dual specificity phosphatase 4; breast; s.m.
102522; BE250944; Hs.183556; solute carrier family 1 (neutr; pros; mAb
102581; AU077228; Hs.77256; enhancer of zeste (Drosophila); blad, EWS, leuk; CTL+s.m.
102610; U65011; Hs.30743; preferentially expressed antig; lung, ovar; CTL
102623; AW249285; Hs.37110; melanoma antigen, family A, 9; lung, blad; mAb+CTL
102669; U71207; Hs.29279; eyes absent (Drosophila) homol; lung, pros; CTL+s.m.
102696; BE540274; Hs.239; forkhead box M1; lung, blad; s.m.
102725; AB026187; Hs.374280; protocadherin 11; EWS; mAb
102742; U79293; Hs.159264; Human clone 23948 mRNA sequenc; breast, ovar ; diag
102745; AW753865; Hs.74376; olfactomedin related ER locali; EWS; diag
102803; H48299; Hs.26126; claudin 10; ovar; mAb
102829; NM_006183; Hs.80962; neurotensin; lung, ovar, headnk; diag
102836; U94320; Hs.158330; neuropeptide Y receptor Y5; EWS; mAb
102852; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
102898; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin; angio, blad, lung, pros; mAb+s.m.
102915; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, ovar; mAb+diag+s.m.
102917; AI016712; Hs.287797; integrin, beta 1 (fibronectin ; angio; mAb
102927; BE512730; Hs.65114; keratin 18; ovar; diag
102968; AU076611; Hs.154672; methylene tetrahydrofolate deh; ovar; s.m.
102994; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
103003; AI910275; Hs.350470; trefoil factor 1 (breast cance; breast, panc; diag
103021; BE001596; Hs.85266; integrin, beta 4; lung blad; mAb
103036; M13509; Hs.83169; matrix metalloproteinase 1 (in; angio, colon, blad, lung, leuk, ovar, headnk, fibro, panc, stom; mAb+diag+s.m.
103037; BE018302; Hs.2894; placental growth factor, vascu; angio; diag
103060; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, lung, ovar, panc; mAb+diag+s.m.
103080; AU077231; Hs.82932; cyclin D1 (PRAD1: parathyroid ; breast, EWS; diag
103095; NM_005424; Hs.78824; tyrosine kinase with immunoglo; angio; mAb
103111; NM_006103; Hs.2719; epididymis-specific, whey-acid; ovar, uter; diag
103119; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, ovar, colon, pros, panc, breast; mAb+diag
103206; X72755; Hs.77367; monokine induced by gamma inte; breast, lung; diag
103210; X72925; Hs.69752; desmocollin 1; pros; mAb
103280; U84722; Hs.76206; cadherin 5, type 2, VE-cadheri; angio, fibro; mAb+s.m.
103299; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar; mAb+s.m.
103312; Y12642; Hs.3185; lysosomal; lung, blad; mAb
103365; X90908; Hs.74126; fatty acid binding protein 6, ; blad; diag

103408; NM_001504; Hs.198252; G protein-coupled receptor 9; breast ; mAb
103478; BE514982; Hs.38991; S100 calcium-binding protein A; lung, blad, headnk; diag
103587; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyc; breast, blad, lung; mAb
103594; AI368680; Hs.816; SRY (sex determining region Y); lung, glio; s.m.
103692; AW137912; Hs.227583; Homo sapiens chromosome X map ; angio; mAb+s.m.
103739; AA115173; ; gb:zn30d02.s1 Stratagene neuro; pros; s.m.
103767; BE244667; Hs.348996; CGI-100 protein; angio; diag
103989; AA315993; Hs.105484; regenerating gene type IV; colon, omuc; mAb+diag
104052; NM_002407; Hs.97644; mammaglobin 2; ovar; diag
104115; AF183810; Hs.26102; opposite strand of: trichorhi; breast; mAb
104252; AF002246; Hs.210863; cell adhesion molecule with ho; ovar; diag
104301; AA768491; Hs.6783; hypothetical protein FLJ22724; ovar; diag
104308; N25117; Hs.355957; ribosomal protein S26; pros; diag
104394; AA129551; Hs.172129; Homo sapiens cDNA: FLJ21409 fi; colon; diag
104542; R29657; ; gb:F1-1179D 22 week old human ; pros; diag
104608; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb
104659; AW969769; Hs.100343; ESTs; EWS; diag
104660; BE298665; Hs.14846; Homo sapiens mRNA; cDNA DKFZp5; uter, colon, pros; mAb
104667; AI239923; Hs.63931; dachshund (Drosophila) homolog; breast, pros, colon; diag
104689; AA420450; Hs.380088; Plakophilin; lung; diag
104691; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
104755; T49951; Hs.9029; DKFZP434G032 protein; breast, colon; diag
104764; AI039243; Hs.278585; ESTs; angio; diag
104786; AA027167; Hs.380438; KIAA0955 protein; angio; CTL+s.m.
104877; AI138635; Hs.22968; intron of VEGFR; renal; diag
104888; AW939591; Hs.5940; mucin 13, epithelial transmemb; colon, stom, uter; mAb+s.m.
104919; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis; breast, cerv, uter; mAb+s.m.
104943; AF072873; Hs.114218; frizzled (Drosophila) homolog ; ovar; mAb+s.m.
104954; AW250651; Hs.26213; Human DNA sequence from clone ; colon; diag
104971; BE311926; Hs.15830; hypothetical protein FLJ12691; blad; CTL
105012; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad; CTL
105038; AW503733; Hs.9414; KIAA1488 protein; breast, angio; CTL+s.m.
105039; AA907305; Hs.36475; ESTs; breast; diag
105093; AL137566; Hs.32405; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
105149; BE089288; Hs.8958; Homo sapiens cDNA FLJ12024 fis; pros; diag
105175; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; colon, lung; mAb
105263; AW388633; Hs.6682; solute carrier family 7, (cati; angio, lung, ovar, blad, panc; mAb+s.m.
105298; BE387790; Hs.26369; hypothetical protein FLJ20287; ovar, lung; diag
105301; AW352357; Hs.7457; MAGE1 protein; EWS; diag
105316; AI671245; Hs.24835; hypothetical protein FLJ14594; EWS; mAb
105329; AA234561; Hs.22862; ESTs; breast, pros; CTL+s.m.
105330; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
105370; AF179274; Hs.22791; transmembrane protein with EGF; pros ; mAb+s.m.
105500; AW602166; Hs.222399; CEGP1 protein; breast, pros; diag
105503; AW963624; Hs.31707; ESTs, Weakly similar to YEW4_Y; pros, breast, colon; CTL+s.m.
105507; BE268348; Hs.380963; CCR4-NOT transcription complex; colon; diag
105516; AK001269; Hs.30738; hypothetical protein FLJ10407; ovar; diag
105564; BE616694; Hs.288042; hypothetical protein FLJ14299; breast; diag
105645; AW294631; Hs.351270; ESTs; pros; diag
105715; BE621800; Hs.29444; putative small membrane protei; colon; diag
105743; BE246502; Hs.9598; sema domain, immunoglobulin do; breast, lung; mAb+s.m.
105746; AW151952; Hs.46679; hypothetical protein FLJ20739; breast; CTL+s.m.
105777; R42755; Hs.23096; ESTs; breast; diag
105782; H09748; Hs.57987; B-cell CLL/lymphoma 11B (zinc ; EWS; CTL+s.m.
105826; AA478756; Hs.194477; E3 ubiquitin ligase SMURF2; angio; s.m.
105990; AI690586; Hs.29403; hypothetical protein FLJ22060; breast; diag
106000; AW194426; Hs.20726; ESTs; breast; diag
106012; AI240665; Hs.352537; ESTs; breast, lung; diag
106014; AF123094; Hs.180566; mucosa associated lymphoid tis; leuk; diag
106063; BE260415; Hs.348198; hypothetical protein FLJ20262; pros; diag
106066; AW274357; Hs.301406; hypothetical protein PP3501; mela; CTL+s.m.
106111; AW875398; Hs.6451; PRO0659 protein; EWS; CTL+s.m.
106124; H93366; Hs.7567; branched chain aminotransferas; angio; s.m.
106155; AA425414; Hs.33287; nuclear factor I/B; breast, pros, angio; diag
106373; AW503807; Hs.21907; histone acetyltransferase; breast; s.m.
106400; BE397649; Hs.279607; Homo sapiens cDNA FLJ13634 fis; colon; diag
106414; BE568205; Hs.28827; mitogen-activated protein kina; breast; s.m.
106448; Z42061; Hs.27004; ESTs; pros; diag
106533; AL134708; Hs.145998; ESTs; EWS; diag
106574; BE044325; Hs.227280; U6 snRNA-associated Sm-like pr; colon; diag
106579; AA456135; Hs.23023; ESTs; pros; diag
106632; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk; mAb+diag
106738; AW149266; Hs.25130; Homo sapiens cDNA FLJ14923 fis; ovar; diag
106793; H94997; Hs.16450; ESTs; angio; diag
106844; AA485055; Hs.158213; sperm associated antigen 6; breast; mAb+CTL
106906; AA861271; Hs.222024; transcription factor BMAL2; lung, blad; diag
106990; AA280722; Hs.24758; ESTs, Weakly similar to I38022; breast; diag
107036; AI973016; Hs.15725; hypothetical protein SBBI48; pros; diag
107102; AB037765; Hs.30652; KIAA1344 protein; pros, breast; diag
107105; AW963419; Hs.155223; stanniocalcin 2; breast; diag
107136; AV661958; Hs.8207; GK001 protein; breast, colon; diag
107151; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; breast, colon, leuk, lung, blad; mAb+diag
107216; D51069; Hs.211579; melanoma cell adhesion molecul; angio; diag

107248; AW263124; Hs.350547; nuclear receptor co-repressor/; breast, colon, pros; mAb+s.m.
107284; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung; mAb+s.m.
107385; NM_005397; Hs.16426; podocalyxin-like; angio; diag
107901; L42612; Hs.335952; keratin 6B; breast, blad, lung; diag
107922; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung; mAb
107932; AW392555; Hs.18878; hypothetical protein FLJ21620; lung; CTL
108055; AJ404672; Hs.334483; hypothetical protein FLJ23571; breast, ovar; diag
108059; S69002; Hs.234773; Homo sapiens cDNA: FLJ22281 fi; ovar; CTL+s.m.
108153; AW519204; Hs.40808; ESTs; pros; diag
108186; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
108242; AA062746; Hs.355244; gb:zm03g12.s1 Stratagene corne; pros; diag
108282; AA065142; ; gb:zm50h11.r1 Stratagene fibro; pros; diag
108505; AA083376; ; gb:zn09g08.s1 Stratagene hNT n; pros; diag
108679; AA115963; Hs.323423; ESTs, Moderately similar to B ; pros; diag
108695; AB029000; Hs.70823; KIAA1077 protein; breast, colon, lung; diag
108732; AA258888; Hs.107476; ATP synthase, H+ transporting,; pros; s.m.
108778; AF133123; Hs.90847; general transcription factor I; ovar; diag
108828; AK001693; Hs.273344; DKFZP564O0463 protein; breast; diag
108860; AA133334; Hs.816; ESTs; lung; s.m.
109001; AI056548; Hs.72116; hypothetical protein FLJ20992 ; angio; CTL+diag
109032; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
109077; AI732617; Hs.182362; ESTs; blad; diag
109112; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
109141; AF174600; Hs.5978; ESTs, Highly similar to AF1746; colon; CTL+s.m.
109166; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, breast, colon, ovar, headnk, EWS; s.m.
109220; AW958181; Hs.189998; ESTs; pros; diag
109273; AA375752; Hs.348140; Homo sapiens mRNA; cDNA DKFZp5; breast; diag
109292; AW975746; Hs.188662; KIAA1702 protein; breast; diag
109454; AA232255; Hs.295232; ESTs, Moderately similar to A4; ovar; diag
109456; AW956580; Hs.42699; ESTs; angio, panc; diag
109514; AA234087; Hs.262346; ESTs, Weakly similar to S72482; breast ; diag
109530; AA908645; Hs.19597; KIAA1694 protein; pros; CTL+s.m.
109648; H17800; Hs.7154; ESTs; ovar; diag
109680; AB037734; Hs.4993; KIAA1313 protein; ovar; diag
110009; BE075297; Hs.6614; ESTs, Weakly similar to A43932; breast, colon; diag
110151; H18835; Hs.31608; hypothetical protein FLJ20041; pros, EWS; diag
110156; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
110240; AI668594; Hs.176588; ESTs, Weakly similar to CP4Y_H; breast; diag
110278; AF061573; Hs.19492; protocadherin 8; EWS; mAb+s.m.
110675; H89355; Hs.249159; adrenergic, alpha-2A-, recepto; pros; mAb+s.m.
110728; AA737106; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
110844; AI740792; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
110915; BE092285; Hs.29724; hypothetical protein FLJ13187; breast, pros; diag
110971; AI760098; Hs.21411; ESTs; pros; diag
111157; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
111179; AK000136; Hs.10760; asporin (LRR class 1); breast, colon; CTL+s.m.
111185; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad; mAb+diag
111223; AA852773; Hs.334836; KIAA1866 protein; breast, colon, lung, EWS; mAb
111299; AB033091; Hs.355925; KIAA1265 protein; ovar; diag
111357; BE314949; Hs.87128; hypothetical protein FLJ23309; breast; diag
111384; N94606; Hs.288969; HSCARG protein; breast; diag
111900; AF131784; Hs.25318; Homo sapiens clone 25194 mRNA ; breast; diag
111929; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
112134; R41823; Hs.7413; ESTs; calsyntenin-2; breast, EWS; diag
112244; AB029000; Hs.70823; KIAA1077 protein; breast, colon, blad, lung; diag
112280; AA863360; Hs.26040; ESTs, Weakly similar to fatty ; breast; s.m.
112283; L14561; Hs.20952; ATPase, Ca++ transporting, pla; ovar; mAb
112287; AB033064; Hs.236463; KIAA1238 protein; breast ; diag
112971; Z42387; Hs.83883; transmembrane, prostate androg; colon, pros, pros; mAb+s.m.
113003; AW292315; Hs.7215; ESTs; EWS; diag
113021; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
113047; AI571940; Hs.7549; ESTs; breast, colon; diag
113073; N39342; Hs.103042; microtubule-associated protein; pros; CTL+s.m.
113168; AW002393; Hs.337629; gb:wu61d05.x1 NCI_CGAP_GC6 Hom; ovar; diag
113195; H83265; Hs.8881; ESTs, Weakly similar to S41044; angio, lung; diag
113230; T61430; ; gb:yc06a03.s1 Stratagene lung ; blad; diag
113361; T79589; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
113374; T79925; Hs.269165; ESTs, Weakly similar to ALU1_H; leuk; diag
113443; AW083920; Hs.16098; claudin 2; colon, panc; mAb
113471; AI765890; Hs.16341; MAWD binding protein; pros; diag
113490; BE178110; Hs.173374; Homo sapiens cDNA FLJ10500 fis; colon; diag
113950; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; breast, pros ; diag
113970; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
114124; W57554; Hs.125019; lymphoid nuclear protein (LAF-; breast; diag
114251; H15261; Hs.21948; ESTs; breast; diag
114292; AI815395; Hs.184641; fatty acid desaturase 2; breast; s.m.
114334; AB037784; Hs.22941; KIAA1363 protein; ovar; diag
114407; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, colon, lung; diag
114452; AI369275; Hs.243010; Homo sapiens cDNA FLJ14445 fis; angio; diag
114480; BE066778; Hs.151678; UDP-N-acetyl-alpha-D-galactosa; breast; s.m.
114531; AA053033; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
114540; AI904232; Hs.75323; prohibitin; breast; diag
114542; AW970128; Hs.91011; anterior gradient 2 (Xenopus l; breast, pros; diag

114587; AF086009; Hs.296398; gb:Homo sapiens full length in; colon; diag
114724; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) b; ovar; CTL+s.m.
114768; AF212848; Hs.182339; ets homologous factor; pros, breast, colon; CTL+s.m.
114798; AA159181; Hs.54900; serologically defined colon ca; pros; CTL+s.m.
114908; AA454985; Hs.54973; cadherin-like protein VR20; pros; diag
114918; BE165762; Hs.23518; hypothetical protein from BCRA; pros; diag
114965; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb
115060; AF052693; Hs.198249; gap junction protein, beta 5 (; lung, blad, headnk; mAb+s.m.
115221; AW365434; Hs.79741; hypothetical protein FLJ10116; ovar; diag
115239; BE251328; Hs.73291; hypothetical protein FLJ10881; colon; diag
115291; BE545072; Hs.122579; hypothetical protein FLJ10461; ovar, lung; CTL+s.m.
115412; AW131168; Hs.372382; ESTs, Weakly similar to I38022; pros; diag
115536; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon; CTL+s.m.
115674; AW992356; Hs.380760; Homo sapiens pyruvate dehydrog; ovar; s.m.
115675; W87707; Hs.82065; interleukin 6 signal transduce; breast, pros; mAb+s.m.
115683; AF255910; Hs.54650; junctional adhesion molecule 2; angio, glio; mAb
115697; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
115719; AW992405; Hs.352406; Homo sapiens, clone IMAGE:3507; pros, breast, colon; CTL+s.m.
115819; AA486620; Hs.41135; endomucin-2; angio; diag
115827; AA428000; Hs.283072; actin related protein 2/3 comp; angio; diag
115844; AI373062; Hs.332938; hypothetical protein MGC5370; pros; diag
115881; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
115892; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
115909; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung; diag
115947; R47479; Hs.94761; KIAA1691 protein; colon; diag
115978; AL035864; Hs.69517; cDNA for differentially expres; lung, blad, breast, pros, ovar, headnk; CTL
116003; BE275469; Hs.66493; Down syndrome critical region ; colon; mAb
116011; AL359053; Hs.57664; Homo sapiens mRNA full length ; breast; diag
116028; H59799; Hs.42644; thioredoxin-like; ovar, lung; diag
116107; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
116202; BE159395; Hs.294092; ESTs; pros; diag
116238; AV660717; Hs.47144; DKFZP586N0819 protein; ovar; diag
116301; AW969706; Hs.293332; ESTs; EWS; diag
116334; AL038450; Hs.48948; ESTs; pros; diag
116335; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk; diag
116393; AI972402; Hs.306051; hypothetical protein MGC2648; pros; diag
116399; AA889120; Hs.110637; homeo box A10; pros; CTL+s.m.
116401; AW893940; Hs.59698; ESTs; ovar; diag
116416; AW753676; Hs.39982; ESTs; ovar; diag
116470; AI272141; Hs.351928; SRY (sex determining region Y); colon, breast, angio, blad; diag
116483; AI346201; Hs.76118; ubiquitin carboxyl-terminal es; angio, lung; s.m.
116610; D80449; Hs.184841; ESTs; pros; diag
116732; AW152225; Hs.165909; ESTs, Weakly similar to I38022; colon; diag
116787; AW362955; Hs.356547; Homo sapiens cDNA FLJ14415 fis; pros, breast, colon, pros; mAb
116962; H79677; ; gb:yu76g10.s1 Soares fetal liv; pros; diag
117027; AW085208; Hs.130093; ESTs; breast ; diag
117280; M18217; Hs.172129; Homo sapiens cDNA: FLJ21409 fi; breast, colon, pros; diag
117284; AK001701; Hs.183779; Homo sapiens cDNA FLJ10590 fis; pros; diag
117320; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung; mAb+diag
117367; AI041793; Hs.42502; ESTs; breast ; diag
117412; N32536; Hs.42645; solute carrier family 16 (mono; breast, ovar ; mAb+s.m.
117425; AK000028; Hs.356100; ribosomal protein S24; pros; diag
117563; AF055634; Hs.44553; unc5 (C.elegans homolog) c; leuk ; diag
117602; N35020; Hs.44685; C3HC4-like zinc finger protein; EWS; CTL+s.m.
117921; AA021459; Hs.306480; Homo sapiens mRNA; cDNA DKFZp7; pros ; diag
117984; AF189723; Hs.106778; ATPase, Ca++ transporting, typ; pros, breast, colon; mAb
118049; N53145; ; gb:yv55f09.s1 Soares fetal liv; pros; diag
118314; N48580; Hs.46692; ESTs; blad, lung; diag
118336; BE327311; Hs.47166; HT021; breast, ovar, blad, pros; CTL+s.m.
118368; N64339; Hs.48956; gap junction protein, beta 6 (; lung, blad; mAb
118417; AF080229; ; gb:Human endogenous retrovirus; pros; s.m.
118472; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
118511; N75620; Hs.43157; ESTs; angio; diag
118901; AW292577; Hs.94445; ESTs; breast; diag
118905; AW973708; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
119018; AA631143; Hs.278695; Homo sapiens prostein mRNA, co; pros, pros; diag
119036; R95872; Hs.117572; chemokine binding protein 2; breast, ovar; mAb
119073; BE245360; Hs.45514; v-ets erythroblastosis virus E; angio, pros; CTL+s.m.
119082; AF252297; Hs.91546; cytochrome P450 retinoid metab; EWS; diag
119126; R45175; Hs.117183; ESTs; pros, breast, colon; diag
119279; N57568; Hs.48028; EST; breast; diag
119307; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
119478; AI624342; Hs.179082; ESTs; breast; diag
119617; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag
119743; AA947552; Hs.58086; branched chain aminotransferas; ovar; s.m.
119771; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast; diag
119780; NM_016625; Hs.191381; hypothetical protein; ovar, lung; CTL+s.m.
119789; BE393948; Hs.50915; kallikrein 5; ovar; diag
119845; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv; mAb+s.m.
119940; AL050097; Hs.272531; DKFZP586B0319 protein; pros; diag
120104; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, lung; diag
120132; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
120147; AI917116; Hs.348941; hemoglobin, beta; EWS; diag

120206; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast ; mAb
120242; AW969587; Hs.86366; ESTs; blad; diag
120328; AA923278; Hs.290905; ESTs, Weakly similar to protea; pros; s.m.
120438; AW015242; Hs.99488; ESTs, Weakly similar to YK54_Y; ovar; diag
120471; AA251944; Hs.104058; CGI-29 protein; colon; diag
120486; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk; diag
120588; AA703226; Hs.16193; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
120624; AW407987; Hs.173518; M-phase phosphoprotein homolog; breast; s.m.
120830; AI568170; Hs.96886; ESTs; EWS; diag
120977; AA398155; Hs.97600; ESTs; breast, ovar; diag
121027; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 fi; blad; mAb
121231; AA814948; Hs.96343; ESTs, Weakly similar to ALUC_H; EWS; diag
121335; AA404418; ; gb:zw37e02.s1 Soares_total_fet; angio; diag
121362; AF050147; Hs.97932; chondromodulin I precursor; EWS; mAb
121457; W07404; Hs.102558; hypothetical protein FLJ22055; colon; diag
121619; AA528339; Hs.178062; ESTs, Weakly similar to phosph; EWS; s.m.
121710; AF163474; Hs.96744; prostate androgen-regulated tr; pros; diag
121721; AL047051; Hs.199961; ESTs, Weakly similar to ALU7_H; pros; diag
121723; AA243499; Hs.104800; hypothetical protein FLJ10134; breast; diag
121748; BE536911; Hs.234545; hypothetical protein NUF2R; breast; diag
121779; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
121791; AA815378; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar; mAb+CTL
121792; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
121913; AI249366; Hs.98558; ESTs; protease inhibitor 15 (; breast, pros; s.m.
121920; AA428300; ; gb:zw18b02.s1 Soares ovary tum; ovar, uter, cerv; diag
122041; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
122520; AW951324; Hs.173609; pregnancy specific beta-1-glyc; colon; diag
122797; AJ251027; Hs.99526; odorant-binding protein 2B (OB; breast; diag
122802; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter; mAb+s.m.
122969; AW821252; Hs.104336; hypothetical protein; ovar; diag
123005; AW369771; Hs.367688; integrin, beta 8; ovar, lung, headnk, glio; mAb+s.m.
123044; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc ; lung; diag
123137; AI073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom; diag
123158; AF161426; Hs.218329; hypothetical protein; breast; diag
123160; AA488687; Hs.284235; ESTs, Weakly similar to I38022; lung; diag
123169; AI950087; Hs.369628; gb:wq05c02.x1 NCI_CGAP_Kid12 H; ovar; diag
123209; AW968543; Hs.203270; ESTs, Weakly similar to ALU1_H; pros; diag
123308; C14187; Hs.157208; ESTs; EWS; diag
123339; AW188464; Hs.101515; ESTs; ovar; diag
123475; BE439553; Hs.12329; Homo sapiens, clone IMAGE:4098; pros; diag
123494; AW179019; Hs.112110; mitochondrial ribosomal protei; ovar; diag
123520; AA608550; ; gb:ae53d12.s1 Stratagene lung ; pros; s.m.
123533; AA608751; ; gb:ae56h07.s1 Stratagene lung ; colon; diag
123619; AA602964; Hs.366318; gb:no97c02.s1 NCI_CGAP_Pr2 Hom; breast; CTL+s.m.
123689; AA399323; Hs.285130; Homo sapiens pinch-2 protein m; ovar; diag
123709; AA706910; Hs.112742; ESTs; breast; diag
123829; AF251237; Hs.112208; XAGE-1 protein; lung, blad, test; CTL
123972; T46848; Hs.70337; immunoglobulin superfamily, me; ovar; diag
124006; AI147155; Hs.279727; ESTs; homologue of PEM-3 [Cion; breast, angio, lung, ovar, EWS; diag
124059; BE387335; Hs.283713; ESTs, Weakly similar to S64054; breast, colon, blad, lung; CTL+diag
124153; AU077333; Hs.160483; erythrocyte membrane protein b; pros; mAb
124352; AA640891; Hs.102406; ESTs; breast, pros, ovar, lung; diag
124526; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros; mAb+s.m.
124579; AI693815; Hs.127179; cryptic gene; panc; diag
124777; R41933; Hs.140237; ESTs, Weakly similar to ALU1_H; pros, breast; diag
125103; AA570056; Hs.122730; ESTs, Moderately similar to KI; colon; mAb
125154; W38419; ; gb:zc78a07.s1 Pancreatic Islet; ovar; diag
125250; W26524; Hs.356686; protein phosphatase 4 regulato; ovar; CTL+s.m.
125266; W90022; Hs.186809; ESTs, Highly similar to LCT2_H; angio; diag
125453; BE385523; Hs.18048; melanoma antigen, family A, 10; blad; mAb+CTL
125666; AL390172; Hs.317432; Homo sapiens cDNA: FLJ21270 fi; ovar; diag
125770; AA143045; Hs.81665; v-kit Hardy-Zuckerman 4 feline; EWS; diag
125976; AA436760; Hs.35552; gb:zv67d11.r1 Soares_total_fet; pros; diag
126399; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
126645; AA316181; Hs.61635; six transmembrane epithelial a; pros, breast, lung, panc, headnk, EWS; mAb+CTL
126758; AI559444; Hs.104679; ESTs; pros, breast; mAb
126799; AW753865; Hs.74376; olfactomedin related ER locali; EWS; diag
126872; AW450979; ; gb:UI-H-BI3-ala-a-12-0-UI.s1 N; blad; diag
126892; AF121856; Hs.284291; sorting nexin 6; ovar; diag
126960; AL390172; Hs.317432; branched chain aminotransferas; ovar; s.m.
126966; R38438; Hs.118747; solute carrier family 15 (H+/p; pros; mAb
127003; AW816515; Hs.173540; ATPase, Class V, type 10D; pros; mAb
127221; BE062109; Hs.241551; chloride channel, calcium acti; lung, blad, headnk, cerv; mAb+s.m.
127240; AJ005683; Hs.86998; nuclear factor of activated T-; pros; CTL+s.m.
127425; AF183810; Hs.26102; trichorhinophalangeal syndrome; breast; mAb
127479; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc; diag
127537; AI926047; Hs.162859; ESTs; pros; diag
127664; AA806164; Hs.116502; ESTs; EWS; diag
128046; AA873285; Hs.357313; gb:oh68h05.s1 NCI_CGAP_Kid5 Ho; pros, breast, colon; diag
128305; AI954968; Hs.365706; matrix Gla protein; breast; diag
128478; AA708205; Hs.100343; ESTs; EWS; CTL+s.m.
128515; BE395085; Hs.334762; type I transmembrane protein F; panc; mAb
128595; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.

128610; N48373; Hs.10247; activated leucocyte cell adhes; breast, pros, lung, ovar; diag
128734; AB008390; Hs.104570; kallikrein 8 (neuropsin/ovasin; ovar; diag
128790; AF026692; Hs.105700; secreted frizzled-related prot; breast, colon, pros, ovar, uter, panc; diag
128797; NM_002975; Hs.105927; stem cell growth factor; lymph; EWS, leuk; diag
128854; BE159181; Hs.168232; hypothetical protein FLJ13855; breast; diag
128925; R67419; Hs.21851; Homo sapiens cDNA FLJ12900 fis; breast; diag
128949; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc; mAb+diag+s.m.
128969; Z42047; Hs.107479; Homo sapiens PRO2751 mRNA, com; pros; diag
129041; BE382756; Hs.169902; solute carrier family 2 (facil; lung, blad; mAb+s.m.
129097; BE243933; Hs.108642; zinc finger protein 22 (KOX 15; ovar; CTL+s.m.
129099; AF146074; Hs.108660; ATP-binding cassette, sub-fami; lung, blad, headnk ; mAb+s.m.
129184; AW161450; Hs.109201; CGI-86 protein; pros; mAb
129260; AF077200; Hs.279813; hypothetical protein; colon; diag
129284; AA318224; Hs.296141; ESTs; colon; diag
129362; U30246; Hs.110736; solute carrier family 12 (sodi; colon, breast, pros; mAb
129366; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA ; breast; diag
129389; NM_012445; Hs.288126; spondin 2, extracellular matri; colon, pros; diag
129404; AI267700; Hs.351201; ESTs; pros, ovar, lung, blad, headnk, panc; diag
129466; L42583; Hs.334309; keratin 6A; lung, blad; diag
129482; AA188185; Hs.289043; spindlin; breast; diag
129534; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
129571; X51630; Hs.1145; Wilms tumor 1; ovar; CTL+s.m.
129605; AF061812; Hs.115947; keratin 16 (focal non-epidermo; lung, blad, headnk; diag
129620; D79338; Hs.239720; CCR4-NOT transcription complex; breast, angio; diag
129628; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk; s.m.
129650; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
129689; AW748482; Hs.77873; B7 homolog 3; breast; diag
129703; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457; EWS, leuk; diag
129720; AA156214; Hs.12152; APMCF1 protein; breast; diag
129750; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad; mAb+s.m.
129869; AI222069; Hs.13015; hypothetical protein similar t; breast; diag
129912; AF155096; Hs.107213; hypothetical protein FLJ20585; ovar; CTL+s.m.
129936; AJ250717; Hs.1355; cathepsin E; blad; sm+diag
129953; AA412195; Hs.13740; ESTs; breast; diag
129977; NM_000399; Hs.1395; early growth response 2 (Krox-; EWS; CTL+s.m.
130010; AA301116; Hs.142838; nucleolar phosphoprotein Nopp3; ovar; diag
130057; AF027153; Hs.324787; solute carrier family 5 (inosi; breast; mAb
130095; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
130155; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
130181; AF052119; Hs.151608; Homo sapiens clone 23522 mRNA ; pros; diag
130184; H58306; Hs.15165; retinoic acid induced 14; angio; diag
130262; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
130343; AB040914; Hs.278628; KIAA1481 protein; breast; diag
130376; R40873; Hs.155174; CDC5 (cell division cycle 5, S; ovar; CTL+s.m.
130385; AW067800; Hs.155223; stanniocalcin 2; breast, lung; mAb+diag
130455; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
130511; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar; diag
130558; BE564937; Hs.15984; pp21 homolog; pros; CTL+s.m.
130577; M69241; Hs.162; insulin-like growth factor bin; ovar; diag
130604; AA383256; Hs.1657; estrogen receptor 1; breast; mAb+s.m.
130627; BE003054; Hs.1695; matrix metalloproteinase 12 (m; lung, colon, blad, headnk, ovar, panc; mAb+diag+s.m.
130637; AA356764; Hs.17109; integral membrane protein 2A; EWS; mAb+s.m.
130648; AI458165; Hs.17296; hypothetical protein MGC2376; colon; diag
130667; BE246961; Hs.17639; Homo sapiens ubiquitin protein; breast; s.m.
130690; AB006625; Hs.139033; paternally expressed 3; ovar; diag
130714; AI348274; Hs.18212; DNA segment on chromosome X (u; breast; diag
130760; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
130800; AI187292; Hs.19574; hypothetical protein MGC5469; colon, lung; diag
130839; AB011169; Hs.380875; similar to S. cerevisiae SSM4; angio; diag
130844; U76248; Hs.20191; seven in absentia (Drosophila); breast; diag
130892; AL120837; Hs.20993; high-glucose-regulated protein; breast; CTL+s.m.
130941; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
130967; AA393071; Hs.182579; leucine aminopeptidase; ovar; s.m.
130972; D81866; Hs.374468; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
130987; BE613269; Hs.21893; hypothetical protein DKFZp761N; colon; diag
131046; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, fibro; diag
131080; NM_001955; Hs.2271; endothelin 1; angio; diag
131083; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros; mAb
131148; AW953575; Hs.303125; p53-induced protein PIGPC1; breast, colon, angio; diag
131216; AI815486; Hs.243901; Homo sapiens cDNA FLJ20738 fis; colon, breast; diag
131228; AW207469; Hs.24485; chondroitin sulfate proteoglyc; ovar; diag
131244; AI638429; Hs.24763; RAN binding protein 1; lung, blad, headnk; CTL+s.m.
131288; AA278482; Hs.25328; ESTs, Moderately similar to AL; pros; diag
131289; AA296696; Hs.333418; FXYD domain-containing ion tra; colon; diag
131307; NM_000025; Hs.2549; adrenergic, beta-3-, receptor; EWS; mAb
131313; R96290; Hs.75874; ribosomal protein L44; EWS; diag
131492; AI452601; Hs.288869; nuclear receptor subfamily 2, ; pros; mAb+s.m.
131544; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
131559; AL078599; Hs.10784; hypothetical protein FLJ20037; breast; diag
131564; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast; diag
131603; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad; s.m.
131643; AW410601; Hs.30026; HSPC182 protein; breast; diag
131739; AF017986; Hs.31386; secreted frizzled-related prot; breast; mAb+s.m.

131817; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio; s.m.
131885; BE502341; Hs.3402; ESTs; breast; diag
131919; T15803; Hs.272458; protein phosphatase 3 (formerl; pros, breast; s.m.
131925; AF151048; Hs.183180; anaphase promoting complex sub; breast; diag
131965; W79283; Hs.35962; ESTs; lung, ovar; diag
131985; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
132050; AI267615; Hs.38022; ESTs; angio; diag
132173; X89426; Hs.41716; endothelial cell-specific mole; angio; diag
132180; NM_004460; Hs.418; fibroblast activation protein,; colon, panc, esoph; mAb
132191; AA507576; Hs.288361; Homo sapiens cDNA: FLJ22696 fi; ovar; diag
132349; AW975654; Hs.181286; serine protease inhibitor, Kaz; pros, blad; s.m.
132354; BE185289; Hs.1076; small proline-rich protein 1B ; lung; diag
132358; NM_003542; Hs.46423; H4 histone family, member G; pros; CTL+s.m.
132371; AA235448; Hs.222088; PRO2000 protein; breast; diag
132454; BE296227; Hs.250822; serine/threonine kinase 15; blad, breast; s.m.
132490; NM_001290; Hs.4980; LIM domain binding 2; angio; diag
132520; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
132528; T78736; Hs.50758; SMC4 (structural maintenance o; ovar; CTL+s.m.
132543; BE568452; Hs.344037; protein regulator of cytokines; colon, lung; diag
132572; AI929659; Hs.237825; signal recognition particle 72; ovar; diag
132592; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 fi; colon; diag
132624; AA326108; Hs.33829; bHLH protein DEC2; ovar; diag
132632; AU076916; Hs.5398; guanine monphosphate synthetas; ovar, lung; s.m.
132669; W38586; Hs.380933; guanine nucleotide binding pro; colon; diag
132710; W74001; Hs.55279; serine (or cysteine) proteinas; lung, blad, colon, headnk; diag
132725; NM_006276; Hs.184167; splicing factor, arginine/seri; ovar; CTL+s.m.
132767; BE182592; Hs.11261; small proline-rich protein 2A; lung; diag
132791; AB029551; Hs.7910; RING1 and YY1 binding protein; pros; CTL+s.m.
132837; AA370362; Hs.57958; EGF-TM7-latrophilin-related pr; angio; diag
132856; NM_001448; Hs.58367; glypican 4; breast, colon, pros; mAb
132888; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epim; pros; s.m.
132902; AI936442; Hs.59838; hypothetical protein FLJ10808; colon; diag
132939; AB009284; Hs.61152; exostoses (multiple)-like 2; ovar; diag
132964; AI362575; Hs.303171; ESTs; pros; diag
132967; AA316181; Hs.61635; six transmembrane epithelial a; pros, pros; mAb+CTL
132990; X77343; Hs.334334; transcription factor AP-2 alph; breast, lung; CTL+s.m.
132994; AA112748; Hs.279905; clone HQ0310 PRO0310p1; colon, breast; s.m.
133006; AW978436; Hs.62515; KIAA0494 gene product; colon; diag
133015; AJ002744; Hs.246315; UDP-N-acetyl-alpha-D-galactosa; breast, colon, pros; s.m.
133016; AI439688; Hs.6289; hypothetical protein FLJ20886; breast; diag
133061; AI186431; Hs.296638; prostate differentiation facto; angio, pros, blad; diag
133063; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
133070; U92649; Hs.380136; a disintegrin and metalloprote; leuk; diag
133179; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
133199; AF231981; Hs.250175; homolog of yeast long chain po; breast, angio; CTL+s.m.
133260; AA403045; Hs.6906; Homo sapiens cDNA: FLJ23197 fi; angio; diag
133272; NM_002776; Hs.69423; kallikrein 10; colon, ovar; diag
133314; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); breast, panc; mAb
133321; T79526; Hs.179516; integral type I protein; breast; diag
133391; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, blad, lung; diag
133415; X69699; Hs.73149; paired box gene 8; ovar; CTL
133477; AW502935; Hs.740; PTK2 protein tyrosine kinase 2; breast; s.m.
133579; X75346; Hs.75074; mitogen-activated protein kina; pros; diag
133626; AW836130; Hs.75277; hypothetical protein FLJ13910; pros; diag
133736; D49958; Hs.75819; glycoprotein M6A; pros; mAb
133829; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; ovar; diag
133860; S78296; Hs.76888; hypothetical protein MGC12702; blad; diag
133944; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
133975; C18356; Hs.295944; tissue factor pathway inhibito; angio, panc; CTL+diag
133976; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; breast, blad; mAb+s.m.
134100; AA460085; Hs.171075; replication factor C (activato; pros; diag
134110; U41060; Hs.79136; LIV-1 protein, estrogen regula; breast, blad, ovar, pros; mAb
134169; AI690916; Hs.178137; transducer of ERBB2, 1; breast; CTL+s.m.
134219; NM_000402; Hs.80206; glucose-6-phosphate dehydrogen; breast; s.m.
134319; BE304999; Hs.285754; fumarate hydratase; colon; s.m.
134326; AW903838; Hs.81800; chondroitin sulfate proteoglyc; ovar, breast, panc, lung; diag
134348; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
134374; N22687; Hs.8236; ESTs; pros; diag
134390; R35528; Hs.8258; DKFZP434D1335 protein; pros; CTL+s.m.
134401; AI916662; Hs.211577; kinectin 1 (kinesin receptor); pros, breast; mAb+s.m.
134405; AW067903; Hs.82772; collagen, type XI, alpha 1; breast, lung, ovar, headnk; CTL
134470; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, headnk; s.m.
134520; BE091005; Hs.349506; activated RNA polymerase II tr; ovar; s.m.
134529; AW411479; Hs.848; FK506-binding protein 4 (59kD); breast; diag
134570; U66615; Hs.172280; SWI/SNF related, matrix associ; EWS; CTL+s.m.
134654; AK001741; Hs.8739; hypothetical protein FLJ10879; breast ; diag
134666; BE391929; Hs.8752; transmembrane protein 4; breast; mAb+s.m.
134691; AW382987; Hs.88474; prostaglandin-endoperoxide syn; ovar; s.m.
134727; X80507; Hs.84520; yes-associated protein 65 kDa; blad; diag
134731; D89377; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
134786; T29618; Hs.89640; TEK tyrosine kinase, endotheli; angio; s.m.
134824; S78723; Hs.298623; 5-hydroxytryptamine (serotonin; blad; mAb
134856; BE281128; Hs.9030; TONDU; blad; CTL+s.m.

134868; AB020689; Hs.90419; KIAA0882 protein; breast; diag
134924; BE294029; Hs.279903; Ras homolog enriched in brain ; breast; mAb
134972; AL033527; Hs.169252; v-myc avian myelocytomatosis v; ovar; CTL+s.m.
134975; R50333; Hs.92186; Leman coiled-coil protein; breast; diag
134989; AW968058; Hs.92381; nudix (nucleoside diphosphate ; colon; diag
135073; W55956; Hs.94030; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
135117; W52493; Hs.94694; Homo sapiens cDNA FLJ10561 fis; breast; diag
135166; AA135867; Hs.280858; ESTs, Highly similar to A35661; pros; diag
135235; AW298244; Hs.266195; ESTs; angio; diag
135242; AI583187; Hs.9700; cyclin E1; ovar; CTL+s.m.
135243; BE463721; Hs.97101; putative G protein-coupled rec; colon; mAb+s.m.
135255; Y13645; Hs.97234; uroplakin 2; blad; mAb
135309; AI564123; Hs.355689; ADP-ribosylation factor-like 5; pros; diag
135315; H81136; Hs.334604; Homo sapiens mRNA for KIAA1870; pros; diag
135389; U05237; Hs.99872; fetal Alzheimer antigen; pros, breast, colon; CTL+s.m.
135400; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
300254; AW183618; Hs.55610; solute carrier family 30 (zinc; pros, breast; mAb+s.m.
300256; AW591433; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
300318; AW444502; Hs.256982; ESTs, Weakly similar to NEL1_H; angio; CTL+diag
300605; AI218847; Hs.152670; ESTs; pros; diag
300921; AF146747; Hs.232165; polycythemia rubra vera 1; cel; pros; mAb+s.m.
300923; AW136372; Hs.1852; acid phosphatase, prostate; pros; s.m.
301042; AI659131; Hs.366053; hypothetical protein MGC2849; pros; mAb
301043; AI160316; Hs.149155; voltage-dependent anion channe; pros; mAb+s.m.
301050; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung; CTL+s.m.
301341; AA887801; Hs.208229; G protein-coupled receptor; breast, lung; mAb+s.m.
302001; AB020711; Hs.374965; KIAA0904 protein; breast ; CTL+s.m.
302005; BE252922; Hs.123119; MAD (mothers against decapenta; pros; diag
302067; BE542706; Hs.222399; CEGP1 protein; breast; diag
302167; NM_006227; Hs.283007; phospholipid transfer protein; pros; mAb
302225; NM_007231; Hs.162211; solute carrier family 6 (neuro; panc; mAb+s.m.
302276; AW057736; Hs.323910; HER2 receptor tyrosine kinase ; breast; mAb+s.m.
302290; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp5; pros, breast; diag
302372; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros ; mAb+s.m.
302384; AI678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
302410; NM_004917; Hs.218366; kallikrein 4 (prostase, enamel; pros; diag
302468; AL133561; Hs.380155; DKFZP434B061 protein; pros; diag
302562; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad; mAb
302881; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
303295; AA205625; Hs.208067; ESTs; blad; diag
303380; AW962764; Hs.303171; olfactory receptor, family 51,; pros; mAb
303506; AA340605; Hs.105887; ESTs, Weakly similar to Homolo; pros, breast, colon ; diag
303699; BE143707; Hs.19525; hypothetical protein FLJ22794; pros; diag
303753; AW503733; Hs.9414; KIAA1488 protein; pros, breast, colon; CTL+s.m.
305503; AA759177; Hs.298148; ESTs, Weakly similar to KIAA05; pros; diag
306273; AA936290; ; gb:on70a01.s1 Soares_NFL_T_GBC; pros; diag
306676; AI005603; ; gb:ov15c10.s1 NCI_CGAP_GC3 Hom; lung; diag
306840; AI077477; Hs.307912; ESTs; angio; diag
309177; AI951118; Hs.326736; Homo sapiens breast cancer ant; breast, pros; mAb+CTL
309583; AW170035; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
309931; AW341683; Hs.343663; gb:hd13d01.x1 Soares_NFL_T_GBC; lung; mAb
310382; AI734009; Hs.127699; KIAA1603 protein; pros; diag
310431; AI420227; Hs.366053; ESTs, Weakly similar to A46010; pros; diag
310573; AW292180; Hs.156142; ESTs; pros; diag
310636; AI814373; Hs.164175; ESTs; lung; diag
310781; AI380797; Hs.158992; ESTs; breast ; diag
310955; AI476732; Hs.263912; ESTs; breast, angio; diag
311034; BE567130; Hs.311389; ESTs, Highly similar to NKGD_H; lung; mAb+s.m.
311166; AI821005; Hs.118599; intron of: BFF9 (GDNFRa).; breast ; diag
311251; AI655662; Hs.197698; ESTs; pros; diag
311557; AF200492; Hs.211238; interleukin-1 homolog 1; lung; diag
311596; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
311630; AI915444; Hs.372037; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
311877; AA084248; Hs.372651; G protein-coupled receptor 39; ovar, angio, glio; mAb+s.m.
311911; R19175; Hs.169793; ribosomal protein L32; pros; diag
311928; T62216; Hs.378028; ESTs; pros; diag
312182; T94344; Hs.326263; ESTs; pros; diag
312252; AI128388; Hs.143655; ESTs; blad; diag
312319; AA906997; Hs.180780; TERA protein; colon; CTL+s.m.
312521; AI263307; Hs.356901; H2B histone family, member L; pros, breast, lung; diag
312544; AA516420; Hs.352340; ESTs, Weakly similar to I38022; breast; diag
312742; AI650363; Hs.116462; ESTs; colon; diag
312795; AW975014; Hs.26; ferrochelatase (protoporphyria; pros; s.m.
312857; BE083868; Hs.126914; KIAA1430 protein; colon, pros; CTL+s.m.
312922; AA329256; Hs.378739; ESTs, Moderately similar to al; pros; diag
313328; AW449211; Hs.105445; GDNF family receptor alpha 1; breast ; mAb+s.m.
313513; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
313556; AA628517; Hs.118502; ESTs; angio; diag
313665; AW751201; Hs.120932; ESTs; angio; diag
313774; AI916058; Hs.144583; ESTs; colon; CTL
313915; C18863; Hs.163443; intron of periostin (OSF-2os); breast; diag
313978; AI870175; Hs.13957; ESTs; angio; diag
314078; AW129357; Hs.329700; ESTs; breast; diag

314097; AA648744; Hs.269493; ESTs; breast; diag
314121; AI732083; Hs.187619; ESTs; pros, breast ; diag
314171; AI821895; Hs.193481; ESTs; pros; diag
314506; AA833655; Hs.206868; Homo sapiens cDNA FLJ14056 fis; breast; diag
314547; AA399272; Hs.144341; ESTs; breast ; diag
314558; AI873274; Hs.370280; ESTs; breast, pros; diag
314589; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad; diag
314691; AW207206; Hs.356962; ESTs; breast, pros; diag
314785; AI538226; Hs.32976; guanine nucleotide binding pro; colon, pros; diag
314907; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
315006; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
315033; AI493046; Hs.146133; ESTs; colon; diag
315051; AW292425; Hs.163484; ESTs; breast, pros, blad; diag
315052; AA876910; Hs.134427; ESTs; pros, breast ; diag
315196; AI367347; Hs.44898; Homo sapiens clone TCCCTA00151; breast; diag
315368; AB037745; Hs.104696; KIAA1324 protein; pros; diag
315408; AW273261; Hs.216292; ESTs; pros; diag
315634; AA837085; Hs.372254; ESTs; breast, pros; diag
315720; AA292998; Hs.163900; ESTs; blad; diag
316177; AI904982; Hs.293102; downstream of breast cancer an; breast; mAb+CTL
316442; AA760894; Hs.125350; ESTs; pros; diag
316580; AA938198; Hs.146123; poly(A) polymerase gamma; breast, angio; s.m.
316886; AA836331; Hs.170261; ESTs; breast ; diag
316943; AW014875; Hs.137007; ESTs; blad; diag
317079; BE159984; Hs.125395; ESTs; blad; mAb+s.m.
317140; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
317224; X73608; Hs.93029; sparc/osteonectin, cwcv and ka; pros, angio; diag
317548; BE568568; Hs.159066; ESTs; pros; CTL+s.m.
317803; AW664964; Hs.128899; ESTs; breast, lung, ovar, pros; mAb+s.m.
317881; AI827248; Hs.224398; Homo sapiens cDNA FLJ11469 fis; breast, lung ; diag
318240; AI085377; Hs.143610; ESTs; lung; diag
318524; AK001050; Hs.159066; hypothetical protein FLJ10188; pros, colon; CTL+s.m.
318532; AW139377; Hs.127179; cryptic gene; panc; diag
318744; AI793124; Hs.144479; ESTs; breast; diag
318754; W21423; Hs.44222; CGI-90 protein; pros; diag
319080; AW967646; Hs.23023; ESTs; pros; diag
319795; AB037821; Hs.146858; protocadherin 10; pros, glio; mAb+s.m.
320066; BE305242; Hs.16098; claudin 2; colon, panc; diag
320167; AA984373; Hs.90790; Homo sapiens cDNA: FLJ22930 fi; breast, pros; diag
320203; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar; mAb+s.m.
320211; AL039402; Hs.125783; DEME-6 protein; breast, pros; CTL
320322; AF077374; Hs.139322; small proline-rich protein 3; lung; diag
320324; AF071202; Hs.139336; ATP-binding cassette, sub-fami; pros; mAb
320561; AF085808; Hs.159330; uroplakin 3; pros, blad; diag
320590; U67058; Hs.154299; Human proteinase activated rec; pros; mAb+s.m.
320635; N50617; Hs.80506; small nuclear ribonucleoprotei; angio lung; diag
320736; AA315361; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
320796; AK001541; Hs.31218; secretory carrier membrane pro; pros, colon ; diag
320896; BE019924; Hs.271580; uroplakin 1B; lung, blad, ovar, headnk; mAb+diag
321023; AW294316; Hs.125608; ESTs; colon; diag
321107; AI732643; Hs.144151; downstream of breast cancer an; breast; mAb+CTL
321412; AI674383; Hs.22891; solute carrier family 7 (catio; pros; mAb+s.m.
321441; AF107493; Hs.201675; Homo sapiens LUCA-15 protein m; pros, breast ; diag
321644; AW975944; Hs.237396; ESTs; breast, pros ; diag
321717; AW956580; Hs.42699; ESTs; angio; diag
321906; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
321911; AF026944; Hs.293797; ESTs; angio, lung, blad; diag
322035; AL137517; Hs.306201; hypothetical protein DKFZp564O; breast, blad; mAb
322521; AF147347; ; gb:Homo sapiens full length in; breast ; diag
322706; AA018899; Hs.127179; cryptic gene; panc; diag
322782; AA056060; Hs.202577; Homo sapiens cDNA FLJ12166 fis; pros; diag
322818; AW043782; Hs.293616; ESTs; pros, breast, angio, glio ; diag
322882; AW248508; Hs.279727; Homo sapiens cDNA FLJ14035 fis; breast, lung, ovar, angio, blad; diag
322975; C16391; ; intron of breast cancer antige; breast ; mAb+CTL
323168; AL120862; Hs.124165; programmed cell death 9 (PDCD9; breast ; diag
323226; AF055019; Hs.355279; Homo sapiens clone 24670 mRNA ; pros; diag
323262; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
323287; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
323332; AI829520; ; gb:wl19c06.x1 NCI_CGAP_Ut1 Hom; breast ; diag
323335; AI655499; Hs.161712; ESTs; pros, breast; mAb
323587; AI299709; Hs.131886; Homo sapiens cDNA: FLJ22113 fi; colon; diag
323817; AA410943; ; NAME OMITTED ... receptor kinase; breast ; mAb
324261; BE069341; ; gb:QV3-BT0381-270100-073-c08 B; breast; diag
324295; AA434579; Hs.143691; ESTs; pros; diag
324338; AA927668; Hs.145078; regulator of differentiation (; colon; diag
324430; AA464018; Hs.335798; Homo sapiens cDNA: FLJ23241 fi; pros, colon; diag
324432; AA464510; Hs.152812; ESTs; breast, lung, panc; diag
324603; AW993522; Hs.299867; ESTs; pros, breast; diag
324617; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros; diag
324658; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros ; diag
324718; AI557019; Hs.116467; small nuclear protein PRAC; colon, pros; diag
324866; AI541214; Hs.46320; Small proline-rich protein SPR; lung, blad; diag
324871; AI890347; Hs.271923; Homo sapiens cDNA: FLJ22785 fi; colon; diag

324987; AI375572; Hs.172634; ESTs; breast; diag
325372; ; ; Phase 2 & 3 Exons; breast; CTL+s.m.
325544; ; ; Phase 2 & 3 Exons; breast, angio; diag
327036; ; ; Phase 2 & 3 Exons; lung, angio; diag
327075; ; ; Phase 2 & 3 Exons; breast, lung; diag
327414; ; ; Phase 2 & 3 Exons; angio; diag
328700; ; ; Phase 2 & 3 Exons; breast, angio; diag
330211; ; ; Phase 2 & 3 Exons; pros; CTL+s.m.
330468; L10343; Hs.112341; protease inhibitor 3; skin-der; lung, colon, blad; diag
330493; M27826; Hs.334372; endogenous retroviral protease; lung, colon; s.m.
330630; NM_002902; Hs.79088; reticulocalbin 2; EF-hand calc; pros; diag
330762; AW407332; Hs.13014; ADP-ribosylation factor GTPase; pros; CTL+s.m.
330790; AI660243; Hs.318545; Hu01 Chip Redos; pros, blad; diag
330814; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast; diag
330827; AI961486; Hs.249196; ESTs; lung, uter; diag
330892; AF109298; Hs.118258; prostate cancer associated pro; pros; diag
331014; AW770994; Hs.30340; hypothetical protein KIAA1165; colon; diag
331151; R82331; Hs.121602; ESTs; pros, breast ; diag
331183; T40769; Hs.8469; ESTs; colon; diag
331237; W87874; Hs.25277; Homo sapiens cDNA FLJ10717 fis; angio; diag
331490; AF216751; Hs.26813; CDA14; pros; diag
331578; AI246482; Hs.243010; ESTs; angio; diag
331614; N92293; Hs.206832; EST; Moderately similar to ALU; breast ; diag
331811; AW885727; Hs.9914; Hu01 Chip Redos; lung; diag
331889; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
331969; AA526911; Hs.82772; collagen; type XI; alpha 1; breast, lung; CTL
332180; AF134160; Hs.7327; claudin 1; lung; mAb
332247; AA669097; ; ESTs; pros, breast ; diag
332396; AW579842; Hs.380730; hypothetical protein FLJ10697; pros; diag
332453; L42583; Hs.334309; Hu01 Chip Redos; lung; diag
332466; AB018259; Hs.118140; KIAA0716 gene product; angio; diag
332530; M31669; Hs.1735; inhibin; beta B (activin AB be; ovar, pros; diag
332535; AF167706; Hs.19280; cysteine-rich repeat-containin; angio; diag
332640; BE568452; Hs.344037; protein regulator of cytokines; blad, headnk; diag
332645; AA284371; Hs.118064; ESTs; breast, colon; diag
332686; X69699; Hs.73149; paired box gene 8; ovar; CTL+s.m.
332697; X51405; Hs.75360; carboxypeptidase E; pros; diag
332740; BE409669; Hs.286241; Homo sapiens cDNA: FLJ22698 fi; pros; diag
332798; ; ; C22000007:gi|12314195|emb|CAB9; pros, breast ; diag
333769; ; ; NM_005940*:Homo sapiens matrix; breast, colon, lung; mAb+diag+s.m.
333904; ; ; Chromosome 22; pros; diag
334223; ; ; NM_005080*:Homo sapiens X-box ; pros, breast; diag
334447; ; ; NM_012429*:Homo sapiens SEC14 ; pros; diag
335115; ; ; NM_006498*:Homo sapiens lectin; pros; CTL+s.m.
335809; ; ; NM_014509*:Homo sapiens kraken; breast; CTL+s.m.
335824; ; ; ENSP00000249072*:DJ222E13.1 (N; breast, pros; CTL+s.m.
335825; ; ; ENSP00000249072*:DJ222E13.1 (N; breast; diag
335936; ; ; Chromosome 22; lung; diag
336034; ; ; NM_007172:Homo sapiens nucleop; breast, angio; CTL+s.m.
336152; ; ; NM_014246:Homo sapiens cadherl; breast ; mAb
336636; ; ; C22000024*:gi|10645308|gb|AAG2; lung, breast; CTL+s.m.
338008; ; ; NM_005940*:Homo sapiens matrix; lung, breast, colon; mAb+diag+s.m.
338033; ; ; Chromosome 22; lung, angio; diag
338158; ; ; NM_012399*:Homo sapiens phosph; lung, angio; diag
338255; ; ; NM_014323*:Homo sapiens zinc f; pros, breast, colon ; CTL+s.m.
400195; ; Hs.42650; NM_007057*:Homo sapiens ZW10 I; lung; CTL+s.m.
400269; ; Hs.253495; Eos Control; fibro; diag
400285; ; ; Eos Control; lung; diag
400287; S39329; Hs.181350; kallikrein 2, prostatic; pros; diag
400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros,angio, blad, lung; mAb+s.m.
400290; H18836; Hs.31608; hypothetical protein FLJ20041; pros, colon, EWS; mAb
400294; N95796; Hs.278695; Homo sapiens prostein mRNA, co; pros, pros; mAb
400295; W72838; Hs.348419; AI905687:IL-BT095-190199-019 B; breast; diag
400298; AA032279; Hs.61635; six transmembrane epithelial a; panc, lung, headnk, stom, EWS, ovar; mAb+CTL
400328; X87344; ; transporter 2, ATP-binding cas; lung; mAb+s.m.
400409; AF153341; ; Homo sapiens winged helix/fork; blad; CTL+s.m.
400419; AF084545; ; Target; lung, sarc; diag
400440; X63957; Hs.83870; nebulin; sarc; diag
400494; ; ; ENSP00000238970*:CIG30 (Fragme; angio; mAb
400517; ; ; lengsin; stom, cerv, uter, lung, pros, colon, hepC; diag
400651; ; ; ENSP00000228031*:COPPER CHAPER; sarc; s.m.
400665; ; ; NM_002425:Homo sapiens matrix ; lung; mAb+diag+s.m.
400773; ; ; NM_003105*:Homo sapiens sortil; blad; mAb
400844; ; ; NM_003105*:Homo sapiens sortil; blad; s.m.
400846; ; ; sortilin-related receptor, L(D; blad; mAb+s.m.
400881; ; ; NM_025080:Homo sapiens hypothe; ovar; diag
401093; ; ; C12000586*:gi|6330167|db|BAA8; blad, lung; CTL+s.m.
401234; ; ; mitogen-activated protein kina; angio; diag
401424; ; ; NM_001172:Homo sapiens arginas; pros; s.m.
401486; ; ; C4000647*:gi|4758508|ref|NP_00; headnk; mAb
401704; ; ; NM_021195*:Homo sapiens claudi; test; mAb
401732; ; ; NM_001176*:Homo sapiens Rho GD; panc; diag
401747; ; ; Homo sapiens keratin 17 (KRT17; blad, lung, headnk, mela; diag

401760; ; ; Target Exon; blad, lung, headnk, esoph; diag
401780; ; ; NM_005557*:Homo sapiens kerati; lung, blad, headnk, esoph, mela; diag
401781; ; ; Target Exon; lung, blad, headnk, esoph, cerv; diag
401785; ; ; NM_002275*:Homo sapiens kerati; lung; diag
401797; ; ; Target Exon; sarc; diag
401994; ; ; Target Exon; lung; diag
402145; ; ; Target Exon; test; CTL+s.m.
402199; ; ; Target Exon; test; CTL+s.m.
402230; ; ; Fgenesh predicted: CYTOCHROME ; blad; diag
402239; ; ; Target Exon; blad; diag
402260; ; ; NM_001436*:Homo sapiens fibril; blad; CTL+s.m.
402265; ; ; Target Exon; lung; diag
402305; ; ; C19000735*:gi|4508027|ref|NP_0; blad; CTL+s.m.
402420; ; ; C1000823*:gi|10432400|emb|CAC1; lung; diag
402424; ; ; NM_024901:Homo sapiens hypothe; blad; CTL+s.m.
402447; ; ; C1000201:gi|204416|gb|AAA02627; esoph; mAb
402474; ; ; NM_004079:Homo sapiens catheps; lung, colon, stom, fibro; diag
402550; ; ; Target Exon; fibro; diag
402604; ; ; Target Exon; glio; diag
402605; ; ; Target Exon; glio; diag
402606; ; ; NM_024626:Homo sapiens hypothe; ovar, breast; mAb
402680; ; ; Target Exon; test; mAb
402777; ; ; C1002652*:gi|544327|sp|Q04799|; blad; diag
402860; ; ; ENSP00000239210:DJ50O24.4 (nov; mela; CTL+s.m.
402888; ; ; Target Exon; sarc; diag
402992; ; ; Target Exon; sarc; diag
402994; ; ; NM_002463*:Homo sapiens myxovi; esoph; diag
403046; ; ; NM_005656*:Homo sapiens transm; pros; mAb
403047; ; ; NM_005656*:Homo sapiens transm; pros, blad, colon; mAb
403071; ; ; NM_003319*:Homo sapiens titin ; sarc; diag
403088; ; ; NM_003319*:Homo sapiens titin ; sarc; diag
403171; ; ; C2001472*:gi|5809678|gb|AAB418; test; diag
403328; ; ; Target Exon; mela; diag
403329; ; ; unnamed protein product [Homo ; lung; diag
403381; ; ; ENSP00000231844*:Ecotropic vir; blad; CTL+s.m.
403409; ; ; NM_005929:Homo sapiens antigen; mela; mAb
403433; ; ; NM_001622:Homo sapiens alpha-2; hepC; diag
403478; ; ; NM_022342:Homo sapiens kinesin; lung; CTL+s.m.
403715; ; ; Target Exon; lung; diag
403740; ; ; NM_001076*:Homo sapiens UDP gl; pros, hepC; s.m.
403776; ; ; ENSP00000226542*:Small inducib; panc; diag
403903; ; ; C5001632*:gi|10645308|gb|AAG21; blad; CTL+s.m.
404029; ; ; NM_018936*:Homo sapiens protoc; glio; mAb
404049; ; ; NM_018937*:Homo sapiens protoc; glio; mAb
404210; ; ; NM_005936:Homo sapiens myeloid; panc, uter, cerv, lung, ovar, pros, colon, stom; diag
404240; ; ; NM_018950:Homo sapiens major h; fibro; mAb
404253; ; ; NM_021058*:Homo sapiens H2B hi; lung; CTL+s.m.
404286; ; ; C6001909:gi|704441|dbj|BAA1890; panc; diag
404298; ; ; C6001238*:gi|121715|sp|P26697|; lung; s.m.
404403; ; ; Target Exon; blad; diag
404440; ; ; NM_021048:Homo sapiens melanom; lung, blad; mAb+CTL
404866; ; ; ENSP00000251112*:Sodium/potass; panc; s.m.
404877; ; ; NM_005365:Homo sapiens melanom; lung, blad; CTL+s.m.
404927; ; ; Target Exon; lung, headnk; diag
404996; ; ; Target Exon; lung, headnk, esoph; diag
405001; ; ; interleukin enhancer binding f; sarc; diag
405025; ; ; Homo sapiens bone morphogeneti; angio; diag
405121; ; ; mitogen-activated protein kina; angio, renal; s.m.
405238; ; ; Target Exon; glio; diag
405239; ; ; oxidative 3 alpha hydroxystero; glio; s.m.
405451; ; ; Homo sapiens glutaminyl-peptid; mela; s.m.
405545; ; ; Target Exon; cerv; mAb
405546; ; ; NM_018833*:Homo sapiens transp; cerv; mAb
405547; ; ; NM_018833*:Homo sapiens transp; cerv, mela; mAb
405646; ; ; C12000200:gi|4557225|ref|NP_00; lung; diag
405704; ; ; NM_001844*:Homo sapiens collag; sarc; diag
405770; ; ; NM_002362:Homo sapiens melanom; lung, esoph; mAb+CTL
405849; ; ; Target Exon; panc; diag
405932; ; ; C15000305:gi|3806122|gb|AAC691; blad, lung, headnk, cerv; CTL+s.m.
406081; ; ; Target Exon; blad; diag
406137; ; ; NM_000179*:Homo sapiens mutS (; lung; CTL+s.m.
406173; ; ; ENSP00000250148*:Growth hormon; panc; CTL+s.m.
406348; ; ; Target Exon; breast; CTL+s.m.
406360; ; ; Target Exon; lung, headnk; diag
406399; ; ; NM_003122*:Homo sapiens serine; blad; diag
406434; ; ; NM_030579*:Homo sapiens cytoch; blad; diag
406467; ; ; Target Exon; lung, headnk, blad; diag
406506; ; ; Target Exon; angio; diag
406547; ; ; Target Exon; test; diag
406627; T64904; Hs.163780; ESTs; angio; CTL+s.m.
406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte; panc; mAb
406672; M26041; Hs.198253; major histocompatibility compl; fibro; mAb
406685; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung; mAb+CTL

406687; M31126; Hs.352054; matrix metalloproteinase 11 (s; breast, lung, ovar, cerv, uter, panc, esoph, mela, sarc; mAb+diag+s.m.
406690; M29540; Hs.220529; carcinoembryonic antigen-relat; lung, headnk, panc, stom, blad, colon, cerv; mAb+CTL
406706; X03740; Hs.231581; myosin, heavy polypeptide 1, s; sarc; diag
406850; AI624300; Hs.172928; collagen, type I, alpha 1; sarc; CTL+s.m.
406906; Z25424; ; gb:H.sapiens protein-serine/th; blad, lung; s.m.
406937; U14622; ; gb:Human transketolase-like pr; test; s.m.
406967; M24349; ; gb:Human parathyroid hormone-l; lung; CTL+s.m.
406974; M57293; ; gb:Human parathyroid hormone-r; lung, blad; diag
407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial; sarc; diag
407034; U84540; ; gb:Human dystrobrevin isoform ; glio; diag
407103; AA424881; Hs.256301; hypothetical protein MGC13170; pros; diag
407118; AA156790; Hs.262036; ESTs, Weakly similar to Z223_H; pros; diag
407122; H20276; Hs.31742; ESTs; pros; diag
407137; T97307; ; gb:ye53h05.s1 Soares fetal liv; lung, blad, ovar, pros, panc, headnk; diag
407168; R45175; Hs.117183; ESTs; pros, breast, colon; diag
407178; AA195651; Hs.352312; AP-2 beta transcription factor; breast ; CTL+s.m.
407202; N58172; Hs.109370; ESTs; pros; diag
407216; N91773; Hs.348385; lysyl oxidase; panc; diag
407242; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung, ovar, cerv; mAb
407244; M10014; ; fibrinogen, gamma polypeptide; lung; diag
407245; X90568; Hs.172004; titin; sarc; diag
407251; U67611; Mm.29182; transaldolase 1; pros; s.m.
407252; AA659037; Hs.163780; ESTs; angio; CTL+s.m.
407276; AI951118; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
407289; AA135159; Hs.203349; Homo sapiens cDNA FLJ12149 fis; lung; diag
407366; AF026942; Hs.17518; gb:Homo sapiens cig33 mRNA, pa; ovar, hepC, stom, mela, esoph; diag
407581; R46402; Hs.173508; P3ECSL; blad; CTL+s.m.
407601; AC002300; Hs.37129; sodium channel, nonvoltage-gat; blad; mAb
407619; AL050341; Hs.37165; collagen, type IX, alpha 2; sarc; diag
407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-; lung, headnk; s.m.
407710; AW022727; Hs.23616; ESTs; test; diag
407720; AB037776; Hs.38002; KIAA1355 protein; lung; mAb
407746; AK001962; Hs.38114; hypothetical protein FLJ11100; lung; diag
407756; AA116021; Hs.38260; ubiquitin specific protease 18; panc, lung, esoph, fibro, mela; CTL+s.m.
407758; D50915; Hs.38365; KIAA0125 gene product; lung; diag
407777; AA161071; Hs.71465; squalene epoxidase; panc, esoph; s.m.
407782; AA608956; Hs.112619; ESTs, Moderately similar to PU; lung; diag
407786; AA687538; Hs.38972; tetraspan 1; pros, colon, uter, stom, ovar, cerv; mAb
407788; BE514982; Hs.38991; S100 calcium-binding protein A; headnk, panc, blad, lung, fibro; diag
407818; AL021938; Hs.40154; jumonji (mouse) homolog; test; CTL+s.m.
407824; AA147884; Hs.9812; Homo sapiens cDNA FLJ14388 fis; sarc; diag
407839; AA045144; Hs.161566; ESTs; blad, headnk; mAb
407846; AA426202; Hs.40403; Cbp/p300-interacting transacti; mela; diag
407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homo; colon, stom, renal, breast, ovar, uter, cerv; diag
407856; AA045281; Hs.266175; phosphoprotein associated with; mela; diag
407872; AB039723; Hs.40735; frizzled (Drosophila) homolog ; ovar; mAb
407881; AW072003; Hs.40968; heparan sulfate (glucosamine) ; panc; s.m.
407910; AA650274; Hs.41296; fibronectin leucine rich trans; fibro; mAb
407944; R34008; Hs.239727; desmocollin 2; lung, headnk, esoph; mAb
407949; W21874; Hs.247057; ESTs, Weakly similar to 210926; fibro, blad; diag
407962; AI133530; Hs.62930; ESTs, Weakly similar to S59501; angio; mAb+s.m.
408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (; breast, pros, blad, lung, headnk, cerv, esoph; mAb+CTL
408015; AW136771; Hs.244349; epidermal differentiation comp; mela, sarc; diag
408045; AW138959; Hs.245123; ESTs; breast ; diag
408056; AA312329; Hs.42331; ephrin-A4; ovar; diag
408063; BE086548; Hs.381047; calcineurin-binding protein ca; pros, lung; diag
408081; AW451597; Hs.167409; intron of basic-helix-loop-hel; ovar, glio; diag
408101; AW968504; Hs.278346; CDC2-related protein kinase 7; breast, lung, stom; s.m.
408122; AI432652; Hs.42824; hypothetical protein FLJ10718; lung; diag
408209; NM_004454; Hs.43697; ets variant gene 5 (ets-relate; mela; CTL+s.m.
408296; AL117452; Hs.44155; DKFZP586G1517 protein; angio; diag
408308; AL033377; Hs.44197; hypothetical protein DKFZp564D; panc, renal, colon; mAb
408353; BE439838; Hs.44298; mitochondrial ribosomal protei; lung; diag
408430; S79876; Hs.44926; dipeptidylpeptidase IV (CD26, ; pros; mAb
408522; AI541214; Hs.46320; Small proline-rich protein SPR; lung, blad, headnk, eosph, cerv; diag
408561; AI308037; Hs.84120; hypothetical protein MGC13016; mela; CTL+s.m.
408570; AL046406; Hs.103483; KIAA1798 protein; angio; CTL+s.m.
408572; AA055611; Hs.226568; ESTs, Moderately similar to AL; lung; diag
408591; AF015224; Hs.46452; mammaglobin 1; breast, cerv; diag
408611; NM_004367; Hs.46468; chemokine (C-C motif) receptor; mela; mAb
408633; AW963372; Hs.222088; PRO2000 protein; blad, lung, headnk, pros; diag
408660; AA525775; Hs.89040; ESTs, Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag
408726; AL137379; Hs.47125; hypothetical protein FLJ13912; test; diag
408758; NM_003686; Hs.47504; exonuclease 1; mela; CTL+s.m.
408770; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
408771; AW732573; Hs.47584; potassium voltage-gated channe; lung; mAb
408780; D31797; Hs.652; tumor necrosis factor (ligand); leuk; diag
408795; AW749126; Hs.170345; hypothetical protein FLJ13710; ovar; diag
408826; AF216077; Hs.48376; Homo sapiens clone HB-2 mRNA s; panc, pros; diag
408833; AW612232; Hs.254835; ESTs; pros; diag
408877; AA479033; Hs.130315; ESTs, Weakly similar to A47582; breast; diag
408915; NM_016651; Hs.48950; heptacellular carcinoma novel ; panc, sarc; diag
408930; AA146721; Hs.334686; hypothetical protein FLJ21588; blad; CTL+s.m.

408962; BE386436; Hs.44317; SRY (sex determining region Y); mela; diag
408992; AA059325; Hs.30114; guanine nucleotide binding pro; lung; diag
408996; AI979168; Hs.82226; glycoprotein (transmembrane) n; mela; mAb+s.m.
409012; AL117435; Hs.49725; DKFZP434I216 protein; sarc; CTL+s.m.
409038; T97490; Hs.50002; small inducible cytokine subfa; mela; diag
409051; AA080912; ; gb:zn04d03.r1 Stratagene hNT n; pros; s.m.
409077; AA063037; Hs.66803; ESTs; lung; diag
409093; BE243834; Hs.50441; CGI-04 protein; lung; diag
409123; AA063403; ; gb:zm04d12.s1 Stratagene corne; pros; s.m.
409142; AL136877; Hs.50758; SMC4 (structural maintenance o; ovar, lung, mela; diag
409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibro; diag
409200; AL042914; Hs.51039; KIAA0076 gene product; sarc; CTL+s.m.
409203; AA780473; Hs.687; cytochrome P450, subfamily IVB; fibro, blad, ovar; diag
409228; R16811; Hs.22010; ESTs, Weakly similar to 210926; lung; mAb
409231; AA446644; Hs.692; GA733-2 antigen; epithelial gl; pros, ovar, breast, uter, panc, colon, stom; mAb
409243; AB037761; Hs.51743; KIAA1340 protein; test; diag
409262; AK000631; Hs.52256; hypothetical protein FLJ20624; pros; CTL+s.m.
409264; NM_014937; Hs.52463; KIAA0966 protein; mela; CTL+s.m.
409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-li; breast, ovar, lung, panc, uter; mAb
409327; L41162; Hs.53563; collagen, type IX, alpha 3; colon, panc, sarc; CTL+s.m.
409340; BE174629; Hs.321130; hypothetical protein MGC2771; mela; CTL+s.m.
409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; test; CTL+s.m.
409348; AI401535; Hs.146090; ESTs; renal, glio; diag
409361; NM_005982; Hs.54416; sine oculis homeobox (Drosophi; blad, lung, pros; CTL+s.m.
409389; AB007979; Hs.301281; Homo sapiens mRNA, chromosome ; glio; diag
409395; U46745; Hs.336678; dystrobrevin, alpha; glio; diag
409402; AF208234; Hs.695; cystatin B (stefin B); blad; diag
409415; AA579258; Hs.6083; Homo sapiens cDNA: FLJ21028 fi; mela; diag
409421; AA199883; Hs.67624; ESTs; test; diag
409430; R21945; Hs.346735; splicing factor, arginine/seri; mela; diag
409432; D49372; Hs.54460; small inducible cytokine subfa; stom, esoph; diag
409433; AA074382; Hs.135255; ESTs; glio, sarc; diag
409509; AL036923; Hs.322710; ESTs; angio; diag
409512; AW979187; Hs.293591; melanoma differentiation assoc; mela, esoph; CTL+s.m.
409542; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
409582; R27430; Hs.271565; ESTs; lung; diag
409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyper; headnk, mela, sarc; CTL+s.m.
409633; AW449822; Hs.55200; ESTs; sarc; diag
409637; AA323948; Hs.55407; Homo sapiens mRNA; cDNA DKFZp4; renal; diag
409638; AW450420; Hs.21335; ESTs; glio; diag
409670; AI368109; Hs.381163; KIAA1856 protein; test; CTL+s.m.
409703; NM_006187; Hs.56009; 2'-5'-oligoadenylate synthetas; panc, esoph, mela; s.m.
409705; M37762; Hs.56023; brain-derived neurotrophic fac; lung; diag
409719; AI769160; Hs.108681; Homo sapiens brain tumor assoc; lung; diag
409731; AA125985; Hs.56145; thymosin, beta, identified in ; pros, sarc; CTL+s.m.
409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal ; ovar, renal; CTL+s.m.
409935; AW511413; Hs.187393; ESTs; lung; diag
409958; NM_001523; Hs.57697; hyaluronan synthase 1; panc, ovar; mAb
409986; N27687; Hs.334334; transcription factor AP-2 alph; mela; diag
410006; AW732308; Hs.57783; eukaryotic translation initiat; test; diag
410037; AB020725; Hs.58009; KIAA0918 protein; pros; diag
410044; BE566742; Hs.58169; highly expressed in cancer, ri; blad; diag
410048; W76467; Hs.343874; proline oxidase homolog; test; s.m.
410076; T05387; Hs.7991; ESTs; lung, pros; diag
410079; U94362; Hs.380757; glycogenin 2; mela; diag
410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; pros; diag
410102; AW248508; Hs.279727; ESTs; homologue of PEM-3 [Cion; ovar, breast, blad, lung, angio, sarc; diag
410174; AA306007; Hs.59461; DKFZP434C245 protein; mela; diag
410240; AL157424; Hs.61289; synaptojanin 2; angio; diag
410247; AF181721; Hs.61345; RU2S; ovar; CTL+s.m.
410268; AA316181; Hs.61635; six transmembrane epithelial a; panc, pros, EWS; mAb+CTL
410290; AA402307; Hs.322844; hypothetical protein DKFZp564A; mela; diag
410310; J02931; Hs.62192; coagulation factor III (thromb; pros, panc; mAb
410361; BE391804; Hs.62661; guanylate binding protein 1, i; mela, esoph, hepC, fibro, uter; diag
410438; AW748012; Hs.45207; hypothetical protein KIAA1335; lung; CTL+s.m.
410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; breast, colon, uter, stom; diag
410480; R97457; Hs.63984; cadherin 13, H-cadherin (heart; angio; mAb
410491; AA465131; Hs.64001; Homo sapiens clone 25218 mRNA ; mela, esoph; diag
410530; M25809; Hs.64173; ATPase, H transporting, lysoso; ovar; mAb
410553; AW016824; Hs.272068; hypothetical protein MGC14128; blad, lung; diag
410555; U92649; Hs.380136; a disintegrin and metalloprote; leuk, lung; mAb
410561; BE540255; Hs.6994; Homo sapiens cDNA: FLJ22044 fi; lung; diag
410566; AA373210; Hs.43047; Homo sapiens cDNA FLJ13585 fis; panc; diag
410600; AW575742; Hs.351676; ESTs, Moderately similar to S6; mela; mAb+s.m.
410621; AA194329; Hs.172004; titin; sarc; diag
410681; AW246890; Hs.65425; calbindin 1, (28kD); lung; diag
410687; U24389; Hs.65436; lysyl oxidase-like 1; panc; diag
410733; D84284; Hs.66052; CD38 antigen (p45); pros; mAb+CTL
410763; AF279145; Hs.8966; hypothetical protein FLJ21776; panc; mAb
410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; test; CTL+s.m.
410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); panc; diag
410870; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
410883; D43767; Hs.66742; CCL17 chemokine (TARC) (SCYA1; leuk; diag

410889; X91662; Hs.66744; twist (Drosophila) homolog (ac; sarc; CTL+s.m.
410929; H47233; Hs.30643; ESTs; ovar, test; diag
411078; AI222020; Hs.182364; CocoaCrisp; pros, glio, breast; diag
411089; AA456454; Hs.214291; cell division cycle 2-like 1 (; lung, fibro; CTL+s.m.
411243; AB039866; Hs.69319; CA11; esoph; diag
411248; AA551538; Hs.69321; Homo sapiens cDNA FLJ14408 fis; blad; diag
411257; AA628967; Hs.115274; Indian hedgehog protein (IHH) ; ovar; diag
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centro; lung, blad, headnk; CTL+s.m.
411296; BE207307; Hs.10114; growth suppressor 1; sarc; diag
411358; R47479; Hs.94761; KIAA1691 protein; mela,renal, sarc; mAb
411388; X72925; Hs.69752; desmocollin 1; headnk, mela; mAb
411393; AW797437; Hs.69771; B-factor, properdin (COMPLEMEN; ovar; diag
411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); panc, pros, stom, breast, uter, cerv, ovar; mAb
411573; AB029000; Hs.70823; KIAA1077 protein; panc, headnk, lung, stom; diag
411579; AC005258; Hs.70830; U6 snRNA-associated Sm-like pr; lung; diag
411732; U47924; Hs.71642; guanine nucleotide binding pro; lung; diag
411768; NM_013371; Hs.71979; interleukin 19; ovar, uter, cerv; diag
411789; AF245505; Hs.72157; Adlican; breast, panc, lung, stom, headnk, ovar, uter, esoph, sarc; diag
411825; AK000334; Hs.352415; solute carrier family 39 (zinc; colon, ovar; mAb
411828; AW161449; Hs.72290; wingless-type MMTV integration; ovar; diag
411869; W20027; Hs.23439; ESTs; angio; diag
411874; AA096106; Hs.20403; ESTs; blad; diag
411880; AW672477; ; gb:hm30f03.x1 NCI_CGAP_Thy4 Ho; blad; diag
411945; AL033527; Hs.92137; L-myc-2 protein (MYCL2); blad, ovar; CTL+s.m.
412006; AW451618; Hs.380683; ESTs; sarc; diag
412026; AA383618; Hs.73073; testis-specific ankyrin motif ; test; diag
412045; AA099802; Hs.83883; transmembrane, prostate androg; pros; mAb+s.m.
412099; U64198; Hs.73165; interleukin 12 receptor, beta ; leuk, mela; mAb
412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN; panc, fibro; diag
412115; AK001763; Hs.73239; hypothetical protein FLJ10901; lung, blad; CTL+s.m.
412116; AW402166; Hs.784; Epstein-Barr virus induced gen; panc; mAb
412133; U83460; Hs.380728; solute carrier family 31 (copp; pros; mAb
412228; AW503785; Hs.73792; complement component (3d/Epste; mela; mAb
412247; AF022375; Hs.73793; vascular endothelial growth fa; renal, glio, blad, colon; diag
412265; AA101325; Hs.86154; hypothetical protein FLJ12457; test; CTL+s.m.
412326; R07566; Hs.73817; small inducible cytokine A3 (h; pros, leuk; diag
412351; AL135960; Hs.73828; T-cell acute lymphocytic leuke; angio; CTL+s.m.
412420; AL035668; Hs.73853; bone morphogenetic protein 2; blad, glio, lung, stom, angio; diag
412448; L12964; Hs.73895; tumor necrosis factor receptor; leuk; mAb
412471; M63193; Hs.73946; endothelial cell growth factor; cerv, mela, esoph; diag
412490; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 fi; mela; diag
412519; AA196241; Hs.73980; troponin T1, skeletal, slow; sarc; diag
412530; AA766268; Hs.266273; hypothetical protein FLJ13346; blad, lung; diag
412564; X83703; Hs.355934; cardiac ankyrin repeat protein; angio; diag
412580; AA113262; Hs.17901; similar to CABLES [Homo sapien; mela; diag
412610; X90908; Hs.74126; fatty acid binding protein 6, ; blad; diag
412661; N32860; Hs.24611; ESTs, Weakly similar to I54374; blad; CTL+s.m.
412715; NM_000947; Hs.74519; primase, polypeptide 2A (58kD); pros; s.m.
412723; AA648459; Hs.335951; hypothetical protein AF301222; lung, blad, headnk, colon, stom, uter; diag
412755; BE144306; Hs.179891; ESTs, Weakly similar to P4HA_H; angio; s.m.
412811; H06382; Hs.349705; ESTs; lung; diag
412817; AL037159; Hs.74619; proteasome (prosome, macropain; lung; s.m.
412843; AF007555; Hs.74624; protein tyrosine phosphatase, ; pros; mAb
412856; BE386745; Hs.74631; basigin (OK blood group); mela; mAb
412926; AI879076; Hs.75061; macrophage myristoylated alani; mela; CTL+s.m.
412939; AW411491; Hs.75069; eukaryotic translation elongat; mela, renal; diag
412970; AB026436; Hs.177534; dual specificity phosphatase 1; breast, mela; s.m.
412986; X81120; Hs.75110; cannabinoid receptor 1 (brain); glio; mAb
413004; T35901; Hs.75117; interleukin enhancer binding f; lung; diag
413011; AW068115; Hs.821; biglycan; lung; CTL+s.m.
413049; NM_002151; Hs.823; hepsin (transmembrane protease; pros; mAb
413095; AA494359; Hs.30715; potassium voltage-gated channe; panc, stom, renal, colon; mAb+s.m.
413125; BE244589; Hs.75207; glyoxalase I; pros; s.m.
413126; AW419203; Hs.174174; ESTs; angio; diag
413129; AF292100; Hs.104613; RP42 homolog; lung; diag
413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent; angio; CTL+s.m.
413142; M81740; Hs.75212; ornithine decarboxylase 1; lung; s.m.
413163; Y00815; Hs.75216; protein tyrosine phosphatase, ; pros; mAb
413171; AA318325; Hs.75219; tyrosinase-related protein 1; mela; mAb
413190; AA151802; Hs.40368; adaptor-related protein comple; mela; diag
413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis; esoph, cerv; diag
413223; AI732182; Hs.191866; ESTs; lung; diag
413268; AL039079; Hs.75256; regulator of G-protein signall; headnk; CTL+s.m.
413281; AA861271; Hs.222024; transcription factor BMAL2; lung, blad, headnk, panc, angio; diag
413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; test; s.m.
413328; Y15723; Hs.75295; guanylate cyclase 1, soluble, ; pros; s.m.
413335; AI613318; Hs.48442; ESTs; ovar; diag
413364; BE536218; Hs.137516; fidgetin-like 1; lung; diag
413372; H55532; Hs.349695; tubulin, alpha 2; test; diag
413435; X51405; Hs.75360; carboxypeptidase E; pros, glio, panc, sarc; diag
413436; AF238083; Hs.68061; sphingosine kinase 1; sarc; s.m.
413472; BE242870; Hs.75379; solute carrier family 1 (glial; glio; mAb
413566; AW604451; Hs.381153; sprouty (Drosophila) homolog 4; sarc; CTL+s.m.

413573; AI733859; Hs.149089; ESTs; lung; diag
413582; AW295647; Hs.71331; hypothetical protein MGC5350; lung; diag
413597; AW302885; Hs.117183; ESTs; pros; diag
413623; AA825721; Hs.246973; intron of Bicaudal D homolog 1; ovar, pros; diag
413691; AB023173; Hs.75478; ATPase, Class VI, type 11B; lung; mAb
413711; AW291765; Hs.75486; heat shock transcription facto; renal; diag
413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD; lung, blad, headnk, panc, cerv, esoph, colon; diag
413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); test; diag
413778; AA090235; Hs.75535; myosin, light polypeptide 2, r; sarc; diag
413794; AF234532; Hs.61638; myosin X; mela; diag
413804; T64682; ; gb:yc48b02.r1 Stratagene liver; blad; diag
413808; J00287; Hs.350038; Homo sapiens mRNA for caldesmo; esoph; diag
413813; M96956; Hs.75561; teratocarcinoma-derived growth; colon; diag
413833; Z15005; Hs.75573; centromere protein E (312kD); lung; CTL+s.m.
413842; M29383; Hs.856; interferon, gamma; leuk; diag
413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; fibro, renal; mAb
413880; AI660842; Hs.110915; interleukin 22 receptor; panc, colon; mAb+s.m.
413924; AL119964; Hs.75616; seladin-1; pros, breast, ovar; diag
413943; AW294416; Hs.144687; Homo sapiens cDNA FLJ12981 fis; blad, lung; CTL+s.m.
413985; AI018666; Hs.75667; synaptophysin; glio, sarc; mAb
414004; AA737033; Hs.7155; ESTs, Moderately similar to 21; panc, mela; diag
414020; NM_002984; Hs.75703; CCL4 Chemokine (C-C motif) lig; pros; diag
414034; U89277; Hs.305985; early development regulator 1 ; test; CTL+s.m.
414035; Y00630; Hs.75716; serine (or cysteine) proteinas; lung, cerv, headnk, blad; s.m.
414053; BE391635; Hs.75725; transgelin 2; blad; diag
414061; NM_000699; Hs.300280; amylase, alpha 2A; pancreatic; ovar; diag
414065; AW515373; Hs.271249; Homo sapiens cDNA FLJ13580 fis; pros; diag
414085; AA114016; Hs.75746; aldehyde dehydrogenase 1 famil; pros, panc, sarc; s.m.
414142; AW368397; Hs.334485; hemicentin (fibulin 6); fibro, panc, sarc; diag
414161; AA136106; Hs.184852; KIAA1553 protein; test; diag
414166; AW888941; Hs.75789; N-myc downstream regulated; pros, renal; diag
414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fi; glio; diag
414219; W20010; Hs.75823; ALL1-fused gene from chromosom; sarc; diag
414221; AW450979; ; gb:UI-H-BI3-ala-a-12-0-UI.s1 N; blad; diag
414251; AL042306; Hs.97689; VASA protein; test; CTL+s.m.
414259; W44633; Hs.301296; integrin, beta-like 1 (with EG; panc; diag
414334; AA824298; Hs.21331; hypothetical protein FLJ10036; test; diag
414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadher; breast, ovar, uter, pros, colon, panc, sarc; mAb
414368; W70171; Hs.75939; uridine monophosphate kinase; lung; s.m.
414386; X00442; Hs.75990; haptoglobin; ovar; diag
414416; AW409985; Hs.76084; hypothetical protein MGC2721; blad, lung; CTL+s.m.
414420; AA043424; Hs.76095; immediate early response 3; panc, colon; diag
414430; AI346201; Hs.76118; ubiquitin carboxyl-terminal es; lung; s.m.
414443; AU077268; Hs.76144; platelet-derived growth factor; sarc, panc, headnk; mAb
414476; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
414477; U41635; Hs.76228; amplified in osteosarcoma; sarc; diag
414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antig; mela; mAb
414521; D28124; Hs.76307; neuroblastoma, suppression of ; breast, ovar, uter, pros, blad, panc, colon, stom, fibr; diag
414565; AA502972; Hs.183390; hypothetical protein FLJ13590; pros; diag
414569; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
414575; H11257; Hs.375743; Homo sapiens clone IMAGE:45193; renal; diag
414595; AA641726; Hs.289015; hypothetical protein MGC4171; blad; diag
414602; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; pros; mAb
414683; S78296; Hs.76888; hypothetical protein MGC12702; blad, lung, test; diag
414732; AW410976; Hs.77152; minichromosome maintenance def; test, blad; diag
414761; AU077228; Hs.77256; enhancer of zeste (Drosophila); lung, blad, test; CTL+s.m.
414776; AA155598; Hs.212839; hypothetical protein FLJ14195;; angio; diag
414786; AI246482; Hs.243010; Homo sapiens cDNA FLJ14372 fis; angio; diag
414799; AI752416; Hs.77326; insulin-like growth factor bin; renal; diag
414806; D14694; Hs.77329; phosphatidylserine synthase 1; lung; mAb
414807; AI738616; Hs.77348; hydroxyprostaglandin dehydroge; blad; s.m.
414809; AI434699; Hs.77356; transferrin receptor (p90, CD7; lung; mAb+s.m.
414825; X06370; Hs.77432; epidermal growth factor recept; glio, lung, renal, esoph, panc, headnk, leuk ; mAb+s.m.
414915; NM_002462; Hs.76391; myxovirus (influenza) resistan; esoph; diag
414918; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
414921; BE390551; Hs.77628; steroidogenic acute regulatory; breast; diag
414945; BE076358; Hs.77667; lymphocyte antigen 6 complex, ; mela; mAb
414987; AA524394; Hs.294022; hypothetical protein FLJ14950; blad, panc, esoph; diag
414998; NM_002543; Hs.77729; oxidised low density lipoprote; fibro, ovar, panc, colon; mAb
415003; M11437; Hs.77741; kininogen; panc; diag
415025; AW207091; Hs.72307; ESTs; blad; diag
415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Coe; lung, headnk; s.m.
415178; D80503; Hs.46692; ESTs; blad; diag
415214; AI445236; Hs.125124; EphB2; colon, stom; mAb
415314; N88802; Hs.5422; glycoprotein M6B; mela; mAb
415457; AW081710; Hs.7369; Homo sapiens testes specific A; fibro, ovar, uter; CTL+s.m.
415511; AI732617; Hs.182362; ESTs; blad, ovar, renal; diag
415542; R13474; Hs.290263; ESTs, Weakly similar to I38022; blad; diag
415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SM; test; CTL+s.m.
415752; BE314524; Hs.78776; putative transmembrane protein; endo, uter, breast, stom, blad, mela; mAb
415786; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
415787; H01463; Hs.93534; ESTs; pros; diag
415819; AU077330; Hs.360791; transcription elongation facto; test; CTL+s.m.

415829; AW450198; Hs.163742; ESTs; test; diag
415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis; lung, test; diag
415910; U20350; Hs.78913; chemokine (C-X3-C) receptor 1; glio; mAb
415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colo; test; diag
415989; AI267700; Hs.351201; ESTs; pros,ovar, blad, lung, headnk, panc, colon, sarc; diag
415992; C05837; Hs.145807; hypothetical protein FLJ13593; pros, fibro; mAb
415999; AA172179; Hs.294029; ESTs; pros, uter ; diag
416018; AW138239; Hs.78977; proprotein convertase subtilis; colon, panc, lung; diag
416030; H15261; Hs.21948; ESTs; breast, fibro; diag
416065; BE267931; Hs.78996; proliferating cell nuclear ant; blad, lung, headnk, mela; CTL+s.m.
416111; AA033813; Hs.79018; chromatin assembly factor 1, s; lung, stom; CTL+s.m.
416188; BE157260; Hs.79070; v-myc avian myelocytomatosis v; pros; diag
416201; AA467752; Hs.195161; ESTs; test; diag
416208; AW291168; Hs.41295; ESTs, Weakly similar to MUC2_H; lung; diag
416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calc; ovar; diag
416225; AA577730; Hs.188684; ESTs, Weakly similar to PC4259; pros, blad; diag
416350; AF188625; Hs.189507; phospholipase A2, group IID; test, mela, fibro; diag
416370; N90470; Hs.203697; CD38 antigen (p45); pros, glio; mAb+CTL
416373; AA195845; Hs.73680; ESTs, Weakly similar to S12658; sarc; diag
416402; NM_000715; Hs.1012; complement component 4-binding; fibro; diag
416448; L13210; Hs.79339; lectin, galactoside-binding, s; ovar, colon, stom; diag
416498; U33632; Hs.79351; potassium channel, subfamily K; panc, stom, breast, ovar, colon; mAb
416539; Y07909; Hs.79368; epithelial membrane protein 1; pros, headnk; diag
416602; NM_006159; Hs.367895; Protein kinase C-binding prote; breast; diag
416640; BE262478; Hs.13406; neuron-specific protein; mela; diag
416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; blad, lung, headnk, cerv, panc, angio; diag
416773; AK000340; Hs.79828; hypothetical protein FLJ20333; test; CTL+s.m.
416815; U41514; Hs.80120; UDP-N-acetyl-alpha-D-galactosa; angio; s.m.
416819; U77735; Hs.80205; pim-2 oncogene; lung, test; diag
416881; N32520; Hs.141358; ESTs; mela; diag
416929; N20535; Hs.43265; melastatin 1; mela; diag
416975; NM_004131; Hs.1051; granzyme B (granzyme 2, cytoto; mela; s.m.
417003; AL038170; Hs.80756; betaine-homocysteine methyltra; blad; s.m.
417070; Z19077; Hs.172004; titin; sarc; diag
417105; X60992; Hs.81226; CD6 antigen; fibro; mAb
417115; AW952792; Hs.334612; small nuclear ribonucleoprotei; test; CTL+s.m.
417124; BE122762; Hs.25338; ESTs; angio; diag
417148; AA359896; Hs.374554; hypothetical protein FLJ14902; panc; diag
417151; AA194055; Hs.293858; ESTs; blad; diag
417153; X57010; Hs.81343; collagen, type II, alpha 1 (pr; pros, sarc; diag
417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte; lung; mAb+s.m.
417237; H86385; Hs.81737; palmitoyl-protein thioesterase; mela; s.m.
417259; AW903838; Hs.81800; chondroitin sulfate proteoglyc; panc, breast; diag
417275; X63578; Hs.295449; parvalbumin; blad; diag
417295; AW993524; Hs.43148; epithelial membrane protein 1; pros; diag
417308; H60720; Hs.81892; KIAA0101 gene product; lung, headnk, blad, cerv, angio, mela, sarc; diag
417312; AW888411; Hs.250811; leukemia-associated phosphopro; blad; CTL+s.m.
417333; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
417355; D13168; Hs.82002; endothelin receptor type B; glio, mela; mAb
417365; D50683; Hs.82028; transforming growth factor, be; fibro, angio; mAb
417366; BE185289; Hs.1076; small proline-rich protein 1B ; lung, blad, headnk, panc, esoph, mela; diag
417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; fibro, mela; diag
417391; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
417400; AA663486; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
417407; AA923278; Hs.290905; ESTs, Weakly similar to protea; test, pros; s.m.
417409; BE272506; Hs.82109; syndecan 1; blad; diag
417412; X16896; Hs.82112; interleukin 1 receptor, type I; fibro, pros, panc; mAb
417426; NM_002291; Hs.82124; laminin, beta 1; angio; diag
417437; U52682; Hs.82132; interferon regulatory factor 4; mela; CTL+s.m.
417512; X76534; Hs.82226; glycoprotein (transmembrane) n; lung, mela, headnk, panc, breast; mAb
417515; L24203; Hs.82237; ataxia-telangiectasia group D-; lung, headnk, blad; diag
417542; J04129; Hs.82269; progestagen-associated endomet; lung, mela; diag
417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383; test; diag
417599; AA204688; Hs.62954; ESTs; blad, esoph; diag
417621; AV654694; Hs.82316; interferon-induced, hepatitis ; esoph; diag
417696; BE241624; Hs.82401; CD69 antigen (p60, early T-cel; pros; mAb
417705; AW134952; Hs.175220; hypothetical protein FLJ14541; test; mAb
417715; AW969587; Hs.86366; ESTs; blad, lung, headnk; diag
417720; AA205625; Hs.208067; ESTs; blad, lung, esoph, headnk; diag
417750; AI267720; Hs.260523; synovial sarcoma, translocated; sarc; diag
417777; AI823763; Hs.7055; ESTs, Weakly similar to I78885; test; s.m.
417791; AW965339; Hs.44269; ESTs; ovar, blad, lung, headnk; CTL+s.m.
417801; AA417383; Hs.82582; integrin, beta-like 1 (with EG; panc, fibro; diag
417805; U38545; Hs.82587; phospholipase D1, phophatidylc; angio; s.m.
417831; H16423; Hs.82685; CD47 antigen (Rh-related antig; ovar; mAb
417843; W07361; Hs.22545; Homo sapiens cDNA FLJ12935 fis; pros; diag
417847; AI521558; Hs.7331; hypothetical protein FLJ22316; ovar; diag
417849; AW291587; Hs.82733; nidogen 2; angio, headnk; diag
417874; BE616160; Hs.82829; protein tyrosine phosphatase, ; panc; mAb+s.m.
417880; BE241595; Hs.82848; selectin L (lymphocyte adhesio; mela; mAb
417886; AA214584; ; ESTs; test, ovar; diag
417900; BE250127; Hs.82906; CDC20 (cell division cycle 20,; lung, stom, test, blad, headnk, cerv, esoph; CTL+s.m.
417911; AA333387; Hs.82916; chaperonin containing TCP1, su; test; diag

417944; AU077196; Hs.82985; collagen, type V, alpha 2; sarc; diag
417975; AA641836; Hs.30085; hypothetical protein FLJ23186; colon, stom, lung; mAb
417976; BE565892; Hs.83077; interleukin 18 (interferon-gam; colon, stom, fibros; diag
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 famil; lung, headnk, esoph; s.m.
418036; Z37976; Hs.83337; latent transforming growth fac; angio; diag
418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lung, angio, test, sarc; diag
418067; AI127958; Hs.83393; cystatin E/M; headnk, panc, blad; diag
418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUSS; blad; s.m.
418113; AI272141; Hs.83484; SRY (sex determining region Y); blad, breast, uter, colon, lung, ovar, glio, test, sarc; CTL+s.m.
418134; AA397769; Hs.86617; ESTs; test; diag
418140; BE613836; Hs.83551; microfibrillar-associated prot; lung, headnk, esoph, ovar, sarc; diag
418156; W17056; Hs.83623; nuclear receptor subfamily 1, ; fibro; mAb+s.m.
418203; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, test, mela, stom; s.m.
418216; AA662240; Hs.283099; AF15q14 protein; headnk, lung, blad; diag
418245; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
418283; S79895; Hs.83942; cathepsin K (pycnodysostosis); breast, cerv, ovar, uter, pros, headnk, lung, panc, colon, stom; diag
418318; U47732; Hs.84072; transmembrane 4 superfamily me; panc, pros, colon, stom, omuc; mAb
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibi; headnk, lung, blad; s.m.
418338; NM_002522; Hs.84154; neuronal pentraxin I; sarc; diag
418339; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
418345; AJ001696; Hs.241407; serine (or cysteine) proteinas; cerv, lung; s.m.
418371; M13560; Hs.84298; CD74 antigen (invariant polype; renal; mAb
418379; AA218940; Hs.137516; fidgetin-like 1; lung; diag
418394; AF132818; Hs.84728; Kruppel-like factor 5 (intesti; panc; CTL+s.m.
418396; AI765805; Hs.26691; SLC2A12 Solute carrier family ; pros; mAb
418397; NM_001269; Hs.84746; chromosome condensation 1; lung; diag
418399; AF131781; Hs.84753; hypothetical protein FLJ12442; test, blad, sarc; diag
418406; X73501; Hs.84905; cytokeratin 20; blad, colon; diag
418432; M14156; Hs.85112; insulin-like growth factor 1 (; pros, fibro; diag
418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide; fibro; mAb
418462; BE001596; Hs.85266; integrin, beta 4; lung, blad, cerv, headnk, ovar; mAb
418543; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb
418576; AW968159; Hs.302740; Epithelial calcium channel 2, ; pros; mAb+s.m.
418610; AW245993; Hs.32417; hypothetical protein MGC2742; pros; diag
418641; BE243136; Hs.86947; a disintegrin and metalloprote; cerv, lung, panc, blad, headnk, stom; mAb
418655; AA226354; Hs.111240; ESTs; pros; diag
418661; NM_001949; Hs.1189; E2F transcription factor 3; ovar, lung, mela; CTL+s.m.
418663; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk, cerv, esoph; mAb
418683; U90908; Hs.87241; hypothetical protein from clon; angio; CTL+s.m.
418686; Z36830; Hs.87268; annexin A8; blad, lung; diag
418693; AI750878; Hs.87409; thrombospondin 1; angio, panc; diag
418696; AW959433; Hs.326290; hypothetical protein FLJ12581; test; diag
418739; AA310964; Hs.88012; SHP2 interacting transmembrane; mela; diag
418756; AA252254; Hs.226949; ESTs; test ; diag
418825; AA228881; Hs.22394; hypothetical protein FLJ10893; angio; diag
418829; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag
418882; NM_004996; Hs.89433; ATP-binding cassette, sub-fami; ovar, pros, breast, lung; diag
418883; BE387036; Hs.1211; acid phosphatase 5, tartrate r; fibro; s.m.
418888; AU076801; Hs.89436; cadherin 17, LI cadherin (live; colon, stom, ovar, uter, panc; mAb+s.m.
418918; X07871; Hs.89476; CD2 antigen (p50), sheep red b; mela, fibro; mAb
418932; L34059; Hs.89484; cadherin 4, type 1, R-cadherin; glio; mAb
418941; AA452970; Hs.239527; E1B-55kDa-associated protein 5; angio, blad; diag
418968; NM_000078; Hs.89538; cholesteryl ester transfer pro; mela; diag
418994; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, angio; mAb
419038; AW134924; Hs.58290; ESTs; pros; diag
419073; AW372170; Hs.183918; transmembrane receptor Unc5H2 ; ovar, renal, blad, lung; mAb
419078; M93119; Hs.89584; insulinoma-associated 1; blad, lung, panc, sarc; diag
419079; AW014836; Hs.18844; ESTs; esoph, lung, stom, colon; diag
419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fibro; diag
419092; J05581; Hs.89603; mucin 1, transmembrane; breast, panc, lung, blad, fibro; mAb
419222; AD001528; Hs.89718; spermine synthase; pros; s.m.
419223; X60111; Hs.1244; CD9 antigen (p24); breast, pros, ovar; mAb
419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227; fibro; diag
419261; X07876; Hs.89791; wingless-type MMTV integration; panc; diag
419264; AA877104; Hs.293672; ESTs, Weakly similar to ALUB_H; pros; diag
419290; AI128114; Hs.112885; spinal cord-derived growth fac; panc; diag
419356; AI656165; Hs.7331; hypothetical protein FLJ22316; uter, ovar; diag
419359; AL043202; Hs.90073; chromosome segregation 1 (yeas; lung, blad, test; diag
419440; AB020689; Hs.90419; KIAA0882 protein; breast; diag
419485; AA489023; Hs.99807; ESTs, Weakly similar to unname; mela; diag
419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cytoto; fibro; s.m.
419519; AI198719; Hs.176376; ESTs; mela; diag
419551; AW582256; Hs.91011; anterior gradient 2 (Xenepus l; panc, pros, breast; diag
419559; Y07828; Hs.91096; ring finger protein; blad, colon, stom; CTL+s.m.
419568; AB026116; Hs.283078; hOAT4; renal; mAb
419569; AI971651; Hs.91143; jagged 1 (Alagille syndrome); headnk, lung; diag
419628; H67546; Hs.49768; ESTs; mela, sarc; diag
419667; AU077005; Hs.92208; a disintegrin and metalloprote; breast, cerv, angio; mAb
419693; AA133749; Hs.301350; FXYD domain-containing ion tra; pros, breast, ovar, panc, lung; mAb
419721; NM_001650; Hs.315369; aquaporin 4; glio, lung, fibro; mAb
419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA ; blad, headnk; diag
419749; X73608; Hs.93029; sparc/osteonectin, cwcv and ke; pros, panc, lung; diag
419752; AA249573; Hs.152618; ESTs, Moderately similar to ZN; lung; diag

419839; U24577; Hs.93304; phospholipase A2, group VII (p; pros, lung; diag
419870; AW403911; Hs.266175; phosphoprotein associated with; mela; diag
419875; AA853410; Hs.93557; proenkephalin; sarc; diag
419948; AB041035; Hs.93847; NM_016931:Homo sapiens NADPH o; angio; mAb
419956; AL137939; Hs.40096; cadherin 19, type 2; mela; mAb
419968; X04430; Hs.93913; interleukin 6 (interferon, bet; lung, panc, esoph; diag
419981; AA897581; Hs.128773; ESTs; angio; diag
420005; AW271106; Hs.133294; ESTs; lung, test, blad, colon; diag
420062; AW411096; Hs.94785; TGF(beta)-induced transcriptio; test; CTL+s.m.
420067; T52431; Hs.94795; Homo sapiens mRNA; cDNA DKFZp5; sarc; diag
420137; AA306478; Hs.95327; CD3D antigen, delta polypeptid; fibro; mAb
420154; AI093155; Hs.95420; G antigen family C 1 protein (; pros, leio; CTL+s.m.
420174; AI824144; Hs.199749; ESTs; angio; CTL+s.m.
420208; BE276055; Hs.95972; silver (mouse homolog) like; mela, sarc; mAb
420209; AA256444; Hs.126485; hypothetical protein FLJ12604;; angio; diag
420218; AW958037; Hs.381105; ribosomal protein L4; mela, pros; diag
420255; NM_007289; Hs.1298; membrane metallo-endopeptidase; pros; mAb
420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadheri; angio, fibro; mAb
420267; N37030; Hs.173337; ESTs; mela, sarc; diag
420281; AI623693; Hs.323494; Predicted cation efflux pump; lung, blad, ovar, panc; mAb
420301; AA767526; Hs.22030; paired box gene 5 (B-cell line; mela; diag
420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339,; mela; mAb
420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide; fibro; mAb
420344; BE463721; Hs.97101; putative G protein-coupled rec; colon, pros, blad, headnk, panc, stom, ovar; mAb
420347; AL033539; Hs.97124; Human DNA sequence from clone ; test; diag
420360; U83171; Hs.97203; small inducible cytokine subfa; leuk; diag
420367; AA259090; Hs.257028; ESTs; test; diag
420376; AL137471; Hs.97266; protocadherin 18; sarc; mAb+s.m.
420378; NM_014143; Hs.97269; B7-H1 protein; leuk; mAb
420380; AA640891; Hs.102406; ESTs; lung; diag
420424; AB033036; Hs.97594; KIAA1210 protein; pros; diag
420462; AF050147; Hs.97932; chondromodulin I precursor; lung, EWS, sarc; mAb
420474; L09753; Hs.1313; tumor necrosis factor (ligand); leuk; mAb
420544; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
420576; AA297634; Hs.54925; KIAA1858 protein; sarc; diag
420596; NM_002692; Hs.99185; polymerase (DNA directed), eps; test; CTL+s.m.
420633; NM_014581; Hs.274480; odorant-binding protein 2B (OB; breast, endo; diag
420656; AA279098; Hs.187636; ESTs; fibro; diag
420710; NM_007009; Hs.99875; zona pellucida binding protein; test; diag
420729; AW964897; Hs.290825; ESTs; pros; diag
420757; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
420759; T11632; Hs.127797; Homo sapiens cDNA FLJ11381 fis; test; diag
420783; AI659838; Hs.99923; lectin, galactoside-binding, s; lung, blad, headnk; diag
420789; AI670057; Hs.199882; ESTs; renal,; diag
420859; AW468397; Hs.100000; S100 calcium-binding protein A; sarc; diag
420908; AL049974; Hs.100261; Homo sapiens mRNA; cDNA DKFZp5; panc; diag
420923; AF097021; Hs.273321; differentially expressed in he; blad, colon; diag
420931; AF044197; Hs.100431; small inducible cytokine B sub; breast, lung, mela; diag
420981; L40904; Hs.100724; peroxisome proliferative activ; colon; mAb+s.m.
421016; AA504583; Hs.101047; transcription factor 3 (E2A im; test; CTL+s.m.
421044; AF061871; Hs.101302; Human DNA sequence from clone ; panc; diag
421059; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
421064; AI245432; Hs.101382; tumor necrosis factor, alpha-i; blad, uter; diag
421070; AA283185; Hs.19327; ESTs; blad; diag
421100; AW351839; Hs.124660; Homo sapiens cDNA: FLJ21763 fi; blad; diag
421133; AA814971; Hs.26410; ESTs; lung; diag
421154; AA284333; Hs.287631; Homo sapiens cDNA FLJ14269 fis; BPH; diag
421155; H87879; Hs.102267; lysyl oxidase; headnk, panc, renal, sarc; diag
421218; NM_000499; Hs.72912; cytochrome P450, subfamily I (; blad, angio; diag
421233; AA209534; Hs.284243; tetraspan NET-6 protein; pros, breast, ovar; mAb
421241; X91817; Hs.102866; transketolase-like 1; test; s.m.
421302; T34462; Hs.103291; neuritin; uter, endo ; diag
421305; BE397354; Hs.324830; diptheria toxin resistance pro; ovar; diag
421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, lung, angio, test, sarc; diag
421341; AJ243212; Hs.279611; deleted in malignant brain tum; panc, lung; diag
421350; AW301608; Hs.278188; ESTs, Moderately similar to I5; test; diag
421373; AA808229; Hs.222088; ESTs; blad; diag
421433; AI829192; Hs.22380; ESTs; pros; diag
421451; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
421458; NM_003654; Hs.104576; carbohydrate (keratan sulfate ; sarc; s.m.
421478; AI683243; Hs.97258; ESTs, Moderately similar to S2; ovar, blad, renal, uter; diag
421481; AW391972; Hs.104696; KIAA1324 protein; pros; diag
421502; AF111856; Hs.105039; solute carrier family 34 (sodi; ovar, fibro; mAb
421506; BE302796; Hs.105097; thymidine kinase 1, soluble; lung, headnk, esoph; s.m.
421508; NM_004833; Hs.105115; absent in melanoma 2; blad, esoph, lung, mela; CTL+s.m.
421535; AB002359; Hs.105478; phosphoribosylformylglycinamid; test; s.m.
421537; BE383488; Hs.105547; neural proliferation, differen; pros; diag
421566; NM_000399; Hs.1395; early growth response 2 (Krox-; pros; CTL+s.m.
421579; NM_002975; Hs.105927; stem cell growth factor; lymph; sarc; mAb
421633; AF121860; Hs.106260; sorting nexin 10; mela; diag
421650; AA781795; Hs.343800; ESTs; mela; diag
421666; AL035250; Hs.1408; endothelin 3; mela; diag
421727; Y13153; Hs.107318; kynurenine 3-monooxygenase (ky; breast; s.m.

421773; W69233; Hs.112457; ESTs; mela, esoph, sarc; diag
421777; BE562088; Hs.108196; HSPC037 protein; esoph, cerv, lung; diag
421779; AI879159; Hs.108219; wingless-type MMTV integration; colon, ovar; diag
421798; N74880; Hs.355462; N-acylsphingosine amidohydrola; fibro; s.m.
421814; L12350; Hs.108623; thrombospondin 2; panc; diag
421831; AA298836; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
421887; AW161450; Hs.109201; CGI-86 protein; pros; mAb
421896; N62293; Hs.45107; ESTs; pros; diag
421917; AB028943; Hs.109445; KIAA1020 protein; test; diag
421920; BE551245; Hs.1438; gamma-aminobutyric acid (GABA); sarc; mAb
421924; BE514514; Hs.109606; coronin, actin-binding protein; fibro; diag
421948; L42583; Hs.334309; keratin 6A; lung, headnk, blad, esoph, cerv, mela; diag
421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); fibro; diag
421991; NM_014918; Hs.110488; KIAA0990 protein; panc; diag
421996; AW583807; Hs.1460; glucagon; panc; diag
422002; X70070; Hs.110642; neurotensin receptor 1 (high a; colon; mAb
422027; AL043100; Hs.288828; fatty acid amide hydrolase; pros; s.m.
422033; AW245805; Hs.110903; claudin 5 (transmembrane prote; glio; mAb
422087; X58968; Hs.111301; matrix metalloproteinase 2 (ge; sarc; diag
422089; AA523172; Hs.103135; ESTs, Weakly similar to SFR4_H; pros; diag
422094; AF129535; Hs.272027; F-box only protein 5; blad, lung; CTL+s.m.
422095; AI868872; Hs.282804; hypothetical protein FLJ22704; lung, panc, ovar, breast; CTL+s.m.
422099; AA156022; Hs.111518; hypothetical protein; angio; CTL+s.m.
422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; lung, esoph; CTL+s.m.
422110; AI376736; Hs.121555; secreted protein, acidic, cyst; panc; diag
422119; AI277829; Hs.111862; KIAA0590 gene product; blad; diag
422134; AW179019; Hs.112110; mitochondrial ribosomal protei; lung; diag
422152; AA909249; Hs.112282; solute carrier family 30 (zinc; blad; mAb+s.m.
422163; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
422164; NM_014312; Hs.112377; cortic al thymocyte receptor (; blad; mAb+s.m.
422168; AA586894; Hs.112408; S100 calcium-binding protein A; lung, blad, headnk, breast, mela, esoph, sarc, cerv; CTL+s.m.
422170; AI791949; Hs.112432; anti-Mullerian hormone; uter, blad; diag
422173; BE385828; Hs.250619; phorbolin-like protein MDS019 ; mela; diag
422247; U18244; Hs.113602; solute carrier family 1 (high ; blad; mAb
422278; AF072873; Hs.114218; frizzled (Drosophila) homolog ; ovar, headnk, blad, cerv, lung, panc, stom; mAb
422309; U79745; Hs.114924; solute carrier family 16 (mono; mela; mAb+s.m.
422311; AF073515; Hs.114948; cytokine receptor-like factor ; lung, fibro; diag
422355; AW403724; Hs.300697; coagulation factor VII (serum ; fibro; diag
422363; T55979; Hs.115474; replication factor C (activato; mela, colon; diag
422398; AI476149; Hs.334489; hypothetical protein FLJ21992; fibro; CTL+s.m.
422406; AF025441; Hs.116206; Opa-interacting protein 5; blad, lung; diag
422420; U03398; Hs.1524; tumor necrosis factor (ligand); colon, panc, stom, leuk; mAb
422423; AF283777; Hs.116481; CD72 antigen; spleen, leuk; mAb
422440; NM_004812; Hs.116724; aldo-keto reductase family 1, ; lung, headnk; s.m.
422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; lung, headnk, panc, sarc; diag
422532; AL008726; Hs.118126; protective protein for beta-ga; renal, mela; s.m.
422565; BE259035; Hs.118400; singed (Drosophila)-like (sea ; panc, test, mela; diag
422573; AW297985; Hs.295726; integrin, alpha V (vitronecti; panc; mAb+s.m.
422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetas; esoph, mela; s.m.
422603; BE242587; Hs.118651; hematopoietically expressed ho; angio; CTL+s.m.
422633; X56832; Hs.118804; enolase 3, (beta, muscle); sarc; s.m.
422658; AF231981; Hs.250175; homolog of yeast long chain po; pros; diag
422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 C; test; diag
422726; U11690; Hs.1572; faciogenital dysplasia (Aarsko; test; diag
422728; AW937826; Hs.103262; MAD (mothers against decapenta; pros; diag
422789; AK001113; Hs.120842; hypothetical protein FLJ10251; test; CTL+s.m.
422835; BE218705; Hs.121378; metallothionein-like 5, testis; breast; diag
422871; AI031228; Hs.121509; collagen, type XI, alpha 2; sarc; diag
422887; AI751848; Hs.49215; ESTs; sarc; CTL+s.m.
422938; NM_001809; Hs.1594; centromere protein A (17kD); lung, test; CTL+s.m.
422963; M79141; Hs.13234; ESTs; lung, panc; diag
422997; BE018212; Hs.122908; DNA replication factor; test; CTL+s.m.
423017; AW178761; Hs.227948; serine (or cysteine) proteinas; blad, headnk, mela; mAb+diag
423052; M28214; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
423189; M59371; Hs.171596; EphA2; colon, ovar; mAb
423196; AK001866; Hs.125139; hypothetical protein FLJ11004; fibro; CTL+s.m.
423198; M81933; Hs.1634; cell division cycle 25A; test; CTL+s.m.
423201; NM_000163; Hs.125180; growth hormone receptor; pros; mAb
423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung, esoph; diag
423271; W47225; Hs.126256; interleukin 1, beta; blad, stom, esoph; diag
423309; BE006775; Hs.126782; sushi-repeat protein; lung, colon; diag
423354; AB011130; Hs.127436; calcium channel, voltage-depen; test, fibro; mAb
423387; AJ012074; Hs.348500; vasoactive intestinal peptide ; pros; mAb
423397; NM_001838; Hs.1652; chemokine (C-C motif) receptor; blad, mela; mAb
423412; AF109300; Hs.351615; prostate cancer associated pro; pros; diag
423422; AC005175; Hs.128425; NY-REN-24 antigen; glio; mAb+CTL
423445; NM_014324; Hs.128749; alpha-methylacyl-CoA racemase; pros; s.m.
423453; AW450737; Hs.128791; CGI-09 protein; lung; CTL+s.m.
423458; AI204212; Hs.351113; ESTs; test; CTL+s.m.
423511; AF036329; Hs.129715; gonadotropin-releasing hormone; lung; diag
423515; AA327017; Hs.176594; ESTs; ovar; diag
423541; AA296922; Hs.129778; serine protease inhibitor, Kaz; colon, panc; diag
423575; C18863; Hs.163443; intron of periostin (OSF-2os); headnk, breast, panc, lung, fibro, esoph; diag

423605; AF047826; Hs.129887; cadherin 19, type 2; mela; mAb
423642; AW452650; Hs.157148; hypothetical protein MGC13204; lung; diag
423662; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc ; lung; diag
423685; BE350494; Hs.49753; uveal autoantigen with coiled ; panc, uter, colon; CTL+s.m.
423725; AJ403108; Hs.132127; hypothetical protein LOC57822; lung, headnk, blad; diag
423739; AA398155; Hs.97600; ESTs; breast, ovar, panc; diag
423761; NM_006194; Hs.132576; paired box gene 9; headnk; CTL+s.m.
423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840; test; diag
423778; Y09267; Hs.132821; flavin containing monooxygenas; fibro; s.m.
423779; AW071837; Hs.57971; TRANSCRIPTION FACTOR HES-5; glio; diag
423787; AJ295745; Hs.236204; nuclear pore complex protein; test, esoph; diag
423798; AF047033; Hs.132904; solute carrier family 4, sodiu; angio; mAb
423799; AW026300; Hs.132906; 19A24 protein; mela; mAb
423849; AL157425; Hs.133315; Homo sapiens mRNA; cDNA DKFZp7; lung; diag
423887; AL080207; Hs.134585; DKFZP434G232 protein; headnk, lung; diag
423899; NM_001427; Hs.134989; engrailed homolog 2; mela; CTL+s.m.
423905; AW579960; Hs.135150; lung type-I cell membrane-asso; test; mAb
423909; AJ223183; Hs.135194; immunoglobulin superfamily, me; test; diag
423934; U89995; Hs.159234; forkhead box E1 (thyroid trans; lung; CTL+s.m.
424001; W67883; Hs.137476; paternally expressed 10; breast, ovar; diag
424012; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk, esoph; diag
424036; AA770686; Hs.348495; H2A histone family, member L; panc, ovar; CTL+s.m.
424054; AA334511; Hs.26638; membrane-spanning 4-domains, s; pros, fibro; mAb
424078; AB006625; Hs.139033; paternally expressed 3; ovar, uter; CTL+s.m.
424081; NM_006413; Hs.139120; ribonuclease P (30kD); test; s.m.
424098; AF077374; Hs.139322; small proline-rich protein 3; lung, blad, headnk, esoph, cerv; diag
424125; M31669; Hs.1735; inhibin, beta B (activin AB be; ovar, pros; diag
424144; AA454033; Hs.41644; AKAP-associated sperm protein; fibro; diag
424153; AA451737; Hs.141496; MAGE-like 2; mela; CTL+s.m.
424165; AW582904; Hs.142255; islet amyloid polypeptide; panc; mAb
424212; NM_005814; Hs.143131; glycoprotein A33 (transmembran; colon, stom, ovar; mAb
424218; AF031824; Hs.143212; cystatin F (leukocystatin); mela, fibro; diag
424244; AV647184; Hs.143601; hypothetical protein hCLA-iso; blad; diag
424252; AK000520; Hs.143811; hypothetical protein FLJ20513; colon, stom; diag
424264; D80400; Hs.239388; Human DNA sequence from clone ; blad; mAb
424308; AW975531; Hs.154443; minichromosome maintenance def; blad, lung, test; diag
424310; AA338648; Hs.50334; testes development-related NYD; fibro; diag
424332; AA338919; Hs.101615; ESTs; pros; diag
424339; BE257148; Hs.145416; endoglycan; pros, lung; diag
424343; AW956360; Hs.4748; adenylate cyclase activating p; glio, ovar, uter; mAb
424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763; lung, blad, headnk, cerv; diag
424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast, uter, headnk; diag
424420; BE614743; Hs.146688; prostaglandin E synthase; lung, blad; s.m.
424440; AA340743; Hs.133208; ESTs; sarc; diag
424441; X14850; Hs.147097; H2A histone family, member X; lung; diag
424450; AL137526; Hs.147472; dynein intermediate chain 2; fibro; diag
424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 9; breast, cerv, ovar, uter, blad, colon, stom; s.m.
424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374; fibro; diag
424578; AK001973; Hs.150890; hypothetical protein; test; CTL+s.m.
424581; M62062; Hs.150917; catenin (cadherin-associated p; glio, ovar, uter; mAb+s.m.
424586; NM_003401; Hs.150930; X-ray repair complementing def; panc; CTL+s.m.
424629; M90656; Hs.151393; glutamate-cysteine ligase, cat; lung; CTL+s.m.
424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 fis; glio; diag
424676; Y08565; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
424704; AI263293; Hs.152096; cytochrome P450, subfamily IIJ; renal; s.m.
424711; NM_005795; Hs.152175; calcitonin receptor-like; angio; mAb
424717; H03754; Hs.152213; wingless-type MMTV integration; blad, lung, headnk; diag
424800; AL035588; Hs.153203; MyoD family inhibitor; test, pros; diag
424806; AA382523; Hs.105689; MSTP031 protein; anglo; mAb
424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad, ovar, headnk, esoph, cerv, uter; diag
424846; AU077324; Hs.1832; neuropeptide Y; pros; diag
424897; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
424902; NM_003866; Hs.153687; inositol polyphosphate-4-phosp; panc, leuk, mela; CTL+s.m.
424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni; mela, colon; CTL+s.m.
424971; AA479005; Hs.154036; tumor suppressing subtransfera; panc, mela; CTL+s.m.
424998; U58515; Hs.154138; chitinase 3-like 2; glio; diag
425023; AW956889; Hs.154210; EDG-1 (endothelial differenti; angio; mAb
425048; H05468; Hs.164502; ESTs; lung, blad; diag
425057; AA826434; Hs.1619; achaete-scute complex (Drosoph; glio, lung; CTL+s.m.
425088; AA663372; Hs.169395; hypothetical protein FLJ12015; glio, mela; diag
425154; NM_001851; Hs.154850; collagen, type IX, alpha 1; sarc; diag
425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase; lung, test; s.m.
425200; BE255203.comp; Hs.155101; ATP synthase, H transporting, ; panc; s.m.
425206; NM_002153; Hs.155109; hydroxysteroid (17-beta) dehyd; blad; mAb
425211; M18667; Hs.1867; progastricsin (pepsinogen C); fibro, esoph, pros; diag
425234; AW152225; Hs.165909; ESTs, Weakly similar to I38022; lung, angio, blad, mela; diag
425235; AA353113; Hs.105468; Homo sapiens cDNA: FLJ22743 fi; angio; diag
425237; U07695; Hs.155227; EphB4; test; mAb
425245; AI751768; Hs.155314; KIAA0095 gene product; lung; diag
425259; AL049280; Hs.145010; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
425262; D87119; Hs.155418; GS3955 protein; mela, renal; CTL+s.m.
425266; J00077; Hs.155421; alpha-fetoprotein; lung; diag
425274; BE281191; Hs.155462; minichromosome maintenance def; test; diag

425289; AW139342; Hs.155530; Interferon, gamma-inducible pr; mela; CTL+s.m.
425308; M97639; Hs.155585; receptor tyrosine kinase-like ; pros, sarc; mAb
425367; BE271188; Hs.155975; protein tyrosine phosphatase, ; fibro; diag
425371; D49441; Hs.155981; mesothelin; ovar, lung, fibro; mAb
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (; lung, blad, panc, angio, test, mela, esoph; CTL+s.m.
425427; AI652662; Hs.317432; branched chain aminotransferas; test; s.m.
425428; AL110261; Hs.157211; DKFZP586B0621 protein; panc; diag
425465; L18964; Hs.1904; protein kinase C, iota; ovar, pros, colon; s.m.
425525; AA356883; Hs.23871; ESTs; sarc; diag
425545; N98529; Hs.158295; Homo sapiens, clone MGC:12401,; sarc; diag
425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fi; fibro; CTL+s.m.
425572; AB011076; Hs.158307; undifferentiated embryonic cel; test; CTL+s.m.
425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; test; CTL+s.m.
425606; U52112; Hs.158331; renin-binding protein; mela; diag
425628; NM_004476; Hs.1915; folate hydrolase (prostate-spe; pros; s.m.
425638; NM_012337; Hs.158450; nasopharyngeal epithelium spec; fibro; CTL+s.m.
425679; X05997; Hs.159177; lipase, gastric; esoph; s.m.
425692; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
425695; NM_005401; Hs.159238; protein tyrosine phosphatase, ; lung; mAb+s.m.
425709; AA383076; Hs.159274; outer dense fibre of sperm tai; test; diag
425710; AF030880; Hs.159275; solute carrier family, member ; pros; mAb
425722; AI659076; Hs.97031; hypothetical protein MGC13047; mela; diag
425726; AF085808; Hs.159330; uroplakin 3; pros, blad; diag
425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA,; test; diag
425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohor; test; diag
425849; AJ000512; Hs.296323; serum/glucocorticoid regulated; lung, headnk; s.m.
425921; NM_007231; Hs.162211; solute carrier family 6 (neuro; stom, panc; mAb
425976; C75094; Hs.334514; NG22 protein; pros, ovar; mAb
426027; NM_002608; Hs.1976; platelet-derived growth factor; sarc; diag
426050; AF017307; Hs.166096; E74-like factor 3 (ets domain ; ovar, blad, stom; CTL+s.m.
426059; BE292842; Hs.166120; interferon regulatory factor 7; esoph, cerv; CTL+s.m.
426067; AW664691; Hs.97053; ESTs; lung; diag
426088; AF038007; Hs.166196; ATPase, Class I, type 8B, memb; blad, lung; mAb
426094; AF034611; Hs.166206; cubilin (intrinsic factor-coba; renal; diag
426116; AA868729; Hs.144694; ESTs; fibro; diag
426125; X87241; Hs.166994; FAT tumor suppressor (Drosophi; colon, stom, panc, pros, renal, fibro, cerv; mAb
426156; BE244537; Hs.167382; natriuretic peptide receptor A; ovar; mAb
426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic ; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; diag
426172; AA371307; Hs.125056; ESTs; pros; diag
426174; AA547959; Hs.115838; Homo sapiens similar to Echino; breast, pros, fibro; diag
426212; S71824; Hs.167988; neural cell adhesion molecule ; glio; mAb
426271; AF026547; Hs.169047; chondroitin sulfate proteoglyc; glio; diag
426274; D38122; Hs.2007; tumor necrosis factor (ligand); fibro, mela; mAb
426300; U15979; Hs.169228; delta-like homolog (Drosophila; ovar, sarc; mAb
426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; breast; mAb
426312; AF026939; Hs.181874; interferon-induced protein wit; esoph, mela; diag
426320; W47595; Hs.169300; transforming growth factor, be; ovar, pros, blad, panc; diag
426350; NM_003245; Hs.2022; transglutaminase 3 (E polypept; cerv; s.m.
426363; M58524; Hs.2025; transforming growth factor, be; pros; diag
426370; R98288; Hs.281706; sortilin 1; sarc; diag
426416; AW612744; Hs.169824; killer cell lectin-like recept; fibro; mAb
426440; BE382756; Hs.169902; solute carrier family 2 (facil; lung, panc, ovar, blad, headnk, esoph; mAb
426462; U59111; Hs.169993; dermatan sulphate proteoglycan; sarc; diag
426470; AA528794; Hs.128644; ESTs; mela; diag
426471; M22440; Hs.170009; transforming growth factor, al; headnk, renal, panc; diag
426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; panc; mAb+s.m.
426501; AW043782; Hs.293616; ESTs; pros, breast, glio, lung, mela; mAb
426502; Y07759; Hs.170157; myosin VA (heavy polypeptide 1; mela; diag
426534; U58096; Hs.2051; testis specific protein, Y-lin; test; CTL+s.m.
426535; AU077012; Hs.170279; ESTs, Weakly similar to ubiqui; angio; diag
426555; NM_000372; Hs.2053; tyrosinase (oculocutaneous alb; mela, sarc; mAb
426559; AB001914; Hs.170414; paired basic amino acid cleavi; hepC, breast, ovar, renal; diag
426575; M74826; Hs.170806; glutamate decarboxylase 2 (pan; panc; s.m.
426627; AF012359; Hs.195685; ESTs; test; diag
426635; BE395109; Hs.129327; hypothetical protein MGC13057; ovar; CTL+s.m.
426682; AV660038; Hs.2056; UDP glycosyltransferase 1 fami; blad, lung; s.m.
426691; NM_006201; Hs.171834; PCTAIRE protein kinase 1; ovar; CTL+s.m.
426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fi; angio; mAb
426721; AA383566; Hs.288545; ESTs, Weakly similar to T29012; fibro; diag
426726; AA488915; Hs.171955; trophinin associated protein (; test; diag
426747; AA535210; Hs.171995; kallikrein 3, (prostate specif; pros; diag
426752; X69490; Hs.172004; titin; sarc; diag
426759; AI590401; Hs.21213; ESTs; mela; diag
426793; X89887; Hs.172350; HIR (histone cell cycle regula; pros; CTL+s.m.
426828; NM_000020; Hs.172670; activin A receptor type II-lik; angio; mAb
426866; U02330; Hs.172816; neuregulin 1; esoph; CTL+s.m.
426897; AW976570; Hs.97387; ESTs; lung; diag
426900; AW163564; Hs.142375; ESTs; blad, pros; mAb
426935; NM_000088; Hs.172928; collagen, type I, alpha 1; test, sarc; CTL+s.m.
426966; AI493134; Hs.349204; sclerostin; lung; diag
426968; U07616; Hs.173034; amphiphysin (Stiff-Mann syndro; blad; mAb+CTL
426991; AK001536; Hs.214410; Homo sapiens cDNA FLJ10674 fis; ovar, sarc; diag
427080; AW068287; Hs.301175; ras-related C3 botulinum toxin; mela; diag

427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosop; headnk, esoph; diag
427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase ; breast; mAb
427244; AA402400; Hs.178045; ESTs; esoph; diag
427260; AA663848; ; gb:ae70b06.s1 Stratagene schiz; lung; diag
427274; NM_005211; Hs.174142; colony stimulating factor 1 re; pros, sarc; mAb
427298; AA400495; ; ESTs; test; diag
427318; AF186081; Hs.175783; zinc transporter; pros; mAb
427333; AF067797; Hs.176658; aquaporin 8; panc, colon; mAb
427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
427356; AW023482; Hs.97849; ESTs; ovar, breast, pros, blad, lung; diag
427398; AW390020; Hs.20415; chromosome 21 open reading fra; pros; diag
427427; AF077345; Hs.177936; lectin, superfamily member 1 (; breast; diag
427441; AA412605; Hs.293266; SPANX family, member C; lung, esoph; CTL+s.m.
427461; AA531527; Hs.332040; hypothetical protein MGC13010; pros; mAb
427474; U13192; Hs.2159; aggrecan 1 (chondroitin sulfat; sarc; diag
427486; AA974433; Hs.362432; fibroblast growth factor 4 (he; test; diag
427510; Z47542; Hs.179312; small nuclear RNA activating c; lung; CTL+s.m.
427515; T79526; Hs.179516; integral type I protein; pros; diag
427521; AW973362; ; ESTs; test; diag
427528; AU077143; Hs.179565; minichromosome maintenance def; mela; CTL+s.m.
427535; R29543; Hs.2164; pro-platelet basic protein (in; fibro; diag
427546; AA405280; Hs.36793; hypothetical protein FLJ23188; lung; diag
427550; BE242818; Hs.311609; nuclear RNA helicase, DECD var; mela; CTL+s.m.
427557; NM_002659; Hs.179657; plasminogen activator, urokina; panc, colon, stom, ovar, cerv, blad, lung, headnk, esoph; mAb
427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_H; test; diag
427583; M62962; Hs.179704; meprin A, alpha (PABA peptide ; colon; mAb
427584; BE410293; Hs.179718; v-myb avian myeloblastosis vir; test; CTL+s.m.
427585; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc,stom, colon, ovar, cerv, sarc; diag
427615; BE410107; Hs.179817; CGI-82 protein, PSDR1; pros; diag
427634; AI399745; Hs.18449; hypothetical protein MGC10820; mela, sarc; diag
427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis; sarc; diag
427666; AI791495; Hs.180142; calmodulin-like skin protein (; breast, cerv, blad, lung, headnk, esoph; diag
427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis; test; diag
427668; AA298760; Hs.180191; hypothetical protein FLJ14904; lung, test; diag
427681; AB018263; Hs.284232; tumor necrosis factor receptor; ovar; mAb+s.m.
427698; AW972594; Hs.335499; ESTs; fibro; CTL+s.m.
427701; AA411101; Hs.243886; nuclear autoantigenic sperm pr; lung; mAb+CTL
427715; BE245274; Hs.180428; KIAA1181 protein; pros; diag
427719; AI393122; Hs.134726; ESTs; test, blad; diag
427730; AW250549; Hs.180577; granulin; mela; diag
427786; BE407863; Hs.256871; ESTs; esoph, blad; diag
427809; M26380; Hs.180878; lipoprotein lipase; ovar; mAb
427811; M81057; Hs.180884; carboxypeptidase B1 (tissue); breast; s.m.
427897; NM_017413; Hs.303084; apelin; peptide ligand for APJ; angio, renal, pros; diag
427912; AL022310; Hs.181097; tumor necrosis factor (ligand); angio; mAb
427958; AA418000; Hs.376771; potassium intermediate/small c; pros, glio; mAb
427961; AW293165; Hs.143134; ESTs; lung, sarc; diag
428001; H97428; Hs.219907; ESTs, Moderately similar to Tr; mela; diag
428004; AA449563; Hs.151393; glutamate-cysteine ligase, cat; lung; s.m.
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fi; lung; diag
428046; AW812795; Hs.337534; ESTs, Moderately similar to I3; lung, colon ; diag
428062; AA420683; Hs.98321; hypothetical protein FLJ14103; angio; diag
428087; AA100573; Hs.182421; troponin C2, fast; sarc; CTL+s.m.
428141; D50402; Hs.182611; solute carrier family 11 (prot; glio; mAb
428153; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
428169; AI928984; Hs.182793; golgi phosphoprotein 2; pros; diag
428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar, sarc; CTL+s.m.
428183; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
428206; AB020643; Hs.183006; KIAA0836 protein; angio; mAb
428221; U96781; Hs.183075; ATPase, Ca transporting, cardi; sarc; s.m.
428227; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, headnk, fibro, colon, stom, cerv, leuk, renal, test, mela, esoph, hepC; diag
428248; AI126772; Hs.40479; ESTs; sarc; diag
428293; BE250944; Hs.183556; solute carrier family 1 (neutr; pros; mAb
428305; AA446628; Hs.2799; cartilage linking protein 1; sarc; diag
428329; AA426091; Hs.98453; ESTs, Moderately similar to R2; test; diag
428336; AA503115; Hs.183752; microseminoprotein, beta-; pros; diag
428355; BE256452; Hs.2257; vitronectin (serum spreading f; colon; diag
428398; AI249366; Hs.98558; ESTs; pros, breast ; diag
428405; Y00762; Hs.2266; cholinergic receptor, nicotini; esoph, sarc; mAb
428423; AU076517; Hs.184276; solute carrier family 9 (sodiu; ovar; CTL+s.m.
428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA s; lung, fibro; diag
428467; AK002121; Hs.184465; hypothetical protein FLJ11259; fibro; mAb
428471; X57348; Hs.184510; stratifin; lung, headnk, colon, panc; diag
428645; AA431400; Hs.98729; ESTs, Weakly similar to 201720; lung; s.m.
428651; AF196478; Hs.188401; annexin A10; blad, stom, panc; diag
428667; AI375550; Hs.346868; nucleolar protein p40; homolog; fibro, uter; diag
428722; U76456; Hs.190787; tissue inhibitor of metallopro; glio; diag
428728; NM_016625; Hs.191381; hypothetical protein; ovar, lung, BPH; CTL+s.m.
428771; AB028992; Hs.193143; KIAA1069 protein; lung; CTL+s.m.
428784; Y12851; Hs.193470; purinergic receptor P2X, ligan; glio, mela; mAb
428800; M57627; Hs.193717; interleukin 10; fibro; diag
428801; AW277121; Hs.254881; ESTs; pros; diag
428804; AK000713; Hs.193736; hypothetical protein FLJ20706; mela; diag

428810; AF068236; Hs.193788; nitric oxide synthase 2A (indu; lung; s.m.
428819; AL135623; Hs.193914; KIAA0575 gene product; pros; CTL+s.m.
428824; W23624; Hs.173059; ESTs; panc; diag
428832; AA578229; Hs.324239; ESTs, Moderately similar to ZN; panc, uter; diag
428841; AI418430; Hs.104935; ESTs; renal; diag
428848; NM_000230; Hs.194236; leptin (murine obesity homolog; sarc; diag
428862; NM_000346; Hs.2316; SRY (sex determining region Y); pros, sarc; CTL+s.m.
428927; AA441837; Hs.90250; Homo sapiens hypothetical prot; fibro; mAb+diag
428928; BE409838; Hs.194657; cadherin 1, type 1, E-cadherin; pros, breast, stom, blad; mAb
428949; AA442153; Hs.104744; hypothetical protein DKFZp434J; sarc; diag
428957; NM_003881; Hs.194679; WNT1 inducible signaling pathw; cerv; diag
428959; AF100779; Hs.194680; WNT1 inducible signaling pathw; sarc; diag
428977; AK001404; Hs.194698; cyclin B2; test; CTL+s.m.
428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_H; sarc; diag
429002; AW248439; Hs.2340; junction plakoglobin; blad; CTL+s.m.
429010; Y18198; Hs.194725; one cut domain, family member ; panc; diag
429038; AL023513; Hs.194766; seizure related gene 6 (mouse); lung; mAb
429058; AF138863; Hs.35254; hypothetical protein FLB6421; esoph; diag
429065; AI753247; Hs.29643; Homo sapiens cDNA FLJ13103 fis; lung; diag
429083; Y09397; Hs.227817; BCL2-related protein A1; mela; diag
429113; D28235; Hs.196384; prostaglandin-endoperoxide syn; angio, blad, stom; s.m.
429120; AK001673; Hs.196530; hypothetical protein FLJ10811; test; diag
429150; AF120103; Hs.197366; smoothened (Drosophila) homolo; ovar; mAb
429163; AA884766; ; gb:am20a10.s1 Soares_NFL_T_GBC; pros; diag
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; breast, panc,stom, lung, mela; s.m.
429201; X03178; Hs.198246; group-specific component (vite; panc; diag
429220; AW207206; Hs.356962; ESTs; breast, pros, BPH; diag
429228; AI553633; Hs.356828; ESTs; lung, fibro, headnk, esoph; diag
429259; AA420450; Hs.380088; Plakophilin; lung, headnk; diag
429290; AF203032; Hs.198760; neurofilament, heavy polypepti; pros; CTL+s.m.
429299; AI620463; Hs.347408; hypothetical protein MGC13102; pros, cerv; diag
429329; AA456140; Hs.99235; Homo sapiens pannexin 3 (PANX3; sarc; mAb
429345; R11141; Hs.199695; hypothetical protein; blad; diag
429359; W00482; Hs.2399; matrix metalloproteinase 14 (m; headnk, breast, cerv, ovar, blad, lung, esoph, mela, sarc; mAb
429413; NM_014058; Hs.201877; DESC1 protein; lung, blad; diag
429415; NM_002593; Hs.202097; procollagen C-endopeptidase en; sarc; diag
429423; AI016712; Hs.380983; integrin, beta 1 (fibronectin ; angio; mAb
429432; AI678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
429441; AJ224172; Hs.204096; lipophilin B (uteroglobin fami; breast, pros, ovar; diag
429466; M85835; Hs.12827; ESTs; glio, uter; CTL+s.m.
429469; M64590; Hs.380791; glycine dehydrogenase (decarbo; test; s.m.
429486; AF155827; Hs.203963; hypothetical protein FLJ10339; blad, lung, headnk, test; diag
429500; X78565; Hs.289114; hexabrachion (tenascin C, cyto; lung, glio, headnk, mela, sarc; diag
429504; X99133; Hs.204238; lipocalin 2 (oncogene 24p3) (N; ovar, lung, blad; diag
429505; AW820035; Hs.278679; a disintegrin and metalloprote; colon, leuk; mAb
429538; BE182592; Hs.139322; small proline-rich protein 2A; lung, esoph; diag
429563; BE619413; Hs.2437; eukaryotic translation initiat; lung; diag
429586; T73510; Hs.209153; angiopoietin-like 3; hepC; CTL+s.m.
429597; NM_003816; Hs.2442; a disintegrin and metalloprote; panc, colon, stom, lung; mAb
429609; AF002246; Hs.210863; cell adhesion molecule with ho; ovar, mela; diag
429612; AF062649; Hs.252587; pituitary tumor-transforming 1; lung, blad, headnk; diag
429655; U48959; Hs.211582; myosin, light polypeptide kina; pros; s.m.
429663; M68874; Hs.211587; phospholipase A2, group IVA (c; angio, lung; s.m.
429664; L20433; Hs.211588; POU domain, class 4, transcrip; sarc; CTL+s.m.
429736; AF125304; Hs.212680; tumor necrosis factor receptor; lung; mAb
429747; M87507; Hs.2490; caspase 1, apoptosis-related c; colon, stom, fibro; s.m.
429764; BE245076; Hs.216958; KIAA0194 protein; pros; mAb
429769; NM_004917; Hs.218366; kallikrein 4 (prostase, enamel; pros; s.m.
429784; M89796; Hs.30; membrane-spanning 4-domains, s; fibro; mAb
429823; AA459443; Hs.181400; ESTs; sarc; diag
429859; NM_007050; Hs.225952; protein tyrosine phosphatase, ; breast; mAb+s.m.
429918; AW873986; Hs.119383; ESTs; pros, glio; diag
429921; AA526911; Hs.82772; collagen, type XI, alpha 1; headnk, panc, sarc; CTL
429983; W92620; Hs.260855; ESTs; blad; diag
429986; AF092047; Hs.227277; sine oculis homeobox (Drosophi; lung; CTL+s.m.
430014; H59354; Hs.374303; actinin, alpha 4; renal; diag
430016; NM_004736; Hs.227656; xenotropic and polytropic retr; ovar; mAb
430044; AA464510; Hs.152812; ESTs; breast, lung, panc, headnk, ovar, stom, esoph; diag
430056; X97548; Hs.226059; KRAB-associated protein 1; test; CTL+s.m.
430129; BE301708; Hs.233955; hypothetical protein FLJ20401; angio; diag
430130; AL137311; Hs.234074; Homo sapiens mRNA; cDNA DKFZp7; pros; mAb
430144; AI732722; Hs.98927; ERGL protein; ERGIC-53-like pr; pros; diag
430152; AB001325; Hs.234642; aquaporin 3; blad, fibro; mAb
430154; AW583058; Hs.234726; serine (or cysteine) proteinas; pros; diag
430157; BE348706; Hs.278543; ESTs; blad; diag
430168; AW968343; Hs.145582; DKFZP434I1735 protein; blad; diag
430223; NM_002514; Hs.235935; nephroblastoma overexpressed g; mela; diag
430226; BE245562; Hs.2551; adrenergic, beta-2-, receptor,; pros; mAb
430228; AW950939; Hs.6382; ESTs, Highly similar to T00391; glio; diag
430252; AI638774; Hs.105328; testes development-related NYD; test; CTL+s.m.
430253; AK001514; Hs.236844; hypothetical protein FLJ10652; test; CTL+s.m.
430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551; test; CTL+s.m.
430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse h; ovar; CTL+s.m.

430280; AA361258; Hs.237868; interleukin 7 receptor; mela, lung, panc, stom, esoph, headnk, fibro; mAb+s.m.
430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_H; test; diag
430294; AI538226; Hs.32976; guanine nucleotide binding pro; pros; diag
430337; M35707; Hs.239600; calmodulin-like 3; lung; diag
430354; AA954810; Hs.239784; human homolog of Drosophila Sc; ovar; diag
430378; Z29572; Hs.2556; tumor necrosis factor receptor; lung,fibro, breast headnk, blad, breast, colon, stom; diag
430393; BE185030; Hs.241305; estrogen-responsive B box prot; lung; diag
430396; D49742; Hs.241363; hyaluronan-binding protein 2; panc; diag
430407; H23551; Hs.30974; ESTs; panc; diag
430439; AL133561; Hs.380155; DKFZP434B061 protein; lung, test; diag
430451; AA836472; Hs.297939; cathepsin B; ovar, lung, headnk, panc, stom; diag
430454; AW469011; Hs.105635; ESTs; lung; diag
430476; AA447465; Hs.2563; tachykinin, precursor 1 (subst; sarc; diag
430487; D87742; Hs.241552; KIAA0268 protein; pros; diag
430491; AL109791; Hs.241559; Homo sapiens mRNA full length ; ovar; diag
430498; X02910; Hs.241570; tumor necrosis factor (TNF sup; leuk; diag
430508; AI015435; Hs.104637; ESTs; lung; mAb+s.m.
430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; test; CTL+s.m.
430540; AW245422; Hs.106357; Homo sapiens cDNA: FLJ22105 fi; mela; mAb
430563; AA481269; Hs.348628; ATP-binding cassette, sub-fami; lung; diag
430594; AK000790; Hs.246885; hypothetical protein FLJ20783; mela; diag
430634; AI860651; Hs.26685; calcyphosine; ovar; diag
430637; BE160081; Hs.256290; S100 calcium-binding protein A; mela; diag
430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_H; test; diag
430676; AF084866; Hs.372585; gb:Homo sapiens envelope prote; test; diag
430677; Z26317; Hs.359784; desmoglein 2; lung, colon; mAb
430678; AI458174; Hs.192855; ESTs; lung; diag
430686; NM_001942; Hs.2633; desmoglein 1; lung, headnk, mela; mAb
430691; C14187; Hs.157208; aristaless-related homeobox pr; EWS, ovar, panc; diag
430704; AW813091; Hs.335799; ESTs; stom; diag
430770; AA765694; Hs.123296; ESTs; mela; diag
430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom, fibro; diag
430838; N46664; Hs.169395; hypothetical protein FLJ12015; mela; CTL+s.m.
430890; X54232; Hs.2699; glypican 1; glio, lung, cerv, blad, esoph; mAb
430985; AA490232; Hs.27323; ESTs, Weakly similar to I78885; lung; mAb
431009; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad, headnk, esoph; mAb
431053; S40369; Hs.249141; Glutamate receptor subunit; glio; mAb
431070; AW408164; Hs.249184; transcription factor 19 (SC1); blad; diag
431089; BE041395; Hs.374629; ESTs, Weakly similar to unknow; blad, lung, pros, angio, fibro; diag
431099; Y13367; Hs.249235; phosphoinositide-3-kinase, cla; pros; CTL+s.m.
431103; M57399; Hs.44; pleiotrophin (heparin binding ; sarc, mela; diag
431124; AF284221; Hs.59506; doublesex and mab-3 related tr; lung; CTL+s.m.
431151; BE207083; Hs.366053; gb:ba10d10.y1 NIH_MGC_7 Homo s; pros; mAb
431164; AA493650; Hs.94367; thyroid transcription factor 1; fibro; CTL+s.m.
431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endopla; mela, pros, panc, colon, stom; mAb
431211; M86849; Hs.323733; gap junction protein, beta 2, ; colon, blad, lung, panc, headnk, esoph; mAb
431217; NM_013427; Hs.250830; Rho GTPase activating protein ; pros; CTL+s.m.
431221; AA449015; Hs.286145; SRB7 (suppressor of RNA polyme; lung; CTL+s.m.
431222; X56777; Hs.273790; zona pellucida glycoprotein 3A; pros; diag
431250; BE264649; Hs.251377; taxol resistance associated ge; esoph; diag
431322; AW970622; Hs.376626; gb:EST382704 MAGE resequences,; blad, ovar, uter; diag
431347; AI133461; Hs.251664; insulin-like growth factor 2 (; blad; mAb+diag
431354; BE046956; Hs.251673; DNA (cytosine-5-)-methyltransf; test; CTL+s.m.
431360; NM_000427; Hs.251680; loricrin; mela, sarc; diag
431362; AI874223; Hs.293560; ESTs; angio; diag
431369; BE184455; Hs.251754; secretory leukocyte protease i; ovar, blad; diag
431384; BE158000; Hs.334372; gb:MR2-HT0377-150200-202-e03 H; lung; diag
431385; BE178536; Hs.11090; membrane-spanning 4-domains, s; panc; diag
431441; U81961; Hs.2794; sodium channel, nonvoltage-gat; ovar, pros, blad; mAb
431448; AL137517; Hs.306201; hypothetical protein DKFZp564C; blad; mAb
431457; NM_012211; Hs.256297; integrin, alpha 11; headnk; mAb
431474; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
431494; AA991355; Hs.298312; hypothetical protein DKFZp434A; lung; diag
431512; BE270734; Hs.2795; lactate dehydrogenase A; panc; s.m.
431548; AI834273; Hs.9711; novel protein; lung, angio, pros; diag
431553; X78075; Hs.2799; cartilage linking protein 1; sarc; diag
431579; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
431616; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros, panc, colon ; mAb
431674; AA098901; Hs.301642; G-protein coupled receptor; ovar; mAb+s.m.
431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; fibro; diag
431728; NM_007351; Hs.268107; multimerin; angio; diag
431808; M30703; Hs.270833; amphiregulin (schwannoma-deriv; breast, headnk, panc, colon; diag
431836; AF178532; Hs.271411; beta-site APP-cleaving enzyme ; mela; mAb
431870; AW449902; Hs.105500; ESTs; renal; diag
431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alph; blad, headnk, lung, panc, cerv, stom; mAb
431938; AA938471; Hs.54431; specific granule protein (28 k; panc; diag
431939; AW008061; Hs.231994; ESTs; renal, colon; diag
431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis; cerv, glio; diag
431989; AW972870; Hs.291069; ESTs; ovar; diag
431992; NM_002742; Hs.2891; protein kinase C, mu; pros, glio; s.m.
432004; BE018302; Hs.2894; placental growth factor, vascu; renal; diag
432015; AL157504; Hs.159115; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
432023; AW273128; Hs.300268; EST; lung; diag

432097; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
432117; AL036195; Hs.2909; protamine 1; test; CTL+s.m.
432128; AA127221; Hs.66; ESTs; angio; diag
432141; BE410964; Hs.272736; nuclear receptor binding prote; test; mAb+s.m.
432189; AA527941; ; gb:nh30c04.s1 NCI_CGAP_Pr3 Hom; pros; diag
432199; AI693815; Hs.127179; cryptic gene; panc; diag
432210; AI567421; Hs.273330; Homo sapiens, clone IMAGE:3544; ovar, lung, blad; diag
432222; AI204995; ; gb:an03c03.x1 Stratagene schiz; angio, blad, fibro; diag
432231; AA339977; Hs.274127; CLST 11240 protein; fibro; diag
432239; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad, lung, headnk, esoph, sarc; s.m.
432240; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag
432305; M62402; Hs.274313; insulin-like growth factor bin; cerv; diag
432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis; cerv, lung, fibro, pros; diag
432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 n; lung, test,colon; diag
432415; T16971; ; ESTs, Weakly similar to A43932; ovar, pros; diag
432432; AA541323; Hs.115831; ESTs; uter, pros; diag
432435; BE218886; Hs.282070; ESTs; pros, uter, colon, stom, fibro; diag
432441; AW292425; Hs.163484; intron of hepatocyte nuclear f; blad, fibro, pros; diag
432473; AI202703; Hs.152414; ESTs; pros; diag
432481; AW451645; Hs.151504; intron of collagen, type XI, a; sarc; diag
432512; NM_003264; Hs.3017; transition protein 1 (during h; test; CTL+s.m.
432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA; fibro, ovar, uter; CTL+s.m.
432527; AW975028; Hs.102754; ESTs; pros, uter, ovar, cerv ; diag
432542; AW083920; Hs.16098; claudin 2; colon, panc; diag
432583; AW023624; Hs.162282; potassium channel TASK-4; pota; lung; mAb
432615; AA557191; Hs.55026; ESTs, Weakly similar to I54374; pros; diag
432621; AI298501; Hs.21192; ESTs, Weakly similar to T46428; pros; mAb
432629; AW860548; Hs.280658; ESTs; ovar; diag
432653; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros, lung ; mAb+s.m.
432666; AW204069; Hs.351118; ESTs, Weakly similar to unname; test; diag
432706; NM_013230; Hs.286124; CD24 antigen (small cell lung ; colon, ovar, pros; mAb+CTL
432730; AI066520; Hs.131358; ESTs; test; diag
432731; R31178; Hs.287820; fibronectin 1; panc, fibro; diag
432788; AA521091; Hs.178499; Homo sapiens cDNA: FLJ23117 fi; lung, ovar; CTL+s.m.
432800; BE391046; Hs.278962; AIM-1 protein; mela, pros; mAb
432842; AW674093; Hs.334822; hypothetical protein MGC4485; blad, lung, headnk; CTL+s.m.
432850; X87723; Hs.3110; angiotensin receptor 2 (AT2); leio; mAb
432855; AF017988; Hs.279565; secreted frizzled-related prot; panc; diag
432867; AW016936; Hs.233364; ESTs; stom, colon; diag
432878; BE386490; Hs.279663; Pirin; mela; CTL+s.m.
432887; AI926047; Hs.162859; AK056805: Homo sapiens cDNA FL; pros; diag
432938; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
432966; AA650114; Hs.325198; ESTs; pros; diag
433012; NM_004045; Hs.279910; ATX1 (antioxidant protein 1, y; mela; diag
433013; AI697890; Hs.127337; axin 2 (conductin, axil); colon; CTL+s.m.
433043; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
433068; NM_006456; Hs.288215; sialyltransferase; breast, ovar, mela; s.m.
433078; AW015188; Hs.121575; Homo sapiens cDNA FLJ12231 fis; blad; diag
433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, ; blad, lung, headnk, cerv; mAb
433147; AF091434; Hs.43080; platelet derived growth factor; ovar, panc, fibro; diag
433159; AB035898; Hs.150587; kinesin-like protein 2; ovar, uter, colon, blad; diag
433170; AB037816; Hs.8982; KIAA1395; angio; diag
433183; AF231338; Hs.222024; transcription factor BMAL2; lung; diag
433228; F28212; Hs.14953; KIAA1491 protein; test; CTL+s.m.
433258; AI806626; Hs.207300; ESTs, Weakly similar to ALUB_H; lung; diag
433285; AW975944; Hs.237396; ESTs; breast, pros ; diag
433293; AF007835; Hs.32417; hypothetical protein MGC2742; fibro, pros, stom, panc; CTL+s.m.
433323; AA805132; Hs.159142; ESTs; pros; diag
433334; AI927208; Hs.231958; matrix metalloproteinase 28; panc; s.m.
433336; AF017986; Hs.31386; secreted frizzled-related prot; ovar, fibro, headnk, lung, panc, blad; diag
433364; AI075407; Hs.296083; ESTs, Moderately similar to I5; mela; diag
433365; AF026944; Hs.293797; ESTs; blad; diag
433376; AI249361; Hs.74122; caspase 4, apoptosis-related c; angio; s.m.
433388; AI432672; Hs.288539; hypothetical protein FLJ22191; ovar; CTL+s.m.
433404; T32982; Hs.352670; Homo sapiens cDNA FLJ32064 fis; pros; diag
433437; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio, colon; s.m.
433444; AW975324; Hs.129816; ESTs; pros; diag
433466; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
433485; AI493076; Hs.306098; aldo-keto reductase family 1, ; lung; s.m.
433495; AW373784; Hs.71; alpha-2-glycoprotein 1, zinc; breast, pros; diag
433576; BE080715; Hs.161091; ESTs; mela; diag
433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncoge; colon; diag
433671; AW138797; Hs.132906; 19A24 protein; fibro; mAb
433701; AW445023; Hs.15155; ESTs; test; diag
433724; AI827749; Hs.144924; serine/threonine protein kinas; test; CTL+s.m.
433764; AW753676; Hs.39982; zinc finger protein RINZF (NM_; pros, ovar; diag
433800; AI034361; Hs.135150; lung type-I cell membrane-asso; glio, lung, test; mAb
433914; AF108138; Hs.112160; Homo sapiens DNA helicase homo; test; s.m.
434011; AW953437; Hs.5486; clone FLB5214; pros; diag
434105; AW952124; Hs.13094; presenilins associated rhomboi; lung; diag
434217; AW014795; Hs.23349; ESTs; angio; diag
434262; AF121858; Hs.12169; sorting nexin 8; mela; CTL+s.m.
434274; AA628539; Hs.57783; ESTs, Moderately similar to AL; test; diag

434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis; test; diag
434340; AI193043; Hs.353146; ESTs, Weakly similar to T17226; lung; diag
434360; AW015415; Hs.127780; ESTs; lung; diag
434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic re; colon, stom; diag
434377; AW137148; Hs.306593; intron of periostin (OSF-2os); headnk; diag
434398; AA121098; Hs.3838; serum-inducible kinase (SNK); angio, breast; CTL+s.m.
434411; AA632649; Hs.201372; ESTs; stom, leuk; diag
434414; AI798376; ; gb:tr34b07.x1 NCI_CGAP_Ov23 Ho; lung, test, colon; diag
434423; NM_006769; Hs.3844; LIM domain only 4; panc; diag
434449; AW953484; Hs.3849; hypothetical protein FLJ22041 ; sarc; diag
434487; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb+s.m.
434596; T59538; ; gb:yb65g12.s1 Stratagene ovary; angio; s.m.
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; test; CTL+s.m.
434609; R76593; ; gb:yi60c11.r1 Soares placenta ; pros; diag
434636; AA083764; Hs.349208; hypothetical protein MGC3178; angio; diag
434649; AA738254; Hs.165390; ESTs, Highly similar to A40350; test; diag
434665; AA642125; Hs.74502; gb:nr60c01.s1 NCI_CGAP_Lym3 Ho; panc; diag
434666; AF151103; Hs.112259; T cell receptor gamma locus; pros; mAb+s.m.
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis; panc; diag
434826; AF155661; Hs.22265; pyruvate dehydrogenase phospha; mela; s.m.
434846; AW295389; Hs.119768; ESTs; angio; diag
434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; lung, blad; mAb
434927; H46612; Hs.293815; Homo sapiens HSPC285 mRNA, par; angio; diag
434973; AW449285; Hs.313636; EST; pros; diag
435045; BE297155; Hs.143698; ESTs; test; diag
435047; AA454985; Hs.54973; cadherin-like protein VR20; pros; mAb
435066; BE261750; Hs.4747; dyskeratosis congenita 1, dysk; colon; CTL+s.m.
435080; AI831760; Hs.155111; hypothetical protein FLJ14428; renal; mAb
435094; AI560129; Hs.289008; EST; ovar, cerv; diag
435099; AC004770; Hs.4756; flap structure-specific endonu; blad, test, mela; CTL+s.m.
435140; AA668123; Hs.134170; ESTs; fibro; diag
435159; AA668879; Hs.116649; ESTs; lung; diag
435206; AI432364; Hs.160594; ESTs; test; diag
435243; AW292886; Hs.348932; hypothetical protein dJ434O14.; cerv, headnk; diag
435292; N20514; Hs.172965; ESTs; mela; diag
435299; AI745458; Hs.343026; ESTs, Weakly similar to T20593; fibro; diag
435479; AF197137; Hs.155101; ATP synthase, H transporting, ; pros; s.m.
435496; AW840171; Hs.265398; PAR-6 beta; breast, panc, ovar; diag
435563; AF210317; Hs.95497; solute carrier family 2 (facil; blad; mAb+s.m.
435575; AF213457; Hs.44234; triggering receptor expressed ; fibro; mAb+s.m.
435602; AF217515; Hs.283532; uncharacterized bone marrow pr; test; diag
435615; Y15065; Hs.4975; potassium voltage-gated channe; glio; mAb
435652; N32388; Hs.334370; uncharacterized hypothalamus p; panc; diag
435793; AB037734; Hs.4993; KIAA1313 protein; ovar, lung, uter; diag
435849; BE305242; Hs.16098; claudin 2; colon, panc; diag
435876; AW612586; Hs.160271; G protein-coupled receptor 48; pros; mAb
435897; AF269223; Hs.128322; t-complex 11 (a murine tcp hom; test; diag
435904; AF261655; Hs.8910; 1,2-alpha-mannosidase IC; blad; s.m.
435916; AF263538; Hs.86232; growth differentiation factor ; test; diag
435974; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
436032; AA150797; Hs.109276; latexin protein; panc, anglo; diag
436063; AK000028; Hs.356100; ribosomal protein S24; pros; diag
436120; AI248193; Hs.119860; ESTs; fibro; diag
436199; R38946; Hs.127951; hypothetical protein FLJ14503; renal; diag
436246; AW450963; Hs.119991; ESTs; blad; diag
436251; BE515065; Hs.296585; nucleolar protein (KKE/D repea; colon, test, blad; CTL+s.m.
436278; BE396290; Hs.5097; synaptogyrin 2; pros; mAb
436291; BE568452; Hs.344037; protein regulator of cytokines; lung, blad, headnk; diag
436293; AI601188; Hs.306201; ESTs; blad; diag
436302; AL355841; Hs.99330; hypothetical protein FLJ23588; lung; diag
436315; BE390513; Hs.27935; hypothetical protein MGC4837; mela; diag
436396; AI683487; Hs.152213; wingless-type MMTV integration; lung, headnk, pros, panc; diag
436420; AA443966; Hs.31595; ESTs; angio; mAb
436476; AA326108; Hs.33829; bHLH protein DEC2; panc; diag
436511; AA721252; Hs.291502; ESTs; lung; diag
436553; AW407157; Hs.181125; immunoglobulin lambda locus; lung; diag
436569; BE439539; Hs.301961; glutathione S-transferase M2 (; blad; s.m.
436614; AW104388; Hs.149091; ESTs; mela; CTL+s.m.
436700; AI693690; Hs.301406; hypothetical protein PP3501; mela; mAb
436729; BE621807; Hs.351316; transmembrane 4 superfamily me; panc, colon, stom, ovar, lung, blad; mAb
436772; AW975688; Hs.348918; metallothionein 1E (functional; angio; diag
436775; AA731111; Hs.372225; ESTs; uter, ovar; diag
436839; AA767346; Hs.372277; ESTs; lung; diag
436856; AI469355; Hs.127310; ESTs; mela; diag
436954; AA740151; Hs.130425; ESTs; fibro, uter, ovar; diag
436972; AA284679; Hs.25640; claudin 3; ovar, lung, pros; mAb
437052; AA861697; Hs.120591; ESTs; pros; diag
437099; N77793; Hs.48659; ESTs, Highly similar to S14458; test; diag
437100; AI761073; Hs.14535; Homo sapiens cDNA: FLJ22314 fi; panc, renal; diag
437119; AI379921; Hs.177043; XP_171387 similar to rhotekin; fibro; diag
437145; AF007216; Hs.5462; solute carrier family 4, sodiu; panc, pros, stom; mAb
437156; AI916600; Hs.121194; Homo sapiens cDNA: FLJ21569 fi; stom, renal, colon; diag
437181; AI306615; Hs.125343; ESTs, Weakly similar to KIAA07; blad; mAb+s.m.

437204; AL110216; Hs.355961; ESTs, Weakly similar to I55214; lung; CTL+s.m.
437212; AI765021; Hs.210775; ESTs; renal, uter, ovar; diag
437224; AL117628; Hs.97808; ESTs; test; diag
437259; AI377755; Hs.120695; ESTs; lung; diag
437267; AW511443; Hs.258110; ESTs; BPH; diag
437269; AA334384; Hs.149420; ESTs; angio; diag
437330; AL353944; Hs.50115; Homo sapiens mRNA; cDNA DKFZp7; sarc; diag
437381; NM_003684; Hs.5591; MAP kinase-interacting serine/; glio; CTL+s.m.
437390; AI125859; Hs.112607; ESTs; lung; diag
437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp5; lung; diag
437435; AA249439; Hs.27027; hypothetical protein DKFZp762H; lung; diag
437437; AA226869; Hs.351623; hypothetical protein DKFZp762L; test; CTL+s.m.
437478; AL390172; Hs.317432; branched chain aminotransferas; angio; s.m.
437553; AI829935; Hs.130497; ESTs, Weakly similar to MAT8_H; blad; mAb
437571; AA760894; Hs.125350; ESTs; pros; diag
437623; D63880; Hs.5719; chromosome condensation-relate; test; diag
437740; AA810265; Hs.122915; ESTs; mela; diag
437802; AI475995; Hs.122910; ESTs; panc; diag
437852; AW978107; Hs.5884; Homo sapiens mRNA; cDNA DKFZp5; mela; CTL+s.m.
437908; AI082424; Hs.351043; ESTs; test; diag
437915; AI637993; Hs.202312; Homo sapiens clone N11 NTera2D; lung, headnk, ovar, blad, uter; diag
437931; AI249468; Hs.124434; ESTs; blad; diag
437935; AW939591; Hs.5940; mucin 13, epithelial transmemb; colon, stom, uter, panc; mAb+s.m.
437938; AI950087; Hs.369628; gb:wq05c02.x1 NCI_CGAP_Kid12 H; renal, ovar, uter, cerv, blad; diag
437939; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
437960; AI669586; Hs.369312; ESTs; uter, ovar; diag
438167; R28363; Hs.24286; chemokine binding protein 2 (C; ovar, breast, uter; mAb
438199; AW016531; Hs.122147; hypothetical protein FLJ13189 ; breast; diag
438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nucl; mela; mAb+s.m.
438233; W52448; Hs.56147; ESTs; pros, cerv ; diag
438274; AI918906; Hs.55080; ESTs; headnk; diag
438403; AA806607; Hs.292206; ESTs; lung; mAb
438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
438450; AI050866; Hs.65853; nodal, mouse, homolog; test; diag
438456; AA913381; Hs.279763; ESTs; test; diag
438552; AJ245820; Hs.6314; type I transmembrane receptor ; pros, ovar; diag
438670; AI275803; Hs.123428; ESTs; fibro; CTL+s.m.
438702; AI879064; Hs.7164; ESTs; lung; diag
438707; L08239; Hs.5326; amino acid system N transporte; ovar; mAb
438746; AI885815; Hs.184727; Human melanoma-associated anti; panc, blad, mela, ovar; mAb+CTL
438817; AI023799; Hs.163242; ESTs; ovar, uter, blad, renal; diag
438859; AI559626; Hs.93522; Homo sapiens mRNA for KIAA1647; renal; diag
438866; U44385; Hs.6441; tissue inhibitor of metallopro; mela; diag
438873; AI302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fi; fibro; diag
438898; AI819863; Hs.106243; ESTs; lung; diag
438915; AA280174; Hs.355711; Williams-Beuren syndrome chrom; lung, test, mela; dieg
438929; AW195515; Hs.253177; ESTs; renal; diag
438956; W00847; Hs.135056; Human DNA sequence from clone ; lung; diag
438966; AW979074; ; gb:EST391184 MAGE resequences,; renal; diag
438983; AF085884; Hs.20029; proacrosin binding protein sp3; test; CTL+s.m.
438993; AA828995; ; gb:od77b08.s1 NCI_CGAP_Ov2 Hom; ovar; mAb+s.m.
439053; BE244588; Hs.6456; chaperonin containing TCP1, su; test; diag
439092; AA830149; ; gb:oc44f08.s1 NCI_CGAP_GCB1 Ho; pros; diag
439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096; pros; diag
439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic ; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; mAb
439221; AA737106; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582; mela, fibro; diag
439239; AI031540; Hs.235331; ESTs; blad; diag
439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
439310; AF086120; Hs.102793; ESTs; mela; diag
439318; AW837046; Hs.6527; G protein-coupled receptor 56; colon, breast, ovar, uter, cerv, pros, lung, headnk, blad, mela; mAb+s.m.
439335; AA742697; Hs.62492; NM_052863:Homo sapiens secreto; fibro, uter; diag
439366; AF100143; Hs.6540; fibroblast growth factor 13; pros; CTL+s.m.
439382; BE247684; Hs.103070; ESTs; angio; diag
439394; AA149250; Hs.56105; ESTs; lung; diag
439410; AA632012; Hs.188746; ESTs; angio; diag
439453; BE264974; Hs.6566; thyroid hormone receptor inter; lung, esoph, ovar; mAb+s.m.
439496; BE616501; Hs.32343; Homo sapiens, Similar to RIKEN; mela, esoph; diag
439659; AW970780; Hs.59483; leucine-rich repeat-containing; ovar, stom, mela, colon; mAb
439668; AI091277; Hs.302634; frizzled (Drosophila) homolog ; ovar, uter; mAb
439670; AF088076; Hs.59507; ESTs, Weakly similar to AC0048; lung, headnk, cerv; diag
439702; AW085525; Hs.55964; ESTs; mela; diag
439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung, headnk; diag
439735; AI635386; Hs.142846; hypothetical protein; pros; diag
439737; AI751438; Hs.41271; Homo sapiens mRNA full length ; panc; diag
439750; AL359053; Hs.57664; Homo sapiens mRNA full length ; panc, fibro, breast; diag
439755; AW748482; Hs.77873; B7 homolog 3; sarc; mAb
439759; AL359055; Hs.67709; Homo sapiens mRNA full length ; colon, stom, panc, leuk, lung; diag
439778; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
439780; AL109688; ; gb:Homo sapiens mRNA full leng; blad, esoph; diag
439820; AL360204; Hs.283853; Homo sapiens mRNA full length ; ovar, uter, cerv, breast, pros ; diag
439864; AI720078; Hs.291997; ESTs, Weakly similar to A47582; test; diag
439867; AA847510; Hs.161292; ESTs; panc; diag

439920; H05430; Hs.288433; neurotrimin; panc; mAb+diag
439926; AW014875; Hs.137007; ESTs; blad, esoph, lung, cerv; diag
439963; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
440042; AI073387; Hs.133898; ESTs; ovar; CTL+s.m.
440086; NM_005402; Hs.6906; v-ral simian leukemia viral on; angio; diag
440099; AL080058; Hs.6909; DKFZP564G202 protein; panc; diag
440119; AA865455; Hs.125331; ESTs, Moderately similar to un; test; diag
440138; AB033023; Hs.318127; hypothetical protein FLJ10201; lung; CTL+s.m.
440151; AA868167; ; gb:ak38e07.s1 Soares_testis_NH; sarc; diag
440207; AI371978; Hs.128326; ESTs; test; diag
440209; H05049; Hs.247837; neurexin 3; fibro; diag
440210; AW674562; Hs.122128; ESTs; glio; diag
440225; BE295782; Hs.159; tumor necrosis factor receptor; glio; mAb
440238; AW451970; Hs.155644; paired box gene 2; ovar; diag
440260; AI972867; Hs.7130; copine IV; pros; diag
440273; AI805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fi; lung, fibro; diag
440274; R24595; Hs.7122; scrapie responsive protein 1; sarc; diag
440311; AI733079; Hs.125407; ESTs, Moderately similar to AL; renal; diag
440325; NM_003812; Hs.7164; a disintegrin and metalloprote; lung; mAb
440333; AI378424; Hs.288761; hypothetical protein FLJ21749; pros; CTL+s.m.
440449; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
440452; AI925136; Hs.55150; ESTs, Weakly similar to CAYP_H; fibro; diag
440457; BE387593; Hs.21321; Homo sapiens clone FLB9213 PRO; mela; diag
440484; BE328156; Hs.150356; ESTs; panc; diag
440529; AW207640; Hs.16478; Homo sapiens cDNA: FLJ21718 fi; pros; diag
440659; AF134160; Hs.7327; claudin 1; lung; mAb
440704; M69241; Hs.162; insulin-like growth factor bin; lung, glio, ovar; diag
440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN; test; diag
440801; AA906366; Hs.370038; ESTs; pros; diag
440819; AI809444; Hs.202108; ESTs; pros; diag
440901; AA909358; Hs.128612; ESTs; ovar, pros; diag
440943; AW082298; Hs.146161; hypothetical protein MGC2408; lung; diag
440983; M20681; Hs.7594; solute carrier family 2 (facil; test; mAb
441020; W79283; Hs.35962; ESTs; lung, panc; diag
441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; lung, panc, colon; CTL+s.m.
441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis; panc, ovar, stom, uter, lung; diag
441134; W29092; Hs.346950; cellular retinoic acid-binding; sarc; diag
441247; AW118681; Hs.128051; Homo sapiens thymic stromal ly; pros; diag
441321; H17182; Hs.7771; B-cell associated protein; test; diag
441345; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
441350; AB020690; Hs.7782; paraneoplastic antigen MA2; panc; mAb+CTL
441377; BE218239; Hs.202656; ESTs; uter, endo, lung; diag
441384; AA447849; Hs.288660; retinoic acid induced 3; ovar; mAb+s.m.
441392; AW451831; Hs.222119; ESTs, Weakly similar to S30433; renal; diag
441457; AW996651; Hs.43838; ESTs; angio; diag
441495; AW294603; Hs.127039; ESTs; blad; diag
441525; AW241867; Hs.127728; ESTs; lung; diag
441553; AA281219; Hs.121296; ESTs; lung, test, ovar; CTL+s.m.
441633; AW958544; Hs.112242; normal mucosa of esophagus spe; blad, lung, cerv, headnk, colon, panc; diag
441790; AW294909; Hs.132208; ESTs; lung; diag
441801; AW242799; Hs.86366; ESTs; blad; diag
441835; AB036432; Hs.184; advanced glycosylation end pro; fibro; mAb
441859; AW194364; Hs.380444; interleukin-4 induced gene-1 p; ovar, mela, fibro; mAb
441878; AI801869; Hs.127982; ESTs; test; diag
442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482; fibro, angio; CTL+s.m.
442082; R41823; Hs.7413; calsyntenin-2; breast, pros, ovar; diag
442104; L20971; Hs.188; phosphodiesterase 4B, cAMP-spe; angio; CTL+s.m.
442108; AW452649; Hs.343259; ESTs; lung; diag
442242; AV647908; Hs.90424; Homo sapiens cDNA: FLJ23285 fi; BPH; diag
442323; AW016669; Hs.29190; ESTs; breast; diag
442333; AI650877; Hs.129302; ESTs; test; diag
442432; BE093589; Hs.38178; hypothetical protein FLJ23468; blad, lung, panc, esoph, mela; CTL+s.m.
442436; AA995998; Hs.370007; gb:os26b03.s1 NCI_CGAP_Kid5 Ho; uter, ovar, renal; diag
442441; AI820662; Hs.129598; ESTs; breast; diag
442503; AF147078; Hs.375031; p53-responsive gene 5; mela; diag
442506; BE566411; Hs.41726; ESTs; angio; diag
442573; H93366; Hs.7567; branched chain aminotransferas; ovar, panc, angio, test; s.m.
442577; AA292998; Hs.163900; ESTs; blad, panc, colon, stom, ovar; diag
442580; AI733682; Hs.130239; ESTs; breast ; diag
442609; AL020996; Hs.8518; selenoprotein N; mela; diag
442613; AI004002; Hs.130522; Kv channel-interacting protein; glio; diag
442622; NM_000435; Hs.8546; Notch (Drosophila) homolog 3; ovar; mAb
442711; AF151073; Hs.8645; hypothetical protein; angio, mela, sarc; diag
442739; NM_007274; Hs.8679; cytosolic acyl coenzyme A thio; mela; s.m.
442757; AI739528; Hs.28345; ESTs; mela; diag
442816; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
442821; BE391929; Hs.8752; transmembrane protein 4; ovar; diag
442832; AW206560; Hs.253569; ESTs; pros, fibro; diag
442896; R37725; Hs.283093; ESTs; panc; diag
442994; AI026718; Hs.16954; ESTs; blad, fibro; diag
443054; AI745185; Hs.84520; yes-associated protein 65 kDa; blad; diag
443162; T49951; Hs.9029; DKFZP434G032 protein; blad, lung; CTL+s.m.
443171; BE281128; Hs.9030; TONDU; blad, ovar; diag

443184; AI638728; Hs.135159; ESTs; sarc; diag
443211; AI128388; Hs.143655; ESTs; blad, ovar, lung, headnk, stom, colon; diag
443216; W80487; Hs.324521; hypothetical protein DC50; test; diag
443257; AI334040; Hs.11614; HSPC065 protein; fibro; CTL+s.m.
443400; R28424; Hs.250648; ESTs; lung; diag
443523; AK001575; Hs.9536; hypothetical protein FLJ10713; test; CTL+s.m.
443537; D13305; Hs.203; cholecystokinin B receptor; test; mAb
443648; AI085377; Hs.143610; ESTs; lung, headnk; diag
443709; AI082692; Hs.134662; ESTs; fibro; diag
443715; AI583187; Hs.9700; cyclin E1; lung, stom, ovar, colon; CTL+s.m.
443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS pro; glio, uter, ovar; CTL+s.m.
443802; AW504924; Hs.9805; KIAA1291 protein; sarc; diag
443883; AA114212; Hs.9930; serine (or cysteine) proteinas; sarc; s.m.
443885; H91806; Hs.15284; ESTs; mela; diag
443892; AI889572; Hs.246875; ESTs; lung; diag
443950; NM_001425; Hs.9999; epithelial membrane protein 3; mela; mAb
443968; AA287702; Hs.10031; KIAA0955 protein; angio; diag
443983; H04482; Hs.163724; ESTs; mela; mAb
443991; NM_002250; Hs.10082; potassium intermediate/small c; pros, colon, uter; mAb
444009; AI380792; Hs.135104; ESTs; angio; diag
444151; AW972917; Hs.128749; alpha-methylacyl-CoA racemase; pros; mAb
444159; AF116846; Hs.10431; dead ringer (Drosophila)-like ; test; CTL+s.m.
444163; AI126098; ; FGENESH predicted RNaseH domai; blad; s.m.
444301; AK000136; Hs.10760; asporin (LRR class 1); panc; diag
444325; AW152618; Hs.16757; ESTs; esoph; diag
444330; AI597655; Hs.49265; ESTs; angio; diag
444342; NM_014398; Hs.10887; similar to lysosome-associated; hepC, lung, fibro, blad, esoph; diag
444378; R41339; Hs.47860; neurotrophic tyrosine kinase, ; lung, glio; mAb+s.m.
444409; AI792140; Hs.49265; ESTs; angio; diag
444444; AI149332; Hs.14855; ESTs; blad; diag
444471; AB020684; Hs.11217; KIAA0877 protein; glio, lung, colon ; mAb
444476; AF020038; Hs.11223; isocitrate dehydrogenase 1 (NA; blad; s.m.
444484; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
444633; AF111713; Hs.12284; junctional adhesion molecule 1; ovar, uter, breast, cerv, blad, headnk; mAb
444649; AW207523; Hs.371001; ESTs; blad; diag
444670; H58373; Hs.332938; hypothetical protein MGC5370; sarc; diag
444754; T83911; Hs.11881; transmembrane 4 superfamily me; panc, omuc, stom, lung, colon; mAb+s.m.
444809; BE207568; Hs.208219; oculospanin; mela; mAb
444823; BE262989; Hs.12045; putative protein; test; diag
444863; AW384082; Hs.104879; serine (or cysteine) proteinas; mela; s.m.
444895; AI674383; Hs.22891; solute carrier family 7 (catio; ovar; mAb+s.m.
444995; AJ272265; Hs.12230; secreted phosphoprotein 2, 24k; hepC, panc; diag
445019; AI205540; Hs.281295; ESTs; headnk, lung, colon; diag
445070; NM_000677; Hs.258; adenosine A3 receptor; glio, renal; mAb
445076; AI206888; Hs.154131; ESTs; test; diag
445084; H38914; Hs.250848; hypothetical protein FLJ14761; sarc; mAb
445093; AI207197; Hs.156905; ESTs; test; diag
445109; AF039916; Hs.12330; ectonucleoside triphosphate di; pros; s.m.
445119; AF035121; Hs.12337; kinase insert domain receptor ; angio; mAb
445160; AI299144; Hs.101937; sine oculis homeobox (Drosophi; sarc; CTL+s.m.
445182; AW189787; Hs.361778; ESTs; blad; diag
445247; AW274290; Hs.153997; ESTs; mela; diag
445279; R41900; Hs.22245; ESTs; angio; diag
445363; NM_005993; Hs.12570; tubulin-specific chaperone d; test; diag
445413; AA151342; Hs.12677; CGI-147 protein; pros, colon, uter, ovar, lung, panc ; diag
445418; AW139377; Hs.127179; cryptic gene; panc; diag
445424; AB028945; Hs.12696; cortactin SH3 domain-binding p; pros ; diag
445443; AV653838; Hs.295131; ESTs; lung; diag
445654; X91247; Hs.13046; thioredoxin reductase 1; lung; s.m.
445684; AK001696; Hs.13109; Ran binding protein 11; angio; diag
445701; AF055581; Hs.13131; lymphocyte adaptor protein; angio; CTL+s.m.
445784; AI253155; Hs.146065; ESTs; mela; CTL+s.m.
445885; AI734009; Hs.127699; KIAA1603 protein; pros, fibro; diag
445900; AF070526; Hs.125036; Homo sapiens clone 24787 mRNA ; renal, leuk; mAb
445911; AI985987; Hs.145645; ESTs, Moderately similar to AL; blad; diag
445982; BE410233; Hs.13501; pescadillo (zebrafish) homolog; mela; diag
446057; AI420227; Hs.366053; Trp-p8 transient receptor pote; pros; mAb
446082; AI274139; Hs.156452; ESTs; blad; diag
446098; AW072215; Hs.208470; ESTs; angio; diag
446100; AW967109; Hs.13804; hypothetical protein dJ462O23.; pros; diag
446102; AW168067; Hs.317694; ESTs; lung; diag
446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083; test; mAb
446269; AW263155; Hs.14559; hypothetical protein FLJ10540; lung, headnk; CTL+s.m.
446291; BE397753; Hs.14623; interferon, gamma-inducible pr; mela; diag
446292; AF081497; Hs.279682; Rh type C glycoprotein; lung, cerv; mAb
446293; AI420213; Hs.149722; LIM domain transcription facto; ovar, test; diag
446320; AF126245; Hs.14791; acyl-Coenzyme A dehydrogenase ; pros; s.m.
446332; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
446342; BE298665; Hs.14846; solute carrier family 7 (catio; uter, colon, pros, mela; mAb
446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4_H; fibro; diag
446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); lung, test; diag
446608; N75217; Hs.175622; ESTs; uter, fibro; diag
446626; AW292180; Hs.156142; ESTs; pros; diag

446636; AC002563; Hs.15767; citron (rho-interacting, serin; lung; CTL+s.m.
446644; NM_003272; Hs.21065; transmembrane 7 superfamily me; mela; mAb
446673; NM_016361; Hs.15871; LPAP for lysophosphatidic acid; blad; diag
446727; AB011095; Hs.16032; KIAA0523 protein; angio; CTL+s.m.
446733; AA863360; Hs.26040; ESTs, Weakly similar to fatty ; breast; s.m.
446755; AW451473; Hs.16134; serine/threonine kinase 10; mela; CTL+s.m.
446791; AI632278; Hs.195922; ESTs; test; diag
446839; BE091926; Hs.16244; mitotic spindle coiled-coil re; test; diag
446856; AI814373; Hs.164175; ESTs; lung; diag
446868; AV660737; Hs.348297; ESTs; panc; diag
446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G; lung; mAb
446932; AA961459; Hs.125644; ESTs; fibro; diag
446967; AI699629; Hs.156781; ESTs; fibro; diag
446979; AI654443; Hs.197683; ESTs; test; diag
446984; AB020722; Hs.16714; Rho guanine exchange factor (G; angio; CTL+s.m.
446989; AK001898; Hs.16740; hypothetical protein FLJ11036; lung, headnk; diag
446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; panc, fibro; diag
446999; AA151520; Hs.351416; hypothetical protein MGC4485; headnk; diag
447004; AW296968; Hs.157539; FGENESH predicted secreted pro; glio; diag
447078; AW885727; Hs.9914; ESTs; lung; diag
447126; AW150632; Hs.170307; Ral guanine nucleotide exchang; angio; diag
447164; AF026941; Hs.17518; vipirin; similar to inflammat; colon, lung, breast, stom, hepC, esoph, mela; diag
447178; AW594641; Hs.192417; ESTs; mela; diag
447188; H65423; Hs.17631; hypothetical protein DKFZp434E; test; diag
447210; AF035269; Hs.17752; phosphatidylserine-specific ph; pros, mela; s.m.
447289; AW247017; Hs.36978; melanoma antigen, family A, 3; lung, mela; mAb+CTL
447334; AA515032; Hs.91109; ESTs; blad; diag
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392; lung, blad, panc, headnk, mela; mAb+s.m.
447350; AI375572; Hs.172634; v-erb-a avian erythroblastic l; breast, ovar, uter; diag
447377; X77343; Hs.334334; transcription factor AP-2 alph; breast, lung, mela; CTL+s.m.
447395; AI418412; Hs.184793; Homo sapiens cDNA: FLJ21880 fi; panc; diag
447437; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
447499; AW262580; Hs.147674; protocadherin beta 16; pros, glio, ovar ; mAb+s.m.
447532; AK000614; Hs.18791; hypothetical protein FLJ20607; lung, blad; CTL+s.m.
447534; AW953935; Hs.288655; ESTs; lung, test; diag
447578; AA912347; Hs.136585; ESTs, Weakly similar to JC5314; ovar; s.m.
447595; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
447604; AW089933; Hs.301342; hypothetical protein MGC4342; mela; diag
447636; Y10043; Hs.19114; high-mobility group (nonhiston; lung; CTL+s.m.
447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient; test; diag
447749; T53260; Hs.8297; ESTs; renal; diag
447761; AF061573; Hs.19492; protocadherin 8; EWS, glio; mAb
447768; X86400; Hs.19520; FXYD domain-containing ion tra; renal; mAb
447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA ; renal; diag
447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022; renal, ovar, uter; diag
447881; BE620886; Hs.355279; GCN1 (general control of amino; renal; diag
447937; AL109716; Hs.20034; Homo sapiens mRNA full length ; mela; mAb
447993; AW139525; Hs.170362; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
448030; N30714; Hs.325960; membrane-spanning 4-domains, s; panc, leuk, renal, stom lung; mAb
448045; AJ297436; Hs.20166; prostate stem cell antigen; blad, panc, pros; mAb
448105; AW591433; Hs.298241; Transmembrane protease, serine; breast, panc, colon, lung, ovar, stom; mAb+diag+s.m.
448133; AA723157; Hs.73769; folate receptor 1 (adult); ovar, fibro; mAb
448140; AF146761; Hs.20450; BCM-like membrane protein prec; fibro, mela, leuk; mAb
448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase,; test; CTL+s.m.
448181; AF272833; Hs.279763; hypothetical protein FLJ10504; test; diag
448204; AI475124; Hs.170561; ESTs; sarc; diag
448231; AI701916; Hs.202509; ESTs; angio; diag
448258; BE386983; Hs.343214; hypothetical protein FLJ20396; mela, ovar; mAb
448262; AW880830; Hs.186273; ESTs; blad; diag
448275; BE514434; Hs.20830; kinesin-like 2; ovar, esoph, mela; diag
448278; W07369; Hs.11782; ESTs; lung; diag
448290; AK002107; Hs.20843; Homo sapiens cDNA FLJ11245 fis; pros; diag
448321; NM_005883; Hs.20912; adenomatous polyposis coli lik; glio; CTL+s.m.
448357; N20169; Hs.108923; RAB38, member RAS oncogene fam; lung, mela; diag
448410; AK000227; Hs.21126; hypothetical protein FLJ20220; mela; diag
448437; AW470125; Hs.220529; gb:xw60c04.x1 NCI_CGAP_Pan1 Ho; panc, colon; diag
448499; BE613280; Hs.77550; p53-regulated DDA3; glio; diag
448569; BE382657; Hs.21486; signal transducer and activato; panc, headnk, fibro, cerv, mela, renal; CTL+s.m.
448588; AI970276; Hs.156905; KIAA1676; test; CTL+s.m.
448595; AB014544; Hs.21572; KIAA0644 gene product; breast, glio; mAb
448664; AI879317; Hs.334691; splicing factor 3a, subunit 1,; mela; CTL+s.m.
448674; W31178; Hs.154140; ovary-specific acidic protein; angio; diag
448692; AW013907; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
448706; AW291095; Hs.21814; interleukin 20 receptor, alpha; pros, uter, blad, colon; mAb
448719; AA033627; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag
448775; AB025237; Hs.388; nudix (nucleoside diphosphate ; test; diag
448811; AI590371; Hs.199460; ESTs; esoph, panc; mAb
448939; BE267795; Hs.22595; hypothetical protein FLJ10637; test; CTL+s.m.
448966; AW372914; Hs.86149; phosphoinositol 3-phosphate-bi; mela; CTL+s.m.
448981; AI968719; Hs.195387; ESTs; test; diag
448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros, cerv, colon, lung, stom, blad, headnk, ovar, breast; mAb
448993; AI471630; Hs.355952; KIAA0144 gene product; lung, blad; diag
448999; AF179274; Hs.22791; transmembrane protein with EGF; pros, glio ; mAb

449003; X76342; Hs.389; alcohol dehydrogenase 7 (class; lung, headnk; s.m.
449019; AI949095; Hs.67776; ESTs, Weakly similar to T22341; blad, lung; diag
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; blad, colon, ovar; s.m.
449040; NM_012191; Hs.22919; putative tumor suppressor; lung; CTL+s.m.
449078; AK001256; Hs.22975; KIAA1576 protein; mela; diag
449101; AA205847; Hs.23016; G protein-coupled receptor; lung, headnk; mAb
449109; AW270992; Hs.120949; ESTs, Weakly similar to ALU7_H; sarc; diag
449156; AF103907; Hs.171353; prostate cancer antigen 3, non; pros; mAb+CTL
449207; AL044222; Hs.23255; nucleoporin 155kD; lung; diag
449228; AJ403107; Hs.148590; protein related with psoriasis; lung; diag
449230; BE613348; Hs.356392; melanoma cell adhesion molecul; lung, cerv, headnk, blad, ovar, colon; mAb
449317; AW293413; Hs.132906; 19A24 protein; mela; mAb
449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN; headnk, lung, angio; CTL+s.m.
449322; AI638616; Hs.196566; ESTs; test; diag
449338; H73444; Hs.394; adrenomedullin; renal; diag
449394; AA004368; Hs.18160; Homo sapiens cDNA FLJ11550 fis; angio; mAb
449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fi; test; diag
449448; D60730; Hs.57471; ESTs; blad, lung, headnk, breast; diag
449467; AW205006; Hs.197042; ESTs; lung; diag
449494; AW237014; Hs.315369; aquaporin 4; fibro; diag
449569; AI656634; Hs.195389; ESTs; test; diag
449592; AI655494; Hs.195718; ESTs; panc; diag
449618; AI076459; Hs.15978; KIAA1272 protein; angio; diag
449625; NM_014253; Hs.349094; odz (odd Oz/ten-m, Drosophila); pros; diag
449650; AF055575; Hs.23838; calcium channel, voltage-depen; pros; mAb
449680; AI033821; Hs.12160; ESTs; renal; diag
449961; AW265634; Hs.133100; ESTs; glio, esoph, lung, blad ; diag
449976; H06350; Hs.135056; Human DNA sequence from clone ; lung; diag
450096; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
450098; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
450149; AW969781; Hs.132863; Zic family member 2 (odd-paire; sarc; CTL+s.m.
450152; AI138635; Hs.22968; intron of VEGFR; renal; diag
450377; AB033091; Hs.355925; KIAA1265 protein; ovar, colon; diag
450382; AA397658; Hs.60257; Homo sapiens cDNA FLJ13598 fis; pros; diag
450400; AI694722; Hs.279744; ESTs; panc; diag
450431; AW136797; Hs.266041; ESTs; test; diag
450451; AW591528; Hs.202072; ESTs; uter, endo; diag
450506; NM_004460; Hs.418; fibroblast activation protein,; panc, esoph; diag
450534; AI570189; Hs.25132; KIAA0470 gene product; angio; CTL+s.m.
450581; AF081513; Hs.25195; TGF-beta 4; uter, cerv, test; diag
450635; AW403954; Hs.25237; mesenchymal stem cell protein ; blad; mAb
450642; R39773; Hs.7130; copine IV; pros; diag
450656; AA010539; Hs.18912; unnamed protein product; fibro, uter; CTL+s.m.
450663; H43540; Hs.25292; ribonuclease HI, large subunit; mela; s.m.
450676; AI147155; Hs.279727; ESTs; sarc; diag
450684; AA872605; Hs.25333; interleukin 1 receptor, type I; blad, lung, headnk; mAb
450690; AA296696; Hs.333418; FXYD domain-containing ion tra; mela; diag
450693; AW450461; Hs.203965; ESTs; pros, uter; diag
450719; AI096837; Hs.21349; ESTs, Weakly similar to RB8B_H; test; diag
450737; AW007152; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
450785; AA852713; Hs.108886; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
450832; AW970602; Hs.105421; ESTs; lung; diag
451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN; pros, uter, glio; diag
451035; AU076785; Hs.430; plastin 1 (I isoform); panc; diag
451050; AW937420; Hs.351869; ESTs; mela; diag
451099; R52795; Hs.25954; interleukin 13 receptor, alpha; glio, fibro, mela; mAb
451106; BE382701; Hs.25960; N-MYC oncogene; test, ovar; CTL+s.m.
451110; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast, ovar, lung, colon; CTL+s.m.
451181; AI796330; Hs.207461; ESTs; panc; diag
451253; H48299; Hs.26126; claudin 10; lung, ovar, panc; mAb
451291; R39288; Hs.6702; ESTs; lung; diag
451295; AI557212; Hs.17132; ESTs, Moderately similar to I5; panc; diag
451320; AW118072; Hs.350251; diacylglycerol kinase, zeta (1; lung; s.m.
451346; NM_006338; Hs.26312; glioma amplified on chromosome; ovar; mAb
451386; AB029006; Hs.26334; spastic paraplegia 4 (autosoma; lung; diag
451398; AI793124; Hs.144479; ESTs; breast, ovar; diag
451411; AA017492; Hs.135655; EST; pros; diag
451497; H83294; Hs.284122; Wnt inhibitory factor-1; uter, fibro, pros, colon, sarc; diag
451541; BE279383; Hs.26557; plakophilin 3; lung, blad, ovar; diag
451592; AI805416; Hs.213897; ESTs; lung, headnk; diag
451635; AA018899; Hs.127179; cryptic gene; panc; diag
451663; AI872360; Hs.209293; ESTs; pros; diag
451720; AW970985; Hs.290853; ESTs; pros; diag
451743; AW074266; Hs.336428; ESTs; lung; diag
451820; AW058357; Hs.199248; ESTs; panc; mAb
451844; T61430; ; gb:yc06a03.s1 Stratagene lung ; blad; diag
451982; F13036; Hs.27373; Homo sapiens mRNA; cDNA DKFZp5; pros, blad; mAb
451999; AW176401; Hs.380623; DEAD/H (Asp-Glu-Ala-Asp/His) b; test; CTL+s.m.
452046; AB018345; Hs.27657; KIAA0802 protein; lung, uter; CTL+s.m.
452208; AA024792; Hs.31895; hypothetical protein MGC4093; renal; diag
452240; AI591147; Hs.61232; ESTs; blad, lung, headnk, panc, cerv; diag
452243; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
452244; N33530; Hs.176674; ESTs; mela; diag

452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S; test; CTL+s.m.
452295; BE379936; Hs.28866; programmed cell death 10; lung; diag
452298; AI039243; Hs.278585; ESTs; angio; diag
452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590; lung, panc, blad, stom, esoph, fibro,colon; s.m.
452316; AA298484; Hs.61265; ESTs, Moderately similar to G7; blad; diag
452340; NM_002202; Hs.505; ISL1 transcription factor, LIM; panc, pros; CTL+s.m.
452353; C18825; Hs.29191; epithelial membrane protein 2; pros, breast; mAb
452355; N54926; Hs.29202; G protein-coupled receptor 34; glio, fibro, panc; mAb
452367; U71207; Hs.29279; eyes absent (Drosophila) homol; lung, pros, ovar, uter; CTL+s.m.
452416; AA026115; Hs.114777; ESTs; fibro; diag
452461; N78223; Hs.108106; transcription factor; blad, lung, headnk, ovar, glio, stom, colon, cerv; CTL+s.m.
452571; W31518; Hs.34665; ESTs; stom, lung, panc, colon, fibro; diag
452594; AU076405; Hs.29981; solute carrier family 26 (sulf; ovar; mAb
452613; AA461599; Hs.23459; ESTs; lung; diag
452679; Z42387; Hs.83883; transmembrane, prostate androg; pros, colon, panc, pros; mAb
452705; H49805; Hs.246005; ESTs; panc; diag
452717; AW160399; Hs.30376; hypothetical protein; pros; diag
452721; AJ269529; Hs.301871; solute carrier family 37 (glyc; pros; mAb
452732; BE300078; Hs.80449; Homo sapiens, clone IMAGE:3535; blad; diag
452744; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; mela; diag
452792; AB037765; Hs.30652; KIAA1344 protein; pros, uter, breast ; diag
452795; AW392555; Hs.18878; hypothetical protein FLJ21620; renal, headnk, colon, lung, panc; CTL
452796; AB011100; Hs.30656; KIAA0528 gene product; test; diag
452833; BE559681; Hs.30736; KIAA0124 protein; lung, mela; CTL+s.m.
452865; AI924046; Hs.119567; ESTs, Weakly similar to A47582; lung; diag
452899; M96739; Hs.30956; nescient helix loop helix 1; sarc; CTL+s.m.
452924; AW580939; Hs.97199; complement component C1q recep; angio; diag
452933; AW391423; Hs.288555; Homo sapiens cDNA: FLJ22425 fi; angio; CTL+s.m.
452934; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
452955; AW390282; Hs.31130; transmembrane 7 superfamily me; pros; mAb+s.m.
453006; AI362575; Hs.303171; ESTs; pros; diag
453028; AB006532; Hs.31442; RecQ protein-like 4; blad, lung, test; CTL+s.m.
453085; AW954243; Hs.351573; KIAA0251 protein; angio; diag
453096; AW294631; Hs.351270; ESTs; pros; diag
453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog ; lung, headnk, colon; mAb
453107; NM_016113; Hs.279746; vanilloid receptor-like protei; mela; mAb
453134; AA032211; Hs.118493; ESTs; blad; diag
453142; AA033648; Hs.7473; Homo sapiens gap junction prot; fibro; mAb
453160; AI263307; Hs.356901; H2B histone family, member L; lung, panc, pros; diag
453210; AL133161; Hs.32360; hypothetical protein FLJ10867; lung; CTL+s.m.
453216; AL137566; Hs.32405; progesterone receptor (PR); blad; mAb+s.m.
453256; AI565587; Hs.32556; KIAA0379 protein; mela; diag
453310; X70697; Hs.553; solute carrier family 6 (neuro; fibro; mAb
453321; AI984381; Hs.232521; ESTs; blad; diag
453323; AF034102; Hs.32951; solute carrier family 29 (nucl; ovar; CTL+s.m.
453331; AI240665; Hs.352537; ESTs; breast, lung, panc, esoph; mAb+diag+s.m.
453344; BE349075; Hs.44571; ESTs; mela; diag
453348; BE272318; Hs.8595; hypothetical protein FLJ12438; test; CTL+s.m.
453365; AA035211; Hs.17404; SOX7 SRY (sex determining regi; angio, blad; CTL+s.m.
453370; AI470523; Hs.139336; ATP-binding cassette, sub-fami; pros; mAb
453389; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; renal, ovar, blad; mAb+s.m.
453392; U23752; Hs.32964; SRY (sex determining region Y); ovar, lung, glio, sarc; CTL+s.m.
453459; BE047032; Hs.257789; ESTs; ovar, cerv, blad, uter, panc, angio, lung; diag
453464; AI884911; Hs.32989; receptor (calcitonin) activity; pros; mAb
453633; AA357001; Hs.34045; hypothetical protein FLJ20764; lung, esoph, test; diag
453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); headnk; mAb
453642; AI370936; Hs.34074; dipeptidylpeptidase VI; glio; mAb
453779; N35187; Hs.43388; 28kD interferon responsive pro; mela; diag
453789; AA628517; Hs.118502; ESTs; angio; diag
453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1; glio, lung, uter, headnk, cerv, panc, pros, sarc; mAb
453883; AI638516; Hs.347524; cofactor required for Sp1 tran; blad, lung; diag
453884; AA355925; Hs.36232; KIAA0186 gene product; lung, ovar, test, esoph; diag
453912; AL121031; Hs.356843; SWI/SNF related, matrix associ; mela; diag
453922; AF053306; Hs.36708; budding uninhibited by benzimi; colon, stom, lung, test; CTL+s.m.
453935; AI633770; Hs.42572; ESTs; panc; diag
453941; U39817; Hs.36820; Bloom syndrome; lung, cerv, headnk; CTL+s.m.
453964; AI961486; Hs.249196; ESTs; lung; diag
453966; BE148734; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
453985; N44545; Hs.251865; ESTs; test; diag
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 famil; lung, headnk; s.m.
454042; H22570; Hs.47860; hypothetical protein FLJ20093; lung; diag
454066; X00356; Hs.37058; calcitonin/calcitonin-related ; lung; diag
454071; AI041793; Hs.42502; ESTs; breast ; diag
454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); test; diag
454098; W27953; Hs.217493; Plakophilin; lung; diag
454117; BE410100; Hs.40368; adaptor-related protein comple; mela; CTL+s.m.
454360; L78207; Hs.54470; ATP-binding cassette, sub-fami; glio; mAb
454429; BE273437; Hs.301406; hypothetical protein PP3501; mela; mAb
454439; AW819152; Hs.154320; DKFZP566O1646 protein; lung; diag
454478; AW805749; Hs.372783; superoxide dismutase 2, mitoch; mela; s.m.
455601; AI368680; Hs.816; SRY (sex determining region Y); lung, cerv, esoph; s.m.
456034; AW450979; ; gb:UI-H-BI3-ala-a-12-0-UI.s1 N; blad, fibro; diag
456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298; fibro, ovar, uter; diag

456177; NM_012391; Hs.79414; prostate epithelium-specific E; breast, pros; diag
456266; L29073; Hs.198726; cold shock domain protein A; panc; CTL+s.m.
456321; NM_001327; Hs.87225; cancer/testis antigen; lung; CTL
456553; AA721325; Hs.189058; ESTs, Highly similar to Simila; panc; diag
456723; Z43902; Hs.4748; adenylate cyclase activating p; glio; mAb+s.m.
456736; AW248217; Hs.1619; achaete-scute complex (Drosoph; lung; diag
456759; BE259150; Hs.127792; delta (Drosophila)-like 3; glio, lung; mAb
456847; AI360456; Hs.86088; ESTs; test; diag
456938; X52509; Hs.161640; tyrosine aminotransferase; breast; s.m.
456977; AK000252; Hs.169758; hypothetical protein FLJ20245; angio; diag
457200; U33749; Hs.197764; thyroid transcription factor 1; fibro; CTL+s.m.
457211; AW972565; Hs.32399; ESTs, Weakly similar to S51797; mela, pros; CTL+s.m.
457292; AI921270; Hs.281462; hypothetical protein FLJ14251; blad; mAb
457313; AF047002; Hs.241520; transcriptional coactivator; test; CTL+s.m.
457411; AW085961; Hs.130093; iroquois-class homeobox protei; breast, fibro; diag
457465; AW301344; Hs.122908; DNA replication factor; test, mela; diag
457498; AI732230; Hs.191737; ESTs; pros; diag
457561; AA331517; Hs.286055; chimerin (chimaerin) 2; glio; mAb
457590; AI612809; Hs.5378; hypothetical protein MGC10724; ovar; diag
457869; AU077186; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
458092; W67353; Hs.350558; KIAA0251 protein; lung; diag
458124; AW005548; Hs.124590; ESTs; fibro; diag
458435; AI418718; Hs.144121; ESTs, Weakly similar to T46916; glio; diag
458471; AV648609; Hs.194240; ESTs; renal, panc, hepC; diag
458933; AI638429; Hs.24763; RAN binding protein 1; lung, test; diag
459373; BE408266; Hs.301406; hypothetical protein PP3501; mela; mAb
459578; AW612538; Hs.304491; EST; mela; diag
459702; AI204995; ; gb:an03c03.x1 Stratagene schiz; blad, fibro; diag
459705; BE082764; Hs.270252; ESTs, Weakly similar to androg; fibro; mAb+s.m.

TABLE 3B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
103739	49403_2	AA115173 AA075709 AA076354 AA083101 AA076396 AA085391 AA070684 AA083368 AA075779 AA075221 AA076395 AA650486 AA083500
108282	108971_1	AA065143 AA065142
113230	2327174_1	AI820546 AI821336 T61430
118417	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951 N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833 AA207155 BI004756 AA206262 AI365204 H77608 AW590511
121335	1369289_1	AA404418 AI217248
126872	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
322521	14637_1	AF147347 T55503 T55426
322975	1784158_1	C16391 C16413
323332	245301_1	AI829520 AI791832 AI791823 AA229315 AA228414 AA229211
323817	887879_1	AA410943 BF366582 AA334202 AA332882 BF371899 AW948953
324261	1026976_1	AL044891 AI908240 AA393080 AW748403 BE069341 BF330573
406685	0_0	M18728
409051	107934_1	AA075419 AA082953 AA080912 AA062835 AA071252 AA084926 AA078992 AA113913 AA081881 AA070343 AA083821 AA062836 AA113892 AA075318 AA076594 AA078900 AA134801 AA063293 AA083403 AW974305
409123	108378_1	AA070050 AA070823 AA063403
409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
411880	1139083_1	BE088101 T05990 AW872477
413804	1556661_1	BE168256 BE168190 T64682
414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
427260	11272_50	AA401424 AA400100 AA663848
427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
429163	1238297_1	AW974271 AA592975 AA447312 AA884766
432189	112710_1	AA527941 AA635266 AI810608 AI620190
432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
432415	11371_1	BG166382 AW161086 N42363 BE935013 BE934998 BG291451 AV700520 BG152773 AI224956 AI079635 AW054706 AA843979 AI744193 F04060 T23457 F04044 AA723859 AA977643 AA283764 AI123609 N21561 BF055052 BE856661 AI804220 AA843394 AI472045 AI740490 AA578830 H09495 AI283334 AA609495 AI122773 AW162643 AW161798 BF940077 AI808825 AI360866 AI123189 R40236 R20726 AW975899 BE764052 N31709 N31708 AI031947 AW194138
434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298

			AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
	434596	14701_1	AF147374 T59538 T59589 T59598 T59542
	434609	14739_1	AF147390 R76593 R76594
	438966	1242593_1	AW979074 AA834841 AA828650
	438993	2580163_1	AI926361 AA834879 AA828995
	439092	919640_1	AW978407 AA830149 M85983 AW503637 BF352096
	439780	49082_1	AL109688 R23665 R26578
	440151	1879911_1	AA868167 F21558 F31418 F35624
	444163	682245_1	BG403189 AI148521 AI184746 AI126098 R05933 BI057330
	451844	2327174_1	AI820546 AI821336 T61430
	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354

TABLE 3C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
325372	5866920	Minus	1117061-1117304
325544	6682452	Plus	171228-171286
327036	6531965	Plus	319951-320040
327075	6531965	Plus	4041318-4041431
327414	5867750	Plus	102461-102586
328700	5868264	Plus	764089-764203
330211	6013592	Plus	59158-59215
332798	Dunham, I. et.al.	Minus	232147-231974
333769	Dunham, I. et.al.	Plus	7696625-7696707
333904	Dunham, I. et.al.	Minus	8217374-8217261
334223	Dunham, I. et.al.	Minus	12734365-12734269
334447	Dunham, I. et.al.	Plus	14308764-14308824
335115	Dunham, I. et.al.	Minus	21388250-21388146
335809	Dunham, I. et.al.	Plus	26310772-26310909
335824	Dunham, I. et.al.	Plus	26376860-26376942
335825	Dunham, I. et.al.	Plus	26378175-26378268
335936	Dunham, I. et.al.	Minus	27360474-27360400
336034	Dunham, I. et.al.	Plus	29014404-29014590
336152	Dunham, I. et.al.	Minus	30156053-30155870
336636	Dunham, I. et.al.	Plus	988418-989185
338008	Dunham, I. et.al.	Plus	7697068-7697236
338033	Dunham, I. et.al.	Plus	8092128-8092271
338158	Dunham, I. et.al.	Minus	11794465-11794343
338255	Dunham, I. et.al.	Minus	15242294-15242231
400494	9714719	Plus	169845-170272
400517	9796686	Minus	49996-50346
400651	8117978	Minus	81488-81646
400665	8118496	Plus	16879-17023
400773	8131629	Minus	44116-44238,48208-48321
400844	9188605	Plus	24746-24872,25035-25204
400846	9188605	Plus	39310-39474
400881	2842777	Minus	91446-91603,92123-92265
401093	8516137	Minus	22335-23166
401234	9929642	Plus	120173-120337
401424	8176894	Plus	24223-24428
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
401704	3097841	Plus	24712-25374
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,2006
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
401797	6730720	Plus	6973-7118
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
402145	8018280	Plus	113086-114800
402199	8576116	Minus	84187-84744
402230	9966312	Minus	29782-29932
402239	7690131	Plus	38175-38304,42133-42266
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
402265	3287673	Plus	21059-21168
402305	7328724	Plus	40832-41362
402420	9796339	Plus	129750-129919
402424	9796344	Minus	64925-65073
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402550	7652009	Minus	80413-80673
402604	9909420	Plus	20393-20767
402605	9909420	Minus	47680-47973

402606	9909429	Minus	81747-82094
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
402777	9588235	Plus	126786-126948
402860	9588237	Minus	76423-76560
402888	9930892	Minus	54727-54901
402992	7767907	Minus	42137-42515
402994	2996643	Minus	4727-4969
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403071	8954241	Plus	136688-137096
403088	8954241	Plus	169894-170193,170504-170806
403171	9838164	Minus	74502-74703
403328	8469086	Minus	120428-120703
403329	8516120	Plus	96450-96598
403381	9438267	Minus	26009-26178
403409	9438598	Plus	6860-7054,12573-12771
403433	9719611	Minus	72225-72437
403478	9958258	Plus	116458-116564
403715	7239669	Plus	85128-85292
403740	7630882	Plus	86504-87227
403776	7770611	Minus	1414-1513,1624-1756
403903	7710671	Minus	101165-102597
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404210	5006246	Plus	169926-170121
404240	5002624	Minus	116132-116407,116653-116922
404253	9367202	Minus	55675-56055
404286	2326514	Plus	51086-51301
404298	9944263	Minus	73591-73723
404403	7272157	Minus	72053-72238
404440	7528051	Plus	80430-81581
404866	9366919	Minus	11743-11929
404877	1519284	Plus	1095-2107
404927	7342002	Plus	68690-69563
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
405001	6015406	Minus	104646-104819
405025	7107727	Plus	105267-105343,106184-106294,106387-10653
405121	8102330	Minus	35816-36004,36587-36684
405238	7249119	Minus	51728-51836
405239	7249119	Plus	144345-144464,144690-144836,151750-15188
405451	7622517	Minus	145949-146227
405545	1054740	Plus	118677-118807,119091-119296,121626-12182
405546	1054740	Plus	124010-124183
405547	1054740	Plus	124361-124520,124914-125050
405646	4914350	Plus	741-969
405704	4204244	Plus	138842-139051
405770	2735037	Plus	61057-62075
405849	7651817	Minus	17705-18287
405932	7767812	Minus	123525-123713
406081	9123861	Minus	38115-38691
406137	9166422	Minus	30487-31058
406173	7230224	Plus	12925-13213
406348	9255985	Minus	71754-71944
406360	9256107	Minus	7513-7673
406399	9256288	Minus	63448-63554
406434	9256651	Minus	17803-17931
406467	9795551	Plus	182212-182958
406506	7711374	Minus	6843-8077
406547	7711513	Minus	172780-174358

Table 4A lists about 425 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues. These genes were selected from a starting collection of about 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 75th percentile value amongst non-malignant adult tissues. Certain predicted protein domains are noted.

Table 5A lists about 231 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected similarly as for Table 1. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 50th percentile value amongst non-malignant adult tissues. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

TABLE 4A: ABOUT 425 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar accession number, GenBank accession number
UniGeneID:	Unigene number
Pred.Prot.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title:	Unigene gene title
R1:	Ratio of 90th percentile of tumor to 75th percentile of normal body tissue

Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGeneTitle	R1

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419551	AW582256	Hs.91011	TM=M;SS=M	anterior gradient 2 (Xenopus laevis	9.7
426174	AA547959	Hs.115838		Homo sapiens similar to Echinoidin	7.0
409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	6.8
428471	X57348	Hs.184510	14-3-3;TM=M;SS=N	stratifin	6.4
417931	W95642	Hs.82961	trefoil;TM=N;SS=M	trefoil factor 3 (intestinal)	6.3
447966	AA340605	Hs.105887	Jacalin;TM=N;SS=M	ESTs, Weakly similar to Homolog of	6.1
406387				Target Exon	6.0
421814	L12350	Hs.108623	EGF,tsp_1,vwc,TSPN,tsp_3;	thrombospondin 2	5.8
406867	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	5.8
426104	AI204418	Hs.190080		ESTs	5.8
421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	5.8
422511	AU076442	Hs.117938	Collagen,none	collagen, type XVII, alpha 1	5.7
426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	5.6
419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXYD domain-containing ion transpor	5.5
419329	AY007220	Hs.288998	S_100;TM=M;SS=N	S100-type calcium binding protein A	5.4
418344	AA216387			gb:nc16b02.s1 NCI_CGAP_Pr1 Homo sap	5.2
407116	AA130986	Hs.271627		ESTs	5.1
417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	5.1
419452	U33635	Hs.90572	ig,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	5.1
421552	AF026692	Hs.105700	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 4	5.1
409453	AI885516	Hs.95612	cadherin,cadherin,Cadheri	ESTs	5.1
409632	W74001	Hs.55279	serpin;TM=N;SS=N	serine (or cysteine) proteinase inh	5.1
417515	L24203	Hs.82237	zf-B_box,zf-UBR1;TM=M;SS=	ataxia-telangiectasia group D-assoc	5.0
411573	AB029000	Hs.70823	Sulfatase;TM=M;SS=N	KIAA1077 protein	5.0
418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	5.0
422087	X58968	Hs.111301	fn2,hemopexin,Peptidase_M	matrix metalloproteinase 2 (gelatin	5.0
421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	4.9
408491	AI088063	Hs.7882		ESTs	4.9
417944	AU077196	Hs.82985	vwc,Collagen,COLFI;TM=N;S	collagen, type V, alpha 2	4.9
409062	AL157488	Hs.50150		Homo sapiens mRNA; cDNA DKFZp564B18	4.9
422281	M36803	Hs.346935	hemopexin;TM=N;SS=M	hemopexin	4.9
425308	M97639	Hs.155585	ig,kringle,pkinase,Fz;TM=	receptor tyrosine kinase-like orpha	4.8
408349	BE546947	Hs.44276	homeobox;TM=M;SS=N	homeo box C10	4.8
449019	AI949095	Hs.67776		ESTs, Weakly similar to T22341 hypo	4.8
435561	AA351978	Hs.4943	MAGE,Cys_knot,EGF,laminin	hepatocellular carcinoma associated	4.8
410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	4.8
429455	AI472111	Hs.278694	lectin_c	CD209 antigen	4.8
414407	AA147026	Hs.76704		ESTs	4.8
419390	AI701162	Hs.331904	PMP22_Claudin,PMP22_Claud	hypothetical protein MGC11138	4.7
453902	BE502341	Hs.3402		ESTs	4.7
411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	4.7
450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	4.7
449717	AB040935	Hs.23954	Glyco_transf_25;TM=N;SS=N	cerebral cell adhesion molecule	4.6
451529	AI917901	Hs.208641	actin,none	ESTs	4.6
435370	AI964074	Hs.225838	EGF,fn3,fibrinogen_C,toxi	ESTs	4.6
411761	AI733848	Hs.71935	zf-C2H2;TM=M;SS=N	putative zinc finger protein from E	4.6
424223	AJ243706	Hs.143323	PHD,ARID,jmjC,jmjN,zf-C5H	putative DNA/chromatin binding moti	4.6
426935	NM_000088	Hs.172928	vwc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	4.5
408796	AA688292	Hs.170345	hormone_rec,zf-C4	ESTs	4.5
407230	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	4.4
422830	AC007954	Hs.121371		hypothetical protein DKFZp434P0111	4.4
447526	AI612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	4.4
430168	AW968343	Hs.145582	efhand,efhand	DKFZP434I1735 protein	4.4
423225	AA852604	Hs.125359	ig,Ribosomal_S19;TM=M;SS=	Thy-1 cell surface antigen	4.4
414822	AA156542	Hs.72127	homeobox,HLH	ESTs	4.4
452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	4.4
444784	D12485	Hs.11951	Somatomedin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	4.4
453857	AL080235	Hs.35861	TM=Y;SS=M	Ras-induced senescence 1 (RIS1)	4.4
413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	4.3
440369	AW176150	Hs.132449		downstream of breast cancer antigen	4.3
418140	BE613836	Hs.83551	TM=M;SS=M	microfibrillar-associated protein 2	4.3
441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	4.3
424464	R68537	Hs.17962	homeobox,none	ESTs	4.3
423582	BE000831	Hs.23837	TGFb_propeptide,TGF-beta,	Homo sapiens cDNA FLJ11812 fis, clo	4.3
432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	4.2
433320	D60647	Hs.250879	rrm	ESTs, Highly similar to CTXN RAT CO	4.2
429165	AW009886	Hs.118258		prostate cancer associated protein	4.2
416984	H38765	Hs.80706	Flavodoxin_2;TM=M;SS=N	diaphorase (NADH/NADPH) (cytochrome	4.2
448913	AA194422	Hs.22564	rrm,zf-RanBP,pkinase,GST_	myosin VI	4.2
430154	AW583058	Hs.234726	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	4.2
400496			TM=Y;SS=N	ENSP00000224716*:GTP-binding protei	4.2
442599	AF078037	Hs.324051	SH3,ank;TM=M;SS=N	RelA-associated inhibitor	4.2
448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	4.2
431309	AW451711	Hs.313760	homeobox,none	ESTs, Weakly similar to I38022 hypo	4.2
426485	NM_006207	Hs.170040	ig;TM=N;SS=M	platelet-derived growth factor rece	4.2
435858	AF254260	Hs.283009	bZIP;TM=M;SS=N	tuftelin 1	4.2
446051	BE048061	Hs.37054	Ephrin_A_deamin,dsrm,z-al	ephrin-A3	4.2
451982	F13036	Hs.27373	NA;NA	Homo sapiens mRNA; cDNA DKFZp564O17	4.2
450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	4.1
431890	X17033	Hs.271986	vwa,integrin_A,FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	4.1
434449	AW953484	Hs.3849	efhand,FKBP;TM=M;SS=N	hypothetical protein FLJ22041 simil	4.1
422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	4.1

423057	AW961597	Hs.130816		ESTs, Moderately similar to I38022	4.1
452063	R53185	Hs.32366	HLH;TM=M;SS=N	ESTs, Weakly similar to TWST_HUMAN	4.1
450680	AF131784	Hs.25318	ras,none	Homo sapiens clone 25194 mRNA seque	4.1
418283	S79895	Hs.83942	Peptidase_C1;TM=N;SS=M	cathepsin K (pycnodysostosis)	4.1
416361	AW204907	Hs.6872		ESTs, Weakly similar to CA13_HUMAN	4.1
426255	BE262530	Hs.2006	GST_C,GST_N;TM=M;SS=N	glutathione S-transferase M3 (brain	4.1
408113	T82427	Hs.194101	7tm_3,none	Homo sapiens cDNA: FLJ20869 fis, cl	4.1
407792	AI077715	Hs.39384	TM=M;SS=Y	putative secreted ligand homologous	4.1
422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	4.1
429359	W00482	Hs.2399	hemopexin,Peptidase_M10;T	matrix metalloproteinase 14 (membra	4.1
442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	4.0
448826	AI580252	Hs.255565		ESTs, Weakly similar to putative p1	4.0
419648	T73661	Hs.91877	TM=N;SS=M	thyroid hormone responsive SPOT14 (	4.0
421485	AA243499	Hs.104800	TM=Y;SS=M	hypothetical protein FLJ10134	4.0
440273	AI805392	Hs.325335		Homo sapiens cDNA: FLJ23523 fis, cl	4.0
417363	AW129357	Hs.329700		ESTs	4.0
451277	AK001123	Hs.26176	TM=Y;SS=M	hypothetical protein FLJ10261	4.0
421823	N40850	Hs.28625		ESTs	4.0
452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	4.0
444286	AI625304	Hs.201008		ESTs	4.0
451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	4.0
451304	M92642	Hs.26208	Collagen,TSPN;TM=M;SS=M	collagen, type XVI, alpha 1	4.0
429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	4.0
441094	U33819	Hs.7647	zf-C2H2,LIM,PHD,TFIIS;TM=	MYC-associated zinc finger protein	4.0
407788	BE514982	Hs.38991	efhand,S_100,S_100,efhand	S100 calcium-binding protein A2	4.0
451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	3.9
437762	T78028	Hs.154679	C2,none	synaptotagmin I	3.9
433399	N46406	Hs.84700	START;TM=M;SS=N	similar to phosphatidylcholine tran	3.9
408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	3.9
404578	AF183810	Hs.26102	zf-C2H2,rubredoxin;TM=M;S	trichorhinophalangeal syndrome I gene	3.9
443883	AA114212	Hs.9930	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	3.9
445084	H38914	Hs.250848	TM=Y;SS=M	hypothetical protein FLJ14761	3.9
453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	3.9
424125	M31669	Hs.1735	TGF-beta,TGFb_propeptide;	inhibin, beta B (activin AB beta po	3.9
437377	AL359573	Hs.124940	ras;TM=M;SS=N	GTP-binding protein	3.9
422562	AI962060	Hs.118397	Zn_carbOpept,F5_F8_type_C	AE-binding protein 1	3.9
422320	AI745249	Hs.23650	TM=Y;SS=N	ESTs, Weakly similar to AAB47496 NG	3.9
433078	AW015188	Hs.121575	asp	Homo sapiens cDNA FLJ12231 fis, clo	3.9
411894	M57609	Hs.72916	zf-C2H2;TM=N;SS=M	GLI-Kruppel family member GLI3 (Gre	3.9
425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	3.9
418113	AI272141	Hs.83484	HMG_box,homeobox;TM=M;SS=	SRY (sex determining region Y)-box	3.9
418753	BE217818	Hs.87016		hypothetical protein FLJ22938	3.8
452679	Z42387	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.8
421030	AW161357	Hs.101174	tubulin-binding;TM=N;SS=M	microtubule-associated protein tau	3.8
431567	N51357	Hs.260855	TM=M;SS=N	Homo sapiens cDNA: FLJ21410 fis, cl	3.8
426363	M58524	Hs.2025	TGF-beta,TGFb_propeptide;	transforming growth factor, beta 3	3.8
447151	AI022813	Hs.92679	kinesin;TM=M;SS=M	Homo sapiens clone CDABP0014 mRNA s	3.8
448717	R67419	Hs.21851	HLH,homeobox,none	Homo sapiens cDNA FLJ12900 fis, clo	3.8
425867	D60385	Hs.12079	cadherin;TM=Y;SS=M	calsyntenin-2	3.8
423940	NM_012429	Hs.277728	CRAL_TRIO;TM=M;SS=N	SEC14 (S. cerevisiae)-like 2	3.8
426742	AA383828	Hs.181131		ESTs	3.8
435818	AA700553	Hs.368614	arf,ras,RecR,none	ESTs	3.8
420005	AW271106	Hs.133294		ESTs	3.8
410867	X63556	Hs.750	EGF,TB,wnt,EB,TIL;TM=N;SS	fibrillin 1 (Marfan syndrome)	3.8
402531	AB037745	Hs.104696	TM=M;SS=M	KIAA1324 protein	3.8
449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	3.8
424806	AA382523	Hs.105689	TM=Y;SS=N	MSTP031 protein	3.8
443933	AI091631	Hs.203845	ion_trans;TM=Y;SS=M	two pore potassium channel KT3.3	3.8
432952	AA813887	Hs.188173		Homo sapiens cDNA FLJ12187 fis, clo	3.8
424036	AA770688	Hs.348495	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member L	3.7
453828	AW970960	Hs.293821	Pep_M12B_propep,Reprolysi	ESTs	3.7
407112	AA070801	Hs.51615	hormone_rec,zf-C4	ESTs, Weakly similar to ALU7_HUMAN	3.7
445669	AI570830	Hs.174870		ESTs	3.7
446091	AW022192	Hs.200197	homeobox,none	ESTs	3.7
424651	AI493206	Hs.120785		ESTs	3.7
409178	BE393948	Hs.50915	trypsin;TM=M;SS=Y	kallikrein 5	3.7
417059	AL037672	Hs.81071	TM=N;SS=Y	extracellular matrix protein 1	3.7
431194	D43704	Hs.250712	Ca_channel_B,RepB_protein	calcium channel, voltage-dependent,	3.7
430397	AI924533	Hs.105607	HCO3_cotransp;TM=Y;SS=N	bicarbonate transporter related pro	3.7
418969	W33191	Hs.28907	SH3;TM=M;SS=N	hypothetical protein FLJ20258	3.7
427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	3.7
424012	AW368377	Hs.137569	SAM,P53;TM=M;SS=N	tumor protein 63 kDa with strong ho	3.7
418840	AI821614	Hs.185831		ESTs	3.7
433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	3.7
433430	AI863735	Hs.369982	thyroglobulin_1,IGFBP,zf-	ESTs	3.7
422491	AA338548	Hs.117546	TM=M;SS=Y	neuronatin	3.7
435114	AA775483	Hs.288936	ODC_AZ,Ribosomal_L9_N;TM=	mitochondrial ribosomal protein L9	3.7
416899	BE262645	Hs.80420	IL8;TM=M;SS=M	small inducible cytokine subfamily	3.7
422110	AI376736	Hs.121555	kazal,none	secreted protein, acidic, cysteine-	3.7
448560	BE613183	Hs.23213	zf-RanBP,MDM2,Ndr	ESTs	3.6
414945	BE076358	Hs.77667	UPAR_LY6;TM=M;SS=M	lymphocyte antigen 6 complex, locus	3.6
422119	AI277829	Hs.111862	WD40;TM=M;SS=N	KIAA0590 gene product	3.6
447335	BE617695	Hs.286192	TM=M;SS=N	hypothetical protein FLJ20940	3.6

450663	H43540	Hs.25292	RNase_HII;TM=N;SS=M	ribonuclease HI, large subunit	3.6
417387	AW021102	Hs.21509	zf-C2H2,none	ESTs	3.6
450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS	tight junction protein 3 (zona occl	3.6
439755	AW748482	Hs.77873	ig;TM=Y;SS=M	B7 homolog 3	3.6
439873	BE159253	Hs.300638		ESTs	3.6
439039	AI656707	Hs.48713	pkinase,none	ESTs	3.6
419235	AW470411	Hs.288433		neurotrimin	3.6
445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	3.6
404394	AF332975	Hs.307004	EGF,fn1,vwc,vwd,MAM,Kerat	Zonadhesin	3.6
452222	AW806287	Hs.21432	Sema,TIG,PSI,GDI	SEX gene	3.6
422961	Y13620	Hs.122607	TM=M;SS=N	B-cell CLL/lymphoma 9	3.6
420988	AW006352	Hs.159643		ESTs, Weakly similar to T32554 hypo	3.6
439680	AW245741	Hs.58461	zf-C2H2,TFIIS,KRAB;TM=M;S	ESTs, Weakly similar to A35659 krue	3.6
426815	D59505	Hs.351344	ig,SET,PHD,zf-CXXC,Adap_c	ESTs, Weakly similar to K1CI_HUMAN	3.6
437446	AA788946	Hs.101302	fn3,vwa,Collagen,TSPN;TM=	ESTs, Moderately similar to CA1C RA	3.6
421690	AW162667	Hs.106857	efhand;TM=M;SS=N	calbindin 2, (29kD, calretinin)	3.5
453939	AA418160	Hs.86043		Homo sapiens cDNA FLJ13558 fis, clo	3.5
426158	NM_001982	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	3.5
439246	AI498072	Hs.351474	ank,pkinase,UPF0073;TM=N;	membrane-associated tyrosine- and t	3.5
410653	BE383768	Hs.65238	zf-C3HC4,AIP3;TM=M;SS=N	95 kDa retinoblastoma protein bindi	3.5
412703	AW984744			gb:RC1-HN0015-040400-011-d03 HN0015	3.5
427871	AW992405	Hs.352406	TM=M;SS=N	Homo sapiens, clone IMAGE:3507281,	3.5
444273	AI903474	Hs.230	LRR,LRRNT;TM=M;SS=M	fibromodulin	3.5
434936	AI285970	Hs.183817	UCH-2	ESTs	3.5
457869	AU077186	Hs.108885	vwa,Collagen;TM=M;SS=M	Homo sapiens, alpha-1 (VI) collagen	3.5
422575	AK000546	Hs.118552	PTR2;TM=Y;SS=M	hypothetical protein FLJ20539	3.5
428343	AL043021	Hs.12705	WD40;TM=N;SS=M	ESTs	3.5
426716	NM_006379	Hs.171921	ig,Sema,PSI;TM=N;SS=M	sema domain, immunoglobulin domain	3.5
423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	3.5
451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	3.5
407926	AW956382	Hs.59771	TYA;TM=N;SS=M	ESTs	3.5
447041	AL135480	Hs.250705		Homo sapiens cDNA FLJ11685 fis, clo	3.5
419073	AW372170	Hs.183918	death,ZU5;TM=N;SS=M	Homo sapiens cDNA FLJ12797 fis, clo	3.5
446945	AI193115	Hs.16611	TM=M;SS=N	tumor protein D52-like 1	3.5
416322	BE019494	Hs.79217	P5CR,NAD_Gly3P_dh,Octopin	pyrroline-5-carboxylate reductase 1	3.5
447347	AA570056	Hs.122730	NA;NA	ESTs, Moderately similar to KIAA121	3.5
448984	AW751955	Hs.22753	TM=M;SS=N	hypothetical protein FLJ22318	3.5
421778	AA428000	Hs.283072	NA;NA	actin related protein 2/3 complex,	3.5
423363	BE544348	Hs.127562	homeobox;TM=M;SS=N	homeo box C11	3.5
432545	X52486	Hs.3041	cyclin,none	uracil-DNA glycosylase 2	3.5
408495	W68796	Hs.237731		ESTs	3.5
406851	AA609784	Hs.352392	ig,MHC_II_beta;TM=M;SS=Y	major histocompatibility complex, c	3.5
418736	T18979	Hs.87908	helicase_C,AT_hook,SNF2_N	Snf2-related CBP activator protein	3.4
410197	NM_005518	Hs.59889	HMG_CoA_synt;TM=N;SS=N	3-hydroxy-3-methylglutaryl-Coenzyme	3.4
453597	BE281130	Hs.33713	KH-domain,Ribosomal_S3_C,	myo-inositol 1-phosphate synthase A	3.4
417259	AW903838	Hs.81800	EGF,ig,lectin_c,sushi,Xli	chondroitin sulfate proteoglycan 2	3.4
453985	N44545	Hs.251865	PH,none	ESTs	3.4
412634	U55984	Hs.356531		heat shock 90kD protein 1, alpha	3.4
407204	R41933	Hs.140237	histone,histone	ESTs, Weakly similar to ALU1_HUMAN	3.4
444371	BE540274	Hs.239	Fork_head;TM=M;SS=N	forkhead box M1	3.4
447334	AA515032	Hs.91109		ESTs	3.4
426530	U24578	Hs.278625	A2M,NTR,ANATO,A2M_N,preny	complement component 4A	3.4
419749	X73608	Hs.93029	kazal,thyroglobulin_1;TM=	sparc/osteonectin, cwcv and kazal-l	3.4
423595	R82826	Hs.220702	homeobox,none	ESTs	3.4
406673	M34996	Hs.198253	ig,MHC_II_alpha;TM=M;SS=M	major histocompatibility complex, c	3.4
434241	AF119913		TM=N;SS=M	Homo sapiens PRO3077 mRNA, complete	3.4
412490	AW803564	Hs.288850		Homo sapiens cDNA: FLJ22528 fis, cl	3.4
452277	AL049013	Hs.28783	ank;TM=M;SS=N	KIAA1223 protein	3.4
431457	NM_012211	Hs.256297	FG-GAP,vwa;TM=Y;SS=M	integrin, alpha 11	3.4
421777	BE562088	Hs.108196	TM=M;SS=N	HSPC037 protein	3.4
453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	3.4
414085	AA114016	Hs.75746	aldedh;TM=N;SS=M	aldehyde dehydrogenase 1 family, me	3.4
440300	N39760	Hs.8859	TM=M;SS=N	Homo sapiens, Similar to RIKEN cDNA	3.4
400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	3.4
433339	AF019226	Hs.8036	ras,arf;TM=M;SS=N	glioblastoma overexpressed	3.4
419301	AA236166	Hs.132957	TM=Y;SS=M	tenomodulin protein	3.4
414792	BE314949	Hs.87128	TM=Y;SS=M	hypothetical protein FLJ23309	3.4
451428	AW083384	Hs.11067		ESTs, Highly similar to T46395 hypo	3.4
432210	AI567421	Hs.273330	EGF,kazal,laminin_EGF,lam	Homo sapiens, clone IMAGE:3544662,	3.4
452242	R50956	Hs.159993		gycosyltransferase	3.4
450676	AI147155	Hs.279727		ESTs	3.4
413014	AW250533	Hs.75139	TM=M;SS=N	partner of RAC1 (arfaptin 2)	3.4
427919	AA173942	Hs.326416	CTF_NFI,none	Homo sapiens mRNA; cDNA DKFZp564H19	3.4
424005	AB033041	Hs.137507	TM=Y;SS=N	vang (van gogh, Drosophila)-like 2	3.4
422072	AB018255	Hs.111138	RhoGAP;TM=M;SS=N	KIAA0712 gene product	3.4
440995	T57773	Hs.10263		ESTs	3.4
426150	NM_003658	Hs.167218	homeobox;TM=N;SS=M	BarH-like homeobox 2	3.3
416877	BE386266	Hs.85658	zf-C2H2;TM=M;SS=N	hypothetical protein FLJ23436	3.3
452191	AU076408	Hs.28309	UDPG_MGDP_dh,UDPG_MGDP_dh	UDP-glucose dehydrogenase	3.3
450273	AW296454	Hs.24743	rrm,none	hypothetical protein FLJ20171	3.3
456177	NM_012391	Hs.79414	Ets,SAM_PNT;TM=M;SS=N	prostate epithelium-specific Ets tr	3.3
423062	NM_003655	Hs.5637	chromo;TM=N;SS=M	ESTs	3.3
421848	X15880	Hs.108885	vwa,Collagen;TM=M;SS=M	collagen, type VI, alpha 1	3.3

433577	AW007080	Hs.284192		ESTs	3.3
409636	AA305729	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	3.3
404730	AA486704	Hs.33287	CTF_NFI,none	Nuclear factor I/B	3.3
422940	BE077458		Sec7,PH,ANF_receptor,lig_	gb:RC1-BT0606-090500-015-b04 BT0606	3.3
410001	AB041036	Hs.57771	trypsin;TM=M;SS=M	kallikrein 11	3.3
427461	AA531527	Hs.332040	TM=Y;SS=M	hypothetical protein MGC13010	3.3
453468	W00712	Hs.32990	TM=M;SS=N	DKFZP566F084 protein	3.3
443807	W52930	Hs.9822	HAT;TM=N;SS=M	HCNP protein; XPA-binding protein 2	3.3
456034	AW450979			gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CG	3.3
424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	3.3
412755	BE144306	Hs.179891		ESTs, Weakly similar to P4HA_HUMAN	3.3
429690	AW956329	Hs.23721	sugar_tr,Ribosomal_S25	ESTs	3.3
423472	AF041260	Hs.129057	TM=M;SS=N	breast carcinoma amplified sequence	3.3
424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	3.3
437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ce	3.3
437464	AA323296	Hs.97837		Homo sapiens mRNA; cDNA DKFZp547J04	3.3
433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	3.3
434931	AW968941	Hs.166254		hypothetical protein DKFZp566I133	3.3
451691	AI809278	Hs.208152	C2	ESTs	3.3
430433	AA478883	Hs.273766	WW,none	ESTs	3.3
429343	AK000785	Hs.199480	VHS,ENTH,UIM;TM=N;SS=M	Homo sapiens, Similar to epsin 3, c	3.3
450835	BE262773	Hs.25584	ArfGap;TM=N;SS=M	hypothetical protein FLJ10767	3.3
414591	AI888490	Hs.248107		ESTs, Weakly similar to ALU8_HUMAN	3.3
452579	AA131657	Hs.23830	CN_hydrolase	ESTs	3.3
409960	BE261944	Hs.355264		hexokinase 1	3.3
406850	AI624300	Hs.172928	vwc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	3.3
453874	AW591783	Hs.36131		collagen, type XIV, alpha 1 (unduli	3.2
425964	AW889928	Hs.9071	homeobox,none	progesterone membrane binding prote	3.2
428412	AA428240	Hs.126083		ESTs	3.2
430316	NM_000875	Hs.239176	fn3,Furin-like,pkinase,Re	insulin-like growth factor 1 recept	3.2
440087	W28969	Hs.7718	KOW,Ribosomal_S4e,S4,rrm;	hypothetical protein FLJ22678	3.2
449933	AW157098	Hs.324104	DUF176,efhand;TM=M;SS=N	Human DNA sequence from clone RP1-6	3.2
441128	AA570256	Hs.348504	TM=Y;SS=M	ESTs, Weakly similar to T23273 hypo	3.2
434182	W20309	Hs.8107	G-gamma;TM=M;SS=N	G-protein gamma-12 subunit	3.2
422737	M26939	Hs.119571	Collagen,COLFI;TM=N;SS=M	collagen, type III, alpha 1 (Ehlers	3.2
408202	AA227710	Hs.43658	OLF;TM=M;SS=N	DKFZP586L151 protein	3.2
424971	AA479005	Hs.154036	PH;TM=M;SS=N	tumor suppressing subtransferable c	3.2
407869	AI827976	Hs.24391	efhand;TM=M;SS=N	hypothetical protein FLJ13612	3.2
444734	NM_001360	Hs.11806	ERG4_ERG24;TM=Y;SS=M	7-dehydrocholesterol reductase	3.2
426991	AK001536	Hs.214410		Homo sapiens cDNA FLJ10674 fis, clo	3.2
414081	AW969976	Hs.365706	gla;TM=N;SS=Y	matrix Gla protein	3.2
408795	AW749126	Hs.170345	hormone_rec,zf-C4	hypothetical protein FLJ13710	3.2
452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	3.2
437879	BE262082	Hs.5894	TM=N;SS=N	hypothetical protein FLJ10305	3.2
407872	AB039723	Hs.40735	Fz,Frizzled,7tm_2,DUF81;T	frizzled (Drosophila) homolog 3	3.2
427289	AI097346	Hs.323878	aminotran_5,SDF,none	phosphoserine aminotransferase	3.2
432375	BE536069	Hs.2962	efhand,S_100;TM=N;SS=M	S100 calcium-binding protein P	3.2
429415	NM_002593	Hs.202097	CUB,NTR;TM=N;SS=M	procollagen C-endopeptidase enhance	3.2
412774	AA120865	Hs.380149	hormone_rec,zf-C4	ESTs	3.2
445942	T80334	Hs.13479	TM=M;SS=N	hypothetical protein FLJ20847	3.2
439456	AI752409	Hs.109314	zf-C2H2;TM=N;SS=M	hypothetical protein FLJ20980	3.2
414774	X02419	Hs.77274	kringle,trypsin,plant_thi	plasminogen activator, urokinase	3.2
433336	AF017986	Hs.31386	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 2	3.2
439905	AW799755	Hs.110953	HLH;TM=M;SS=N	retinoic acid induced 1	3.2
420251	AW374968	Hs.379829		Human DNA sequence from clone RP5-1	3.2
413004	T35901	Hs.75117	TM=M;SS=N	interleukin enhancer binding factor	3.2
418686	Z36830	Hs.87268	annexin;TM=M;SS=N	annexin A8	3.2
410279	BE271977	Hs.61809	ras;TM=M;SS=N	hypothetical protein FLJ14117	3.2
424391	BE550112	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.2
440409	AW294316	Hs.125608	thiored	ESTs	3.2
452689	F33868	Hs.284176	transferrin,KH-domain,rrm	transferrin	3.2
418154	BE165866	Hs.352403	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	3.2
434384	AA631910	Hs.370133		ESTs	3.2
413436	AF238083	Hs.68061	DAGKc;TM=M;SS=N	sphingosine kinase 1	3.2
431663	NM_016569	Hs.267182	T-box;TM=M;SS=N	TBX3-iso protein	3.2
432874	W94322	Hs.279651	SH3;TM=M;SS=Y	melanoma inhibitory activity	3.2
436252	AI539519	Hs.142827		Homo sapiens cDNA FLJ11562 fis, clo	3.2
421044	AF061871	Hs.101302	fn3,vwa,Collagen,TSPN;TM=	Human DNA sequence from clone RP1-2	3.2
419102	AA234098	Hs.42424		ESTs, Weakly similar to 2004399A ch	3.2
419359	AL043202	Hs.90073	CAS_CSE1;TM=M;SS=N	chromosome segregation 1 (yeast hom	3.2
441859	AW194364	Hs.9877	Amino_oxidase,FAD_binding	interleukin-4 induced gene-1 protei	3.1
426418	M90464	Hs.169825	Collagen,C4,VPR;TM=N;SS=M	collagen, type IV, alpha 5 (Alport	3.1
413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	3.1
407874	AI766311	Hs.289047	COQ7	Homo sapiens cDNA FLJ14059 fis, clo	3.1
448019	AW947164	Hs.195641		ESTs, Moderately similar to I38022	3.1
427024	AA397572	Hs.348902		chromosome 11 open reading frame 14	3.1
410281	AF076612	Hs.166186	vwc,W2,MA3,MIF4G	Homo sapiens clone 23928 mRNA seque	3.1
447205	BE617015	Hs.11006	LEA,perilipin;TM=M;SS=N	ESTs, Moderately similar to T17372	3.1
434433	AW629759			gb:hh70e05.y1 NCI_CGAP_GU1 Homo sap	3.1
439737	AI751438	Hs.41271	C1q,Collagen,none	Homo sapiens mRNA full length inser	3.1
450157	AW961576	Hs.60178	PH,Band_41,RhoGEF,none	ESTs	3.1
445989	H97754	Hs.11108		ESTs	3.1
442213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	3.1

402496				Target Exon	3.1
438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	3.1
439335	AA742697	Hs.62492	TM=N;SS=M	NM_052863:Homo sapiens secretoglobi	3.1
412276	BE262621	Hs.73798	MIF,sugar_tr,none	macrophage migration inhibitory fac	3.1
416950	AL049798	Hs.80552		dermatopontin	3.1
456157	AW979153	Hs.336881	transmembrane4,none	ESTs	3.1
452753	AA028049	Hs.277728	CRAL_TRIO,none	SEC14 (S. cerevisiae)-like 2	3.1
414420	AA043424	Hs.76095	TM=M;SS=N	immediate early response 3	3.1
446229	AI744964	Hs.14449	TM=M;SS=N	KIAA1609 protein	3.1
453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	3.1
411441	AL042355	Hs.70202	WD40;TM=M;SS=N	WD repeat domain 10	3.1
422921	BE062045	Hs.351625	AAA,hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23260 fis, cl	3.1
444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	3.1
436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	3.1
427890	AA435761	Hs.373623	RFX_DNA_binding,none	ESTs	3.1
444838	AV651680	Hs.208558	integrin_A,FG-GAP,none	ESTs	3.1
427876	AI494291	Hs.369171		ESTs	3.1
413040	AA193338	Hs.12321	Na_Ca_Ex;TM=Y;SS=M	sodium calcium exchanger	3.1
427515	T79526	Hs.179516	EMP24_GP25L;TM=Y;SS=M	integral type I protein	3.1
451092	AI207256	Hs.13766	filament;TM=N;SS=N	Homo sapiens mRNA for FLJ00074 prot	3.1
442222	AI061301	Hs.164773	trypsin,kringle,UPAR_LY6	ESTs	3.1
452613	AA461599	Hs.23459		ESTs	3.1
447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	3.1
412890	T85247	Hs.351875	COX6C;TM=M;SS=M	cytochrome c oxidase subunit VIc	3.1
418313	BE244231	Hs.84038	TM=Y;SS=N	CGI-06 protein	3.1
440006	AK000517	Hs.6844	AAA,NB-ARC,PAAD_DAPIN;NA;	NALP2 protein; PYRIN-Containing APA	3.1
434042	AI589941	Hs.8254		Homo sapiens, Similar to tumor diff	3.1
420576	AA297634	Hs.54925		KIAA1858 protein	3.1
432269	NM_002447	Hs.2942	pkinase,Sema,PSI,TIG,A4_E	macrophage stimulating 1 receptor (	3.1
424927	AW973666	Hs.153850		hypothetical protein C321D2.4	3.1
440100	BE382685	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.1
452408	AA306477	Hs.29379	TM=M;SS=N	hypothetical protein FLJ10687	3.1
441362	BE614410	Hs.23044	TM=N;SS=N	RAD51 (S. cerevisiae) homolog (E co	3.1
418444	AI902899	Hs.85155	zf-CCCH;TM=M;SS=N	butyrate response factor 1 (EGF-res	3.1
423464	NM_016240	Hs.128856	Collagen;TM=Y;SS=N	CSR1 protein	3.1
424604	AW865388	Hs.151076	TM=M;SS=N	KIAA1243 protein	3.1
420059	AF161486	Hs.94769	ras,none	RAB23, member RAS oncogene family	3.1
453271	AA903424	Hs.6786	LIM;TM=M;SS=N	ESTs	3.1
411274	NM_002776	Hs.69423	trypsin;TM=M;SS=N	kallikrein 10	3.1
434095	AA011117	Hs.3745	EGF,F5_F8_type_C;TM=N;SS=	milk fat globule-EGF factor 8 prote	3.1
403439			ank;TM=M;SS=N	NM_031419*:Homo sapiens molecule po	3.1
413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	3.1
411756	BE294350	Hs.71891	pkinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	3.1
409007	AL122107	Hs.49599		Homo sapiens mRNA; cDNA DKFZp434G08	3.1
452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	3.1
414359	M62194	Hs.75929	cadherin,Cadherin_C_term;	cadherin 11, type 2, OB-cadherin (o	3.1
433212	BE218049	Hs.121820		ESTs	3.1
449123	D50920	Hs.23106	TM=M;SS=N	KIAA0130 gene product	3.1
431176	AI026984	Hs.293662	MCPsignal,laminin_B,lamin	ESTs	3.0
419245	AI732742	Hs.87440		ESTs	3.0
434493	AA635305	Hs.375591		ESTs	3.0
449177	BE616694	Hs.288042		hypothetical protein FLJ14299	3.0
430449	AA352723	Hs.241471	WH1;TM=M;SS=N	RNB6	3.0
452887	AI702223	Hs.107253	K-box;TM=N;SS=M	hypothetical protein DKFZp761F241	3.0
451678	AA374181	Hs.26799		DKFZP564D0764 protein	3.0
445457	AF168793	Hs.12743	Carn_acyltransf;TM=M;SS=N	carnitine O-octanoyltransferase	3.0
407597	AA043925	Hs.339352	fn3,Ig;TM=Y;SS=M	Homo sapiens brother of CDO (BOC) m	3.0
431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	3.0
432302	AA345857	Hs.274307	TIG;TM=M;SS=N	KIAA1442 protein	3.0
442549	AI751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	3.0
437959	AI472068	Hs.375604	eIF5_eIF2B,W2;TM=M;SS=N	KIAA1856 protein	3.0
447400	AK000322	Hs.18457	zf-C3HC4;TM=Y;SS=M	hypothetical protein FLJ20315	3.0
411734	AW374954	Hs.71779		Homo sapiens DNA from chromosome 19	3.0
443547	AW271273	Hs.356487	fn3,none	hypothetical protein FLJ12666	3.0
417000	BE277919	Hs.306019	TM=Y;SS=M	ESTs, Weakly similar to ALU7_HUMAN	3.0
416987	D86957	Hs.80712	GTP_CDC;TM=N;SS=M	KIAA0202 protein	3.0
424494	U78575	Hs.149255	PIP5K;TM=N;SS=M	phosphatidylinositol-4-phosphate 5-	3.0
414496	W73853	Hs.355424	pkinase,F5_F8_type_C,adh_	ESTs	3.0
413336	AI569936	Hs.296178	Occludin;TM=M;SS=N	hypothetical protein FLJ22637	3.0
434314	BE392921	Hs.3797	ras,arf;TM=M;SS=N	RAB26, member RAS oncogene family	3.0
401038			TM=M;SS=N	C11000425:gi|4507721|ref|NP_003310.	3.0
418245	AA088767	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.0
407688	W25317	Hs.37616		Human D9 splice variant B mRNA, com	3.0
456906	AF117646	Hs.156637	zf-C3HC4,Cbl_N,Cbl_N2,Cbl	Cas-Br-M (murine) ectropic retrovir	3.0
424744	AW175781	Hs.152720	TM=M;SS=N	M-phase phosphoprotein 6	3.0
452195	AA994712	Hs.116878		ESTs	3.0
415988	BE407713	Hs.78943	Pept_C1-like;TM=N;SS=M	bleomycin hydrolase	3.0
418399	AF131781	Hs.84753	TM=N;SS=N	hypothetical protein FLJ12442	3.0
420568	F09247	Hs.247735	cadherin,lipocalin;TM=M;S	protocadherin alpha 10	3.0
404661			TM=M;SS=N	C9000306*:gi|12737280|ref|XP_006682	3.0
414152	NM_003248	Hs.75774	EGF,TSPN,tsp_3;TM=M;SS=M	thrombospondin 4	3.0
421307	BE539976	Hs.103305	chromo	Homo sapiens mRNA; cDNA DKFZp434B04	3.0
444868	BE560471	Hs.12101	TM=N;SS=M	hypothetical protein	3.0

450214	BE439763	Hs.227571	RGS;TM=M;SS=N	regulator of G-protein signalling 4	3.0
452664	AA398859	Hs.18397	TM=M;SS=M	hypothetical protein FLJ23221	3.0
422105	AI929700	Hs.111680	TM=M;SS=N	endosulfine alpha	3.0
422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	3.0
434067	H18913	Hs.124023		Homo sapiens cDNA FLJ14218 fis, clo	3.0
412676	NM_000165	Hs.74471	connexin,Connexin43;TM=Y;	gap junction protein, alpha 1, 43kD	3.0
426801	AA486846	Hs.271795		ESTs, Weakly similar to I38022 hypo	3.0
421983	AI252640	Hs.110364	pro_isomerase,none	peptidylprolyl isomerase C (cycloph	3.0
429299	AI620463	Hs.347408	TM=Y;SS=N	hypothetical protein MGC13102	3.0
408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	3.0
438746	AI885815	Hs.184727	transferrin,Guanylate_kin	Human melanoma-associated antigen p	3.0

TABLE 4B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418344	245371_1	AA216387 T63548 AA228876
412703	1243670_1	AW984759 AW984744
434241	63414_1	AF119913 AI207698 R57074
422940	58443_1	BC012771 BG397153 BF366196 AA337277 AA319285 AW843252
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
434433	111338_1	AA633408 AW749955 AW629759 AI651005

TABLE 4C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406387	9256180	Plus	116229-116371,117512-117651
400496	9743564	Plus	41515-41695
402496	9797769	Minus	8615-9103
403439	9719679	Plus	91463-91632
401038	7232177	Minus	4277-4469
404661	9797073	Plus	33374-33675,33769-34008

TABLE 5A: ABOUT 231 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT MAY ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1: Ratio of 90th percentile tumor to 50th percentile of normal body tissue

Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGeneTitle	R1
409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	20.5
421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	16.3
419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXYD domain-containing ion transpor	13.7
417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	13.7
414521	D28124	Hs.76307	DAN;TM=M;SS=M	neuroblastoma, suppression of tumor (DAN)	13.7
438091	AW373062	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	13.4
413815	AL046341	Hs.75562	pkinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	13.2
439180	AI393742	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	13.2
431441	U81961	Hs.2794	ASC;TM=Y;SS=N	sodium channel, nonvoltage-gated 1	12.5
452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	12.4
452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	12.1
441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	11.9
419223	X60111	Hs.1244	transmembrane4;TM=Y;SS=M	CD9 antigen (p24)	11.7
413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	11.5
410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	11.2
422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	10.1
419452	U33635	Hs.90572	ig,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	9.9
427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	9.9
444784	D12485	Hs.11951	Somatomedin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	9.9
436972	AA284679	Hs.25640	PMP22_Claudin;TM=Y;SS=M	claudin 3	9.7
412926	AI879076	Hs.75061	MARCKS;TM=N;SS=M	macrophage myristoylated alanine-ri	9.5
425280	U31519	Hs.1872	PEPCK;TM=M;SS=N	phosphoenolpyruvate carboxykinase 1	9.5
432636	AA340864	Hs.278562	PMP22_Claudin;TM=Y;SS=M	claudin 7	9.4
423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	9.4
424206	NM_003734	Hs.198241	Cu_amine_oxid,Cu_amine_ox	amine oxidase, copper containing 3	9.4
444797	AB018333	Hs.12002	SH3,SAM;TM=M;SS=N	KIAA0790 protein	9.0

402559	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat.type 2B	9.0
443932	AW388222	Hs.9973	SH2,WW,PID,none	tensin	8.9
421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	8.8
433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	8.7
410668	BE379794	Hs.159651	death,TNFR_c6;TM=Y;SS=M	hypothetical protein	8.7
433662	W07162	Hs.150826	ras,ABC_tran,arf;TM=M;SS=	RAB25 RAB25, member RAS oncogene fa	8.6
421853	AL117472	Hs.108924	SH3,Sorb;TM=M;SS=N	SH3-domain protein 5 (ponsin)	8.6
425335	BE394327	Hs.296267	efhand,kazal,arf,ras,7tm_	follistatin-like 1	8.5
400290	H18636	Hs.31608	Cys_knot	hypothetical protein FLJ20041	8.5
438089	W05391	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	8.4
426158	NM_001982	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	8.3
447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	8.2
439941	AI392640	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	8.2
439318	AW837046	Hs.6527	7tm_2,CytC_asm,GPS;TM=Y;S	G protein-coupled receptor 56	8.1
442213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	8.1
412649	NM_002206	Hs.74369	integrin_A,FG-GAP;TM=M;SS	integrin, alpha 7	8.1
448913	AA194422	Hs.22564	rrm,zf-RanBP,pkinase,GST_	myosin VI	8.1
420166	AW732276	Hs.95583	transmembrane4;TM=Y;SS=M	transmembrane 4 superfamily member	8.0
407102	AA007629	Hs.348601	transport_prot,SWIB,ASC	glycerol-3-phosphate dehydrogenase	7.9
452516	AA058630	Hs.29759	TM=N;SS=M	RNA POLYMERASE I AND TRANSCRIPT REL	7.9
413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	7.9
443604	C03577	Hs.9615	efhand;TM=M;SS=N	myosin regulatory light chain 2, sm	7.7
429002	AW248439	Hs.2340	Armadillo_seg;TM=M;SS=N	junction plakoglobin	7.6
432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	7.6
426359	AA376409	Hs.10862	adenylatekinase,none	Homo sapiens cDNA: FLJ23313 fis, cl	7.5
417733	AL048678	Hs.82503	NA;NA	H.sapiens mRNA for 3'UTR of unknown	7.5
451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	7.4
443951	F13272	Hs.356835	PMP22_Claudin,none	ferritin, light polypeptide	7.4
409960	BE261944	Hs.355264		hexokinase 1	7.3
423184	NM_004428	Hs.1624	Ephrin;TM=M;SS=M	ephrin-A1	7.3
405121	X04385	Hs.110802	Cys_knot,TGF-beta,vwa,vwc	von Willebrand factor (VWF), mRNA	7.1
438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	7.1
417771	AA804698	Hs.82547		retinoic acid receptor responder (t	7.0
424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	7.0
402705	X67951	Hs.180909	AhpC-TSA;TM=M;SS=M	peroxiredoxin 1 (PRDX1)	7.0
417115	AW952792	Hs.334612	Sm,pkinase;TM=N;SS=N	small nuclear ribonucleoprotein pol	7.0
442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	6.9
447216	R75812	Hs.169248	cytochrome_c;NA;NA	p75NTR-associated cell death execut	6.9
422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	6.9
414657	AA424074	Hs.76780	TM=M;SS=N	protein phosphatase 1, regulatory (	6.9
447528	AI612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	6.9
436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	6.9
428013	AF151020	Hs.181444	TM=Y;SS=M	hypothetical protein	6.9
444143	AW747996	Hs.160999	Bcl-2,none	ESTs, Moderately similar to A56194	6.8
414443	AU077268	Hs.76144	ig,pkinase;TM=Y;SS=N	platelet-derived growth factor rece	6.7
418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	6.7
448479	H96115	Hs.21293	UDPGP;TM=M;SS=N	UDP-N-acteylglucosamine pyrophospho	6.6
410552	X66945	Hs.748	ig,pkinase,SH2,SH3,C2,PH,	fibroblast growth factor receptor 1	6.6
414883	AA926960	Hs.348669	CKS;TM=N;SS=N	CDC28 protein kinase 1	6.6
417426	NM_002291	Hs.82124	laminin_EGF,laminin_Nterm	laminin, beta 1	6.6
428179	AI127772	Hs.279696	pkinase,PX,pkinase_C;TM=N	serum/glucocorticoid regulated kina	6.6
443195	BE148235	Hs.193063	Aa_trans,none	Homo sapiens cDNA FLJ14201 fis, clo	6.5
424512	X53002	Hs.149846	integrin_B,EGF;TM=Y;SS=M	integrin, beta 5	6.5
421733	AL119671	Hs.1420	ig,pkinase;TM=Y;SS=M	fibroblast growth factor receptor 3	6.5
428950	BE311879	Hs.194673	DED;TM=M;SS=N	phosphoprotein enriched in astrocyt	6.5
450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	6.5
416078	AL034349	Hs.79005		protein tyrosine phosphatase, recep	6.5
408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	6.4
428373	AI751656	Hs.183986	ig;TM=Y;SS=M	poliovirus receptor-related 2 (herp	6.4
449029	N26989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	6.4
406621	X57809	Hs.181125	ig,HSP70,Ppx-GppA;TM=M;SS	immunoglobulin lambda locus	6.4
431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	6.4
428169	AI928984	Hs.182793	photoRC,UPF0118;TM=Y;SS=N	golgi phosphoprotein 2	6.4
443337	Y07604	Hs.9235	NDK;TM=N;SS=N	non-metastatic cells 4, protein exp	6.4
451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	6.4
425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	6.4
426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	6.3
417208	S67773	Hs.81665	ig,pkinase;TM=Y;SS=M	v-kit Hardy-Zuckerman 4 feline sarc	6.3
436278	BE409248	Hs.57988	TFIIS,RNA_POL_M_15KD,UPF0	hypothetical protein FLJ22357 simil	6.3
429455	AI472111	Hs.278694	lectin_c	CD209 antigen	6.3
431685	AW296135	Hs.267659	CH,DAG_PE-bind,PH,RhoGEF,	vav 3 oncogene	6.3
445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	6.3
411756	BE294350	Hs.71891	pkinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	6.3
453902	BE502341	Hs.3402		ESTs	6.3
418005	AI186220	Hs.83164	Collagen,TSPN;TM=M;SS=M	collagen, type XV, alpha 1	6.2
449924	W30681	Hs.146233	SH3,none	Homo sapiens cDNA: FLJ22130 fis, cl	6.2
426520	BE545684	Hs.343566	aa_permeases,pyridoxal_de	KIAA0251 protein	6.2
453064	R40334	Hs.89463		potassium large conductance calcium	6.2
448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	6.2
452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	6.2
402575	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat. type 2B	6.2
444672	Z95636	Hs.11669	laminin_EGF,laminin_G,EGF	laminin, alpha 5	6.2
450440	AB024334	Hs.25001	14-3-3;TM=M;SS=N	tyrosine 3-monooxygenase/tryptophan	6.2

432314	AA533447	Hs.285173	Xlink,none	ESTs	6.1
438564	AA381553	Hs.198253	ig,MHC_II_alpha,none	major histocompatibility complex, c	6.1
444252	R21135	Hs.54985		ESTs	6.1
425184	BE278268	Hs.155048	ig;TM=Y;SS=M	Lutheran blood group (Auberger b an	6.1
431890	X17033	Hs.271986	vwa,integrin_A,FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	6.1
449475	AI348027	Hs.129826	transmembrane4;TM=Y;SS=M	hypothetical protein PP1057	6.1
449538	AI559444	Hs.104679	TM=M;SS=M	ESTs	6.0
414496	W73853	Hs.355424	pkinase,F5_F8_type_C,adh_	ESTs	6.0
414217	AI309298	Hs.279898	NA;NA	Homo sapiens cDNA: FLJ23165 fis, cl	6.0
445333	BE537641	Hs.44278	ras,arf,TK;TM=N;SS=M	hypothetical protein FLJ12538 simil	5.9
431183	NM_006855	Hs.250696	ER_lumen_recept;TM=M;SS=M	KDEL (Lys-Asp-Glu-Leu) endoplasmic	5.9
409645	AI142265	Hs.55498	polyprenyl_synt;TM=M;SS=N	geranylgeranyl diphosphate synthase	5.9
412276	BE262621	Hs.73798	MIF,sugar_tr,none	macrophage migration inhibitory fac	5.9
416137	BE279513	Hs.278607	pkinase,UBA,ThiF;TM=M;SS=	ubiquitin activating enzyme E1-like	5.9
412969	AI373162	Hs.75103	14-3-3;TM=N;SS=M	tyrosine 3-monooxygenase/tryptophan	5.9
414504	AW069181	Hs.115175	pkinase,SAM;TM=M;SS=N	sterile alpha motif and leucine zip	5.9
433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	5.9
436415	BE265254	Hs.343258	Peptidase_M24,Furin-like,	proliferation-associated 2G4, 38kD	5.9
413900	AW409747	Hs.75612	TPR,PDZ,WW,Guanylate_kin;	stress-induced-phosphoprotein 1 (Hs	5.9
441455	AJ271671	Hs.7854	Zip;TM=Y;SS=M	zinc/iron regulated transporter-lik	5.9
444006	BE395085	Hs.334762	Idl_recept_a,PKD,MHC_I;TM	type I transmembrane protein Fn14	5.8
408269	AW888219	Hs.44077	CH;TM=M;SS=N	parvin, alpha	5.8
411372	AI147861	Hs.213289	Glyco_transf_11,EGF,Idl_r	low density lipoprotein receptor (f	5.8
450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS	tight junction protein 3 (zona occl	5.8
456534	X91195	Hs.100623	LIM,PDZ,pkinase;TM=N;SS=M	phospholipase C, beta 3, neighbor p	5.7
451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.7
446812	AL042279	Hs.16206	pkinase	uncharacterized hypothalamus protei	5.7
424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	5.7
405484	XM_093451		TM=N;SS=M	C3002124*:gi|12737280|ref|XP_006682	5.7
425367	BE271188	Hs.155975	TM=M;SS=Y	protein tyrosine phosphatase, recep	5.7
444607	AW405635	Hs.293687	PI-PLC-X,PH,PI-PLC-Y	ESTs	5.7
421456	AW579842	Hs.104557	zf-C2H2,DUF18,efhand,C2,P	hypothetical protein FLJ10697	5.6
412810	M21574	Hs.74615	ig,pkinase,DUF11;TM=M;SS=	platelet-derived growth factor rece	5.6
450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	5.6
453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	5.6
439578	AW263124	Hs.350547	WD40;TM=M;SS=N	nuclear receptor co-repressor/HDAC3	5.6
450954	AI904740	Hs.25691	TM=Y;SS=M	receptor (calcitonin) activity modi	5.6
414555	N98569	Hs.76422	phoslip;TM=M;SS=Y	phospholipase A2, group IIA (platel	5.6
409963	AA133590	Hs.377830	MBOAT,none	calcium/calmodulin-dependent protei	5.6
450463	AW952018	Hs.201398	C1q,Collagen;TM=M;SS=Y	G protein coupled receptor interact	5.6
425177	AF127577	Hs.155017	TM=N;SS=M	nuclear receptor interacting protei	5.5
445496	AB007860	Hs.12802	SH3,ank,PH,ArfGap;TM=M;SS	development and differentiation enh	5.5
428981	BE313077	Hs.93135	rrm	ESTs, Weakly similar to ALU2_HUMAN	5.5
424441	X14850	Hs.147097	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member X	5.5
415662	AW972481	Hs.170610	pkinase,none	ESTs, Highly similar to G01887 MEK	5.5
422105	AI929700	Hs.111680	TM=M;SS=N	endosulfine alpha	5.5
429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	5.5
408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	5.5
425205	NM_005854	Hs.155106	TM=Y;SS=N	receptor (calcitonin) activity modi	5.5
444633	AF111713	Hs.12284	ig;TM=Y;SS=M	junctional adhesion molecule 1	5.5
431565	AF161470	Hs.260622	TM=Y;SS=N	butyrate-induced transcript 1	5.5
429655	U48959	Hs.211582	pkinase,fn3,ig,none	myosin, light polypeptide kinase	5.5
431886	L77964	Hs.271980	pkinase;TM=M;SS=N	mitogen-activated protein kinase 6	5.5
453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	5.4
451863	AL120634	Hs.331803	cpn60_TCP1,E1-E2_ATPase,C	ATPase, Ca transporting, plasma mem	5.4
422293	X94453	Hs.114366	aldedh,aakinase;TM=M;SS=N	pyrroline-5-carboxylate synthetase	5.4
432179	X75208	Hs.2913	EPH_lbd,fn3,pkinase,SAM;T	EphB3	5.4
408048	NM_007203	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.4
448153	Y10805	Hs.20521	NusG;TM=N;SS=M	HMT1 (hnRNP methyltransferase, S. c	5.4
421251	Z28913	Hs.102948	LIM,PDZ;TM=N;SS=M	enigma (LIM domain protein)	5.4
439039	AI656707	Hs.48713	pkinase,none	ESTs	5.4
409882	AJ243191	Hs.56874	HSP20;TM=N;SS=M	heat shock 27kD protein family, mem	5.4
451295	AI557212	Hs.17132	pkinase,DAG_PE-bind,pkina	ESTs, Moderately similar to I54374	5.4
442549	AI751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	5.4
445930	AF055009	Hs.13456	DAGKc,DAGKa,ank,WD40,bZIP	Homo sapiens clone 24747 mRNA seque	5.4
453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	5.4
426432	AF001601	Hs.169857	Arylesterase;TM=M;SS=N	paraoxonase 2	5.4
415753	U52819	Hs.78781	PDGF;TM=M;SS=M	vascular endothelial growth factor	5.4
450778	U81375	Hs.25450	Nucleoside_tran;TM=Y;SS=M	solute carrier family 29 (nucleosid	5.4
414739	U83867	Hs.77196	efhand,SH3,spectrin;TM=N;	spectrin, alpha, non-erythrocytic 1	5.3
421233	AA209534	Hs.284243	transmembrane4;TM=Y;SS=M	tetraspan NET-6 protein	5.3
414774	X02419	Hs.77274	kringle,trypsin,plant_thi	plasminogen activator, urokinase	5.3
414368	W70171	Hs.75939	PRK,CoaE;TM=N;SS=N	uridine monophosphate kinase	5.3
446051	BE048061	Hs.37054	Ephrin,A_deamin,dsrm,z-al	ephrin-A3	5.3
423619	T48691	Hs.249159	7tm_1,7tm_2;TM=Y;SS=M	adrenergic, alpha-2A-, receptor	5.3
440188	AK001812	Hs.7036	ROK;TM=M;SS=N	N-Acetylglucosamine kinase	5.3
414135	NM_004419	Hs.2128	Rhodanese,DSPc,Y_phosphat	dual specificity phosphatase 5	5.3
444838	AV651680	Hs.208558	integrin_A,FG-GAP,none	ESTs	5.3
447918	AI129320	Hs.115175	pkinase,SAM,none	ESTs, Highly similar to JC5818 gamm	5.3
405517	AF000974	Hs.119498	LIM;TM=M;SS=N	thyroid hormone receptor interactor 6	5.3
413588	AA971014	Hs.75432	IMPDH_C,CBS,IMPDH_N;TM=M;	IMP (inosine monophosphate) dehydro	5.2
411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	5.2
416157	NM_003243	Hs.342874	zona_pellucida;TM=Y;SS=M	transforming growth factor, beta re	5.2

407744	AB020629	Hs.38095	ABC_tran,PRK;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.2
446108	AL036596	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.2
422034	AC006486	Hs.333069	Ets;TM=M;SS=N	Ets2 repressor factor	5.2
417098	AB017365	Hs.173859	Frizzled,Fz,7tm_2,toxin_2	frizzled (Drosophila) homolog 7	5.2
430526	AF181862	Hs.242407	7tm_3;TM=Y;SS=M	G protein-coupled receptor, family	5.2
414176	BE140638	Hs.75794	7tm_1,CRCB;TM=Y;SS=N	EDG-2 (endothelial differentiation	5.2
416710	AI268325	Hs.54890	Peptidase_M49,EGF,ig,Neur	hypothetical protein FLJ23590	5.2
417896	AA379770	Hs.82890	DAD;TM=Y;SS=M	defender against cell death 1	5.2
413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	5.2
421837	AF135168	Hs.108802	AAA,cdc48_N,cdc48_2,NB-AR	N-ethylmaleimide-sensitive factor	5.2
429379	NM_014840	Hs.200598	pkinase,RIO1;TM=M;SS=N	KIAA0537 gene product	5.2
429619	AL120751	Hs.211568		eukaryotic translation initiation f	5.2
437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ce	5.1
421071	AI311238	Hs.104476	TM=Y;SS=M	ESTs, Weakly similar to CGHU1E coll	5.1
448581	NM_002709	Hs.21537		protein phosphatase 1, catalytic su	5.1
452568	AA805634	Hs.300870	PI3_PI4_kinase;TM=M;SS=M	Homo sapiens mRNA; cDNA DKFZp547M07	5.1
452069	AB028949	Hs.183994	Metallophos;TM=M;SS=N	KIAA1026 protein	5.1
437175	AW968078	Hs.87773	pkinase,pkinase_C,none	protein kinase, cAMP-dependent, cat	5.1
437056	AI147061		spectrin,SH3,PH,CH	gb:ok33a11.s1 Soares_NSF_F8_9W_OT_P	5.1
450998	BE387614	Hs.25797	rrm;TM=M;SS=N	splicing factor 3b, subunit 4, 49kD	5.1
444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	5.1
448528	BE613248	Hs.172084	PHD;TM=M;SS=N	Homo sapiens, clone IMAGE:3627860,	5.1
452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	5.1
443412	W84893	Hs.9305		angiotensin receptor-like 1	5.1
412853	M34175	Hs.74626	Adaptin_N,Alpha_adaptinC2	adaptor-related protein complex 2,	5.1
439866	AA280717	Hs.6727	rrm,NTF2;TM=M;SS=N	Ras-GTPase activating protein SH3 d	5.1
439975	AW328081	Hs.6817	Ham1p_like;TM=M;SS=N	inosine triphosphatase (nucleoside	5.1
435523	T62849	Hs.11090	TM=Y;SS=M	membrane-spanning 4-domains, subfam	5.1
433423	BE407127	Hs.8997	HSP70,ig,Ppx-GppA;TM=M;SS	heat shock 70kD protein 1A	5.1
412641	M16660	Hs.74335	HSP90,HATPase_c;TM=M;SS=N	heat shock 90kD protein 1, beta	5.1
431236	AV656840	Hs.285115	fn3;TM=Y;SS=M	interleukin 13 receptor, alpha 1	5.1
438552	AJ245820	Hs.6314		type I transmembrane receptor (seiz	5.0
422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	5.0
427502	AI811865	Hs.7133	TM=M;SS=N	Homo sapiens, clone IMAGE:3161564,	5.0
414166	AW888941	Hs.75789	DEAD,helicase_C,rrm,Ndr,C	N-myc downstream regulated	5.0
424954	NM_000546	Hs.1846	P53,WD40,IRK;TM=M;SS=N	tumor protein p53 (Li-Fraumeni synd	5.0
422089	AA523172	Hs.103135	REJ,PLAT,PKD,WSC,LRR	ESTs, Weakly similar to SFR4_HUMAN	5.0
426636	BE242634	Hs.2055	ThiF,UBACT;TM=M;SS=N	ubiquitin-activating enzyme E1 (A1S	5.0
410793	AW581906	Hs.66392	SH3,efhand,C2,PH,RhoGEF,M	intersectin 1 (SH3 domain protein)	5.0

TABLE 5B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
437056	428504_3	AW976398 AI147061 AA765223 AA743380 AI803927

TABLE 5C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405484	5922025	Plus	199214-199579,199672-199920,200262-20049

TABLE 6A: 777 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6A lists777 genes up-regulated in colon cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" colon cancer level was set to the 90th percentile amongst 95 colon cancers. The "average" normal adult tissue level was set to the 90th percentile amongst 209 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 209 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
447033	AI357412	Hs.157601	ESTs	31.35
409041	AB033025	Hs.50081	KIAA1199 protein	29.00
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	26.41
422330	D30783	Hs.115263	epiregulin	24.38
428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	23.55
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	22.70
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	21.60
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	21.15
415989	AI267700	Hs.317584	ESTs	20.95
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.35
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	18.68
421470	R27496	Hs.1378	annexin A3	18.05
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.30
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.15
450531	AW301032	Hs.203800	ESTs	16.60
432867	AW016936	Hs.233364	ESTs	16.35
443211	AI128388	Hs.143655	ESTs	15.80
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	15.10
406964	M21305		gb:Human alpha satellite and satellite 3	15.00
410355	S58544	Hs.153057	sperm associated antigen 1	14.70
441377	BE218239	Hs.202656	ESTs	14.45
413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.35
442409	BE208843	Hs.129544	hypothetical protein MGC15438	14.35
440304	BE159984	Hs.125395	ESTs	14.25
426427	M86699	Hs.169840	TTK protein kinase	13.60
451561	N52812	Hs.177403	ESTs	12.80
434032	AW009951	Hs.206892	ESTs	12.75
428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	12.65
422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	12.55
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.40
446232	AI281848	Hs.194691	retinoic acid induced 3	12.25
424252	AK000520	Hs.143811	hypothetical protein FLJ20513	12.18
450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.85
419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	11.80
422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	11.65
452461	N78223	Hs.108106	transcription factor	11.42
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	11.35
400534				11.00
448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	10.75
453688	AW381270	Hs.194110	hypothetical protein PRO2730	10.75
426890	AA393167	Hs.41294	ESTs	10.60
408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.55
423020	AA383092	Hs.1608	replication protein A3 (14kD)	10.50
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.40
425761	AW664214	Hs.196729	ESTs	10.25
404567				10.15
428536	AI143139	Hs.2288	visinin-like 1	10.10
414972	BE263782	Hs.77695	KIAA0008 gene product	10.05
459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.95
438018	AK001160	Hs.5999	hypothetical protein FLJ10298	9.90
447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.85
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	9.85
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	9.78
451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	9.73
420900	AL045633	Hs.44269	ESTs	9.68
438639	AI278360	Hs.31409	ESTs	9.55
439521	AI808955	Hs.58248	ESTs	9.55
445676	AI247763	Hs.16928	ESTs	9.50
408489	AI082437	Hs.26690	ESTs	9.50
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	9.37
446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.00
423349	AF010258	Hs.127428	homeo box A9	8.96
400195	NA		NA	8.90
411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	8.90
418895	AA894638	Hs.14600	ESTs	8.85
424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.80
448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.75
417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	8.65
414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	8.64
445436	AI224105	Hs.151408	ESTs	8.50
403776				8.50
433447	U29195	Hs.3281	neuronal pentraxin II	8.50
407168	R45175	Hs.117183	ESTs	8.31
419335	AW960146	Hs.284137	hypothetical protein FLJ12888	8.30
422505	AL120862	Hs.124165	ESTs	8.25
458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.20
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	8.15
446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
409687	T51125	Hs.8493	ESTs	8.05

	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.93
	406360	NA		NA	7.80
	443450	N66045	Hs.133529	ESTs	7.75
5	414422	AA147224	Hs.337232	ESTs	7.75
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	7.70
	438604	AA811896	Hs.44604	ESTs	7.60
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.55
	400250	NA		NA	7.53
10	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.50
	404996				7.50
	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	7.45
	445019	AI205540	Hs.281295	ESTs	7.30
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.25
15	448816	AB033052	Hs.22151	KIAA1226 protein	7.25
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	7.25
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	7.20
	433859	AW896758	Hs.273789	ESTs	7.20
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	7.20
20	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.20
	419751	AW195581	Hs.93121	KIAA0761 protein	7.16
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	7.15
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	7.15
	421373	AA808229	Hs.167771	ESTs	7.10
25	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.00
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.96
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	6.95
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.95
	413573	AI733859	Hs.149089	ESTs	6.95
30	442660	AW138174	Hs.130651	ESTs	6.93
	427878	C05766	Hs.181022	CGI-07 protein	6.90
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	6.85
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518 (f	6.82
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.80
35	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.80
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.75
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	6.75
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	6.71
40	401644				6.70
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	6.70
	428479	Y00272	Hs.184572	cell division cycle 2, G1.to S and G2 to	6.69
	406747	AI925153	Hs.217493	annexin A2	6.65
	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.60
45	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	6.60
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.55
	427072	H38046	Hs.303193	ESTs	6.55
	452588	AA889120	Hs.110637	homeo box A10	6.53
	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.50
50	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	6.50
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	6.50
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	6.50
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.50
	410908	AA121686	Hs.10592	ESTs	6.47
55	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	6.47
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.45
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	6.42
	451389	N73222	Hs.279009	matrix Gla protein	6.40
	438202	AW169287	Hs.22588	ESTs	6.40
60	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	6.37
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.36
	436539	AI005457	Hs.275048	ESTs	6.35
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	6.34
65	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	6.32
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	6.31
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.30
	413597	AW302885	Hs.117183	ESTs	6.30
	429529	AA454190	Hs.24283	ESTs, Moderately similar to reduced expr	6.30
70	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.25
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.20
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.20
	438050	BE262816	Hs.6061	protein kinase, AMP-activated, beta 1 no	6.20
	416857	AA188775	Hs.292453	ESTs	6.20
75	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.15
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.15
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.15
	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.11
80	424745	AA214618	Hs.152759	activator of S phase kinase	6.10
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.10
	454438	AA224053	Hs.172405	cell division cycle 27	6.08
	407771	AL138272	Hs.62713	ESTs	6.08

	416057	AI927382	Hs.29857	ESTs	6.05
	442917	AA314907	Hs.85950	ESTs	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	5.96
5	412246	AI160873	Hs.69233	zinc finger protein	5.96
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.95
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.95
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	5.95
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.90
10	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.90
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	5.87
	408908	BE296227	Hs.250822	serine/threonine kinase 15	5.86
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.86
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	5.85
15	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.85
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.85
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.85
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.85
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.82
20	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	459309	AA040620	Hs.5672	hypothetical protein AF140225	5.80
	410060	NM_001448	Hs.58367	glypican 4	5.79
	423806	AA331247	Hs.86617	ESTs	5.77
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5.75
25	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.75
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.75
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.75
	442957	AI949952	Hs.49397	ESTs	5.75
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	5.70
30	426518	Z43039	Hs.170198	KIAA0009 gene product	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	409757	NM_001898	Hs.123114	cystatin SN	5.69
	433687	AA743991		gb:ny57g01.s1 NCI_CGAP_Pr18 Homo sapiens	5.68
35	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.60
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.60
	438777	AA825487	Hs.142179	ESTs	5.60
	417235	AA810278	Hs.24250	ESTs	5.60
	451177	AI969716	Hs.13034	ESTs	5.60
40	415227	AW821113	Hs.72402	ESTs	5.58
	436217	T53925	Hs.107	fibrinogen-like 1	5.56
	452881	AW135220	Hs.241921	ESTs	5.55
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.55
	426235	AI631964	Hs.34447	ESTs	5.55
45	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	5.53
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked mol	5.52
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.47
50	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.47
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	5.47
	420218	AW958037	Hs.286	ribosomal protein L4	5.45
	421155	H87879	Hs.102267	lysyl oxidase	5.45
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	5.45
55	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.45
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	5.44
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	5.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.41
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	5.41
60	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	5.35
	430217	N47863	Hs.336901	ribosomal protein S24	5.33
	417372	T99755	Hs.334728	ESTs	5.30
	415139	AW975942	Hs.48524	ESTs	5.30
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.29
65	424086	AI351010	Hs.102267	lysyl oxidase	5.27
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.27
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	5.26
	452131	AI860677	Hs.72325	Human DNA sequence from clone RP1-187J11	5.25
	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.25
70	449347	AV649748	Hs.295901	KIAA0493 protein	5.25
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.25
	453921	AI824009	Hs.44577	ESTs	5.25
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.25
	421076	AW007988	Hs.233299	ESTs, Weakly similar to I38022 hypotheti	5.25
75	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	5.24
	433384	AI021992	Hs.124244	ESTs	5.23
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	5.21
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.20
	441795	N58115	Hs.21137	AD024 protein	5.20
80	449416	AI651016	Hs.246311	ESTs	5.20
	418379	AA218940	Hs.137516	fidgetin-like 1	5.20
	426753	T89832	Hs.170278	ESTs	5.18
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.17

	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	5.17
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	5.17
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.15
	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.15
5	447713	AI420733	Hs.207083	ESTs	5.15
	425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.15
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	5.15
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	5.13
	441139	AW449009	Hs.126647	ESTs	5.13
10	451121	AW973795	Hs.128927	Homo sapiens cDNA FLJ13903 fis, clone TH	5.10
	435202	AI971313	Hs.170204	KIAA0551 protein	5.10
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	5.10
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	5.09
	422805	AA436989	Hs.121017	H2A histone family, member A	5.07
15	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	5.06
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	5.06
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.05
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.05
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.05
20	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.05
	441675	AI914329	Hs.5461	ESTs	5.00
	449802	AW901804	Hs.23964	hypothetical protein FLJ20147	5.00
	401480	NA		NA	5.00
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	4.95
25	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	4.92
	414718	H95348	Hs.107987	ESTs	4.91
	419139	AI123517	Hs.269940	ESTs	4.90
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I76885 serine/th	4.90
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	4.90
30	408758	NM_003686	Hs.47504	exonuclease 1	4.90
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	4.90
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	4.90
	433927	AI557019	Hs.116467	small nuclear protein PRAC	4.89
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	4.88
35	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	4.87
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.87
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	4.86
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	4.85
	418396	AI765805	Hs.26691	ESTs	4.85
40	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.84
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	4.80
	406414				4.75
	430178	AW449612	Hs.152475	ESTs	4.71
	411901	AA166730	Hs.6966	Human DNA sequence from clone RP1-187J11	4.70
45	404025	NA		NA	4.70
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	4.68
	436662	AI582393	Hs.126695	ESTs	4.68
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	4.68
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	4.65
50	431041	AA490967	Hs.197955	KIAA0704 protein	4.65
	417860	AW408557	Hs.235498	hypothetical protein FLJ14075	4.65
	410658	AW105231	Hs.192035	ESTs	4.65
	425895	AI269484	Hs.161427	zinc finger protein 215	4.65
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.65
55	436397	AA715013	Hs.169835	ESTs	4.60
	439225	AA192669	Hs.45032	ESTs	4.60
	423197	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	4.60
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.60
	412723	AA648459	Hs.335951	hypothetical protein AF301222	4.59
60	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.59
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.58
	430704	AW813091	Hs.335799	ESTs	4.56
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	4.55
	433326	AI379486	Hs.159430	ESTs	4.55
65	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	4.55
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	4.55
	423343	AA324643	Hs.246106	ESTs	4.55
	416467	H57585	Hs.37467	ESTs	4.55
	408867	AA437199	Hs.656	cell division cycle 25C	4.54
70	419423	D26488	Hs.90315	KIAA0007 protein	4.54
	414132	AI801235	Hs.48480	ESTs	4.53
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	4.53
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acyit	4.50
	451009	AA013140	Hs.115707	ESTs	4.50
75	431064	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	4.50
	432725	AL137496	Hs.9001	ESTs	4.50
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	4.50
	410486	AW235094	Hs.69233	zinc finger protein	4.50
	428532	AF157326	Hs.184786	TBP-interacting protein	4.50
80	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.50
	408380	AF123050	Hs.44532	diubiquitin	4.49
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	4.47
	434294	AJ271379	Hs.76194	ribosomal protein S5	4.47

	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.46
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	4.45
	410142	AA081924	Hs.124918	KIAA1795 protein	4.45
	434894	AW977850	Hs.23856	hypothetical protein MGC5297	4.45
5	420092	AA814043	Hs.88045	ESTs	4.45
	400115	NA		NA	4.45
	430967	H16791	Hs.31445	ESTs	4.41
	438078	AI016377	Hs.131693	ESTs	4.41
	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	4.40
10	429774	AI522215	Hs.50883	KIAA1804 protein	4.40
	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	4.40
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.40
	450480	X82125	Hs.25040	zinc finger protein 239	4.40
	421211	AA284966	Hs.266308	mosaic serine protease	4.40
15	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	4.40
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	4.37
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	4.35
	410568	AW162948	Hs.64542	cleavage and polyadenylation specific fa	4.35
	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.35
20	448243	AW369771	Hs.52620	integrin, beta 8	4.35
	438069	N80701	Hs.33790	ESTs	4.35
	446152	AI292036	Hs.150028	ESTs	4.34
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	4.32
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.30
25	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.30
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.30
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.30
	439619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	4.30
	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	4.30
30	450192	AA263143	Hs.24596	RAD51-interacting protein	4.29
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	4.28
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	4.26
	434217	AW014795	Hs.23349	ESTs	4.26
	409723	AW885757	Hs.257862	ESTs	4.25
35	417956	AA210704	Hs.190465	ESTs	4.25
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	4.25
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.24
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	4.22
	424583	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	4.20
40	429436	AA452934	Hs.279813	hypothetical protein	4.20
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila inaD-like	4.20
	448912	D83781	Hs.22559	KIAA0197 protein	4.20
	442671	AI005668	Hs.134779	EST	4.20
	411893	R82845	Hs.273789	ESTs	4.20
45	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.20
	421106	AA877124	Hs.172844	ESTs	4.20
	451401	AI793163		gb:on52g03.y5 NCI_CGAP_Co8 Homo sapiens	4.20
	404516	NA		NA	4.20
	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	4.20
50	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.20
	419229	AI827237	Hs.282884	ESTs	4.18
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	4.16
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	4.16
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.15
55	419247	S65791	Hs.89764	fragile X mental retardation 1	4.15
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	4.15
	422093	AF151852	Hs.111449	CGI-94 protein	4.15
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	4.15
	446999	AA151520	Hs.334822	hypothetical protein MGC4485	4.15
60	414538	AW612228	Hs.107987	ESTs	4.14
	453931	AL121278	Hs.25144	ESTs	4.12
	427718	AI798680	Hs.25933	ESTs	4.11
	453863	X02544	Hs.572	orosomucoid 1	4.10
	440209	H05049	Hs.22269	neurexin 3	4.10
65	435148	AI918049	Hs.124961	ESTs	4.10
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.10
	448692	AW013907	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.10
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	4.10
	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.10
70	457059	BE561665	Hs.177677	exosome component Rrp40	4.10
	407162	N63855	Hs.142634	zinc finger protein	4.10
	406117				4.10
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	4.09
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	4.08
75	448666	NM_014953	Hs.323346	KIAA1008 protein	4.07
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	4.07
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	4.07
	456030	AA136106	Hs.184852	KIAA1553 protein	4.05
	434082	AI373481	Hs.131715	hypothetical protein PRO1777	4.05
80	443646	AI085198	Hs.164226	ESTs	4.05
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.05
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	4.05
	432619	AW291722	Hs.278526	related to the N terminus of tre	4.05

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.05
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.04
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	4.04
	424176	AL137273	Hs.142307	hypothetical protein	4.04
5	452259	AA317439	Hs.28707	signal sequence receptor, gamma (transio	4.04
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.03
	435420	AI928513	Hs.59203	ESTs	4.03
	406666	V00495	Hs.184411	albumin	4.02
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	4.00
10	449448	D60730	Hs.57471	ESTs	4.00
	421037	AI684808	Hs.197653	ESTs	4.00
	448310	AI480316		gb:tm26h09.x1 Soares_NFL_T_GBC_S1 Homo s	4.00
	408155	AB014528	Hs.43133	KIAA0628 gene product	4.00
	413841	M34276	Hs.75576	plasminogen	3.98
15	400110	NA		NA	3.98
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.97
	443715	AI583187	Hs.9700	cyclin E1	3.97
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.97
	450164	AI239923	Hs.30098	ESTs	3.97
20	451592	AI805416	Hs.213897	ESTs	3.95
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome delta	3.95
	426199	AA371865	Hs.97090	ESTs	3.95
	414148	BE084049		gb:PM0-BT0651-270400-003-f02 BT0651 Homo	3.95
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.94
25	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	3.93
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.93
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.92
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.91
	416185	AW975861	Hs.47367	KIAA1785 protein	3.91
30	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.90
	432596	AJ224741	Hs.278461	matrilin 3	3.90
	451229	AW967707	Hs.48473	ESTs	3.90
	413583	AL120806	Hs.5888	ESTs	3.90
	432702	AW973953	Hs.293744	ESTs	3.90
35	437207	T27503	Hs.15929	hypothetical protein FLJ12910	3.90
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.90
	423697	BE088697	Hs.131834	Homo sapiens mRNA; cDNA DKFZp434B0328 (f	3.90
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	3.90
	432289	AI860145	Hs.55118	ESTs	3.89
40	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.88
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.88
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.88
	410094	BE147897	Hs.58593	general transcription factor IIF, polype	3.88
	441826	AW503603	Hs.129915	phosphotriesterase related	3.87
45	444059	R69743	Hs.116774	integrin, alpha 1	3.86
	426262	AI792141	Hs.196270	folate transporter/carrier	3.85
	452641	AW952893	Hs.237825	signal recognition particle 72kD	3.85
	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	3.85
	448315	AW290912	Hs.20797	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.85
50	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	3.85
	409734	BE161664	Hs.56155	hypothetical protein	3.85
	454014	AW016670	Hs.233275	ESTs	3.84
	453116	AI276680	Hs.146086	ESTs	3.83
	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	3.82
55	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.82
	435040	AI932350	Hs.152825	ESTs	3.81
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.81
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	3.81
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.81
60	437631	AA764749	Hs.267245	hypothetical protein FLJ14803	3.80
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.80
	405769				3.80
	438295	AI394151	Hs.37932	ESTs	3.80
	453628	AW243307	Hs.83937	hypothetical protein	3.80
65	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	3.80
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.76
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	3.75
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.75
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.75
70	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.74
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	3.74
	418413	R95735	Hs.117753	ESTs, Weakly similar to A48666 cell prol	3.73
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	3.73
	406667	M12523	Hs.184411	albumin	3.72
75	436411	AW674352		gb:be63c07.y1 NIH_MGC_12 Homo sapiens cD	3.72
	417246	AI760098	Hs.21411	ESTs	3.72
	410664	NM_006033	Hs.65370	lipase, endothelial	3.71
	432686	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fis, clone NT	3.70
	442881	AI023175	Hs.167022	ESTs	3.70
80	432356	AA831032	Hs.111670	ESTs, Highly similar to JC2257 prolyl ol	3.70
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	3.70
	405460	NA		NA	3.70
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.70

	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	3.70
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	3.69
	439857	AA847194	Hs.232002	ESTs	3.69
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	3.69
5	444471	AB020684	Hs.11217	KIAA0877 protein	3.69
	419559	Y07828	Hs.91096	ring finger protein	3.69
	437641	AA811452	Hs.291911	ESTs	3.68
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.67
	417791	AW965339	Hs.111471	ESTs	3.66
10	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.66
	432023	AW273128	Hs.330144	EST	3.66
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.65
	450600	BE079478	Hs.24880	ESTs	3.65
	420595	AA278865	Hs.88523	ESTs	3.65
15	404477	NA		NA	3.65
	457003	S78234	Hs.172405	cell division cycle 27	3.65
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.65
	452220	BE158006	Hs.212296	ESTs	3.65
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.65
20	457465	AW301344	Hs.122908	DNA replication factor	3.64
	436149	AI754308	Hs.159452	ESTs	3.63
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	3.63
	427920	Z11502	Hs.181107	annexin A13	3.63
	424641	AB001106	Hs.151413	glia maturation factor, beta	3.63
25	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.62
	411975	AI916058	Hs.144583	ESTs	3.61
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	3.61
	429628	H09604	Hs.13268	ESTs	3.61
	449722	BE280074	Hs.23960	cyclin B1	3.60
30	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	3.60
	419945	AW290975	Hs.118923	ESTs	3.60
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	3.60
	420585	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	3.60
	407809	AW082279	Hs.244106	ESTs	3.60
35	457708	AA805443	Hs.179909	hypothetical protein FLJ22995	3.60
	427943	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.60
	428771	AB028992	Hs.193143	KIAA1069 protein	3.60
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	3.59
	418688	T85017	Hs.1192	KIAA0074 protein	3.59
40	436961	AW375974	Hs.156704	ESTs	3.58
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1	3.58
	415245	N59650	Hs.27252	ESTs	3.57
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.55
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.55
45	401165	NA		NA	3.55
	415382	AI743539	Hs.72465	ESTs, Weakly similar to non-lens beta ga	3.55
	433968	AL157518	Hs.90421	PRO2463 protein	3.55
	421528	AB037837	Hs.105461	hypothetical protein FLJ20357	3.55
	443325	BE398006	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.55
50	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALU6_HUMAN A	3.55
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.55
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.55
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	3.55
	441065	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.54
55	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.54
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.53
	432542	AW083920	Hs.16098	claudin 2	3.53
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.52
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.51
60	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.51
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	3.50
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.48
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.48
	449915	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukem	3.47
65	427975	AI536065	Hs.122460	ESTs	3.46
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	3.45
	404253				3.45
	435567	AW504944	Hs.162990	Homo sapiens cDNA FLJ14193 fis, clone NT	3.45
	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.45
70	417315	AI060042	Hs.336901	ribosomal protein S24	3.45
	419140	AI982647	Hs.215725	ESTs	3.44
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	3.43
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.42
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.42
75	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	3.41
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.41
	419131	AA406293	Hs.41167	ESTs	3.41
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	3.40
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	3.40
80	453531	AA417940	Hs.271400	ESTs, Weakly similar to JC5795 CDEP prot	3.40
	444826	AI674482	Hs.148441	ESTs	3.40
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	3.40
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.40

	418939	AW630803	Hs.89497	lamin B1	3.40
	418134	AA397769	Hs.86617	ESTs	3.40
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.39
	427927	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.39
5	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.39
	410406	AI969703	Hs.1466	glycerol kinase	3.38
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clone HE	3.38
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	3.38
	446432	AI377320	Hs.150058	ESTs	3.36
10	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	3.35
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.35
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	3.35
	421039	NM_003478	Hs.101299	cullin 5	3.35
	407819	R42185	Hs.274803	ESTs	3.35
15	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.35
	433361	AW469373	Hs.300141	ribosomal protein L39	3.35
	435022	AW183385	Hs.54627	ESTs, Weakly similar to FTDH_HUMAN 10-FO	3.35
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	3.35
	454018	AW016892	Hs.100855	ESTs	3.35
20	439871	R88518	Hs.46736	hypothetical protein FLJ23476	3.35
	453941	U39817	Hs.36820	Bloom syndrome	3.34
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.33
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.33
	438008	AA775026	Hs.203802	ESTs	3.33
25	421246	AW582962	Hs.102697	CGI-47 protein	3.33
	451707	AW051061	Hs.60973	ESTs	3.33
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	3.31
	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.31
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11361 fis, clone HE	3.31
30	438746	AI885815	Hs.184727	ESTs	3.30
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 fem	3.30
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	3.30
	458855	AW361299	Hs.107000	hypothetical protein FLJ11294	3.30
	417221	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	3.30
35	424770	AA425562	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	3.30
	417720	AA205625	Hs.208067	ESTs	3.29
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	3.29
	452862	AW378065	Hs.8687	ESTs	3.28
	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.28
40	437222	AL117588	Hs.12778	ESTs	3.28
	422665	AJ011812	Hs.119018	transcription factor NRF	3.28
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.28
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.27
	447829	AI433029	Hs.164104	ESTs	3.27
45	427576	BE242611	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.27
	456132	BE219771	Hs.237146	hypothetical protein FLJ12752	3.26
	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	3.26
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.26
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	3.25
50	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypotheti	3.25
	453320	AW450240	Hs.257274	ESTs	3.25
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.25
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.25
	410659	AI080175	Hs.68826	ESTs	3.25
55	446202	AI279706	Hs.149474	ESTs	3.25
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	3.25
	439262	AA832333	Hs.333045	ESTs	3.25
	401823	NA		NA	3.25
	441264	AA927170	Hs.23290	ESTs	3.25
60	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.24
	408321	AW405882	Hs.44205	cortistatin	3.24
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	3.24
	404519				3.24
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.23
65	422660	AW297582	Hs.103267	hypothetical protein FLJ22548 similar to	3.23
	427961	AW293165	Hs.143134	ESTs	3.22
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	3.22
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.21
	458652	AW375610	Hs.117102	hypothetical protein FLJ13046 similar to	3.21
70	426472	BE246138	Hs.30853	ESTs	3.21
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.21
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.21
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.20
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.20
75	431678	AW072372	Hs.267446	hypothetical protein FLJ11184	3.20
	430439	AL133561	Hs.241426	DKFZP434B061 protein	3.20
	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.20
	437905	AW363121	Hs.175596	ESTs, Weakly similar to T26935 hypotheti	3.20
	434160	BE551196	Hs.114275	ESTs	3.20
80	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.20
	412966	BE243311	Hs.8024	IK cytokine, down-regulator of HLA II	3.19
	414386	X00442	Hs.75990	haptoglobin	3.19
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.18

	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.18
	433764	AW753676	Hs.39982	ESTs	3.17
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypothetl	3.17
	429616	AI982722	Hs.120845	ESTs	3.17
5	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.16
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.16
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.16
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.15
	443830	AI142095	Hs.143273	ESTs	3.15
10	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.15
	433527	AW235613	Hs.133020	ESTs	3.15
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.15
	457453	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.15
	427687	AW003867	Hs.1570	histamine receptor H1	3.15
15	455068	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.15
	441720	AI346487	Hs.28739	ESTs	3.15
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	3.15
	445921	AW015211	Hs.146181	ESTs	3.15
	429957	AW204530	Hs.99500	ESTs	3.15
20	403137				3.14
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.14
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	3.14
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.14
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.14
25	439277	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.13
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.13
	406668	T62745	Hs.184411	albumin	3.13
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	3.13
	437594	AA761431	Hs.74335	heat shock 90kD protein 1, beta	3.13
30	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.13
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	3.13
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.11
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	3.11
	441790	AW294909	Hs.132208	ESTs	3.11
35	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	3.10
	449664	R06212	Hs.127733	ESTs	3.10
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.10
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.10
	402963				3.10
40	428967	AW978441	Hs.296100	ESTs	3.10
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.10
	407502	U52096		gb:Human zinc finger protein (kr-znf1) m	3.10
	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	3.10
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.10
45	421056	AI076890	Hs.146847	TRAF family member-associated NFKB activ	3.10
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	3.10
	421841	AA908197	Hs.108850	MAK-related kinase	3.10
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.10
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.10
50	433037	NM_014158	Hs.279938	HSPC067 protein	3.09
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.09
	457726	AI217477	Hs.194591	ESTs	3.09
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	3.08
	433013	AI697890	Hs.127337	axin 2 (conductin, axil)	3.08
55	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.08
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL_HUMAN SORTI	3.07
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.07
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	3.07
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.07
60	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.07
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	3.06
	436554	AI985810	Hs.301173	ESTs	3.06
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	3.06
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	3.06
65	445413	AA151342	Hs.12677	CGI-147 protein	3.06
	452909	NM_015368	Hs.30985	pannexin 1	3.06
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	3.05
	425942	AU077195	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Sanf	3.05
	406333				3.05
70	428454	U55936	Hs.184376	synaptosomal-associated protein, 23kD	3.05
	411864	AW948147		gb:RC0-MT0013-280300-031-e03 MT0013 Homo	3.05
	458632	AI744445	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.05
	448292	BE281316	Hs.47334	hypothetical protein FLJ14495	3.05
	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypothetl	3.05
75	402167				3.05
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	3.05
	437828	AW976806	Hs.73149	paired box gene 8	3.05
	404232				3.05
	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	3.05
80	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.05
	452787	AW294022	Hs.222707	KIAA1718 protein	3.05
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.05
	410718	AI920783	Hs.191435	ESTs	3.04

419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.04
446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.03
425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.02
452834	AI638627	Hs.105685	KIAA1688 protein	3.02
410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.02
416568	H64844	Hs.138558	ESTs	3.02
425834	NM_001639	Hs.1957	amyloid P component, serum	3.02
426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	3.01
412719	AW016610	Hs.129911	ESTs	3.01
439586	AA922936	Hs.110039	ESTs	3.01
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	3.01
429703	T93154	Hs.28705	ESTs	3.00
400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.00
415261	T40928	Hs.8346	ESTs	3.00
419435	AI200540	Hs.14877	ESTs, Weakly similar to (defline not ava	3.00
429985	NM_015836	Hs.227274	tryptophanyl tRNA synthetase 2 (mitochon	3.00
423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.00
407182	AA312551	Hs.230157	ESTs	3.00
424202	BE350295	Hs.15032	RAN binding protein 17	3.00
444585	AW170015	Hs.6594	ESTs	3.00
420552	AK000492	Hs.98806	hypothetical protein	3.00
451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	3.00
441928	AI370188	Hs.211454	ESTs	3.00
430868	BE155293	Hs.76064	ribosomal protein L27a	3.00
417806	AI867277	Hs.183733	ESTs	3.00
447175	AI365208	Hs.293606	ESTs	3.00
417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	3.00
435447	AI872932		gb:wm72e03.x1 NCI_CGAP_Ut2 Homo sapiens	3.00
405394				3.00
454975	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.00
441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	3.00
428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.00

TABLE 6B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
411765	125700_1	H43346 AA248302 AA095182
411864	1262055_1	AW948147 BE092316 AW948138 AW948130 AW948148 AW948129 AW948136 AW948152 AW948144 AW948137 AW948160
412359	129085_1	AW837985 AW837938 AA101955 AW837913 AW837935
413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
414148	142133_1	BE084049 AW292907 AA135984
424492	240008_1	AI133482 AI207619 AA341626
430264	315008_1	AA470519 BE303010 BE302954 BE384120
431064	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
433687	373061_1	AA743991 AA604852 AW272737
434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 BE081531 H59570
435447	406400_1	AI872932 AA682306 BE220163 W88695 T81307 H91447
436411	419334_1	AW674352 AA715374 Z25205
443613	575391_1	AI079356 W23287
446901	697809_1	AI347274 AW844024
448310	757918_1	AI480316 AW847535
451401	868474_1	AI793163 AW875182 AW875178 AW875176
454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
454975	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
455838	1374605_1	BE145808 BE145807 BE181883

TABLE 6C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400534	6981826	Minus	278637-279292
401165	9438376	Minus	168244-168423
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401644	8576138	Plus	82655-83959
401823	2262095	Minus	42575-42697,43189-43287,45830-45974
402167	8571795	Plus	109122-110357
402963	5419653	Minus	12950-15959
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403776	7770611	Minus	1414-1513,1624-1756
404025	7341444	Plus	131740-131905
404232	8218045	Minus	71800-71956
404253	9367202	Minus	55675-56055
404477	8080699	Plus	113390-113577
404516	8151967	Plus	114153-114322
404519	8152000	Plus	12817-13000
404567	7249169	Minus	101320-101501
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405394	6624123	Minus	31900-32373
405460	7684569	Minus	52223-52389
405769	3046270	Minus	76844-77193
406117	9142932	Plus	54304-54584
406333	9213235	Plus	64689-64798
406360	9256107	Minus	7513-7673
406414	9256407	Plus	49593-49850

TABLE 7A: 516 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Table 7A lists 516 genes up-regulated in colon cancer compared to normal colon . These were selected as for Table 6A except for using all CEP and colon sample in the normal body tissue list as the normal samples in determining the denominator value and the ratio was equal to or greater than 5.0.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of tumor to normal colon

Pkey	ExAccn	UnigeneID	Unigene Title	R1
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	57.52
406667	M12523	Hs.184411	albumin	49.94
409041	AB033025	Hs.50081	KIAA1199 protein	49.18
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	42.22
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	34.64
429201	X03178	Hs.198246	group-specific component (vitamin D bind	33.38
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	33.10
447033	AI357412	Hs.157601	ESTs	31.24
428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	26.84
438461	AW075485	Hs.286049	phosphoserine aminotransferase	25.40
413841	M34276	Hs.75576	plasminogen	24.68
428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	23.18
452862	AW378065	Hs.8687	ESTs	21.34
415989	AI267700	Hs.317584	ESTs	20.92
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.22
421470	R27496	Hs.1378	annexin A3	17.92
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	17.36
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.28
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.08
421462	AF016495	Hs.104624	aquaporin 9	17.02
424252	AK000520	Hs.143811	hypothetical protein FLJ20513	16.98
452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.70
432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	16.64
433447	U29195	Hs.3281	neuronal pentraxin II	16.59
414386	X00442	Hs.75990	haptoglobin	16.19
425260	L47726	Hs.1870	phenylalanine hydroxylase	16.08
444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	15.82
439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	15.80
443211	AI128388	Hs.143655	ESTs	15.78
439608	AW864696	Hs.301732	hypothetical protein MGC5306	15.52
414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	15.42
412719	AW016610	Hs.129911	ESTs	15.24
439451	AF086270	Hs.278554	heterochromatin-like protein 1	15.18
448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	15.03

	416402	NM_000715	Hs.1012	complement component 4-binding protein,	14.60
	453863	X02544	Hs.572	orosomucoid 1	14.35
	441243	AI767056	Hs.193002	ESTs	14.30
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.30
5	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	13.91
	433213	AW665130	Hs.137190	ESTs	13.80
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	13.52
	438578	AA811244	Hs.164168	ESTs	13.40
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	13.36
10	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	13.00
	449199	AI990122	Hs.196988	ESTs	12.98
	436393	AW022213	Hs.143617	ESTs	12.90
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	12.83
	451561	N52812	Hs.177403	ESTs	12.72
15	420734	AW972872	Hs.293736	ESTs	12.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	12.50
	441377	BE218239	Hs.202656	ESTs	12.45
	435981	H74319	Hs.188620	ESTs	12.38
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	12.38
20	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.38
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	12.34
	430290	AI734110	Hs.136355	ESTs	12.30
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.26
	450628	AW382884	Hs.204715	ESTs	12.24
25	446232	AI281848	Hs.194691	retinoic acid induced 3	12.16
	428223	AA424313	Hs.98402	ESTs	12.08
	432582	AI623817	Hs.168457	ESTs	12.08
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	12.02
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	12.01
30	407202	N58172	Hs.109370	ESTs	11.84
	422109	S73265	Hs.1473	gastrin-releasing peptide	11.68
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	11.68
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	11.67
	443162	T49951	Hs.9029	DKFZP434G032 protein	11.67
35	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.62
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.46
	453909	AW004045	Hs.203365	ESTs	11.42
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	11.34
	452903	AI953425	Hs.246911	ESTs, Weakly similar to I38022 hypotheti	11.32
40	433011	H07960	Hs.306044	CGI-05 protein	11.30
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	11.22
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	11.20
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	11.08
	407168	R45175	Hs.117183	ESTs	10.91
45	407633	NM_007069	Hs.37189	similar to rat HREV107	10.90
	400534				10.88
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.76
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	10.68
	440526	AI832243	Hs.211471	ESTs	10.63
50	427544	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	10.62
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.52
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	10.52
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
	457065	AI476318	Hs.192480	ESTs	10.40
55	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.38
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	10.34
	414718	H95348	Hs.107987	ESTs	10.29
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.28
	404567				10.14
60	428536	AI143139	Hs.2288	visinin-like 1	10.06
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.05
	437267	AW511443	Hs.258110	ESTs	10.00
	420583	H77859	Hs.65450	reticulon 4	10.00
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	9.99
65	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	9.97
	449655	AI021987	Hs.59970	ESTs	9.91
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.90
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	9.90
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	9.88
70	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.84
	448106	AI800470	Hs.171941	ESTs	9.64
	439192	AW970536	Hs.105413	ESTs	9.64
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	9.61
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	9.50
75	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	9.44
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	9.40
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	9.36
	401742	NA		NA	9.30
	416393	N54037	Hs.262869	plasminogen-like	9.28
80	413339	AI818080	Hs.194290	ESTs	9.28
	437641	AA811452	Hs.291911	ESTs	9.28
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	9.22
	431319	AA873350	Hs.302232	ESTs	9.21

434008	AA740878	Hs.112982	ESTs	9.20
446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.16
419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	9.16
413597	AW302885	Hs.117183	ESTs	9.15
440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	9.14
409327	L41162	Hs.53563	collagen, type IX, alpha 3	9.14
444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	9.05
456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	8.98
450164	AI239923	Hs.30098	ESTs	8.95
432867	AW016936	Hs.233364	ESTs	8.93
437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	8.92
421126	M74587	Hs.102122	insulin-like growth factor binding prote	8.92
452712	AW838616		gb:RC5-LT0054-140200-013-D01 LT0054 Homo	8.90
419131	AA406293	Hs.41167	ESTs	8.86
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.82
418895	AA894638	Hs.14600	ESTs	8.82
422665	AJ011812	Hs.119018	transcription factor NRF	8.82
409757	NM_001898	Hs.123114	cystatin SN	8.78
419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	8.74
412446	AI768015	Hs.92127	ESTs	8.71
433285	AW975944	Hs.237396	ESTs	8.68
414538	AW612228	Hs.107987	ESTs	8.64
449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	8.62
430835	AI240006	Hs.192326	ESTs	8.60
445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.59
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	8.52
450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.52
428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	8.50
444478	W07318	Hs.240	M-phase phosphoprotein 1	8.47
439398	AA284267	Hs.221504	ESTs	8.44
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.43
403776				8.42
418973	AA233056	Hs.191518	ESTs	8.42
445436	AI224105	Hs.151408	ESTs	8.38
417958	AA767382	Hs.193417	ESTs	8.34
452838	U65011	Hs.30743	preferentially expressed antigen in mela	8.34
425761	AW664214	Hs.196729	ESTs	8.33
449419	R34910	Hs.119172	ESTs	8.29
407007	U22961		gb:Human mRNA clone with similarity to L	8.28
420900	AL045633	Hs.44269	ESTs	8.25
452503	AB000509	Hs.29736	TNF receptor-associated factor 5	8.23
458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.18
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.16
432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	8.16
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	8.12
446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
416379	AA218940	Hs.137516	fidgetin-like 1	8.07
424560	AA158727	Hs.150555	protein predicted by clone 23733	8.06
453116	AI276680	Hs.146086	ESTs	8.04
419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.04
409687	T51125	Hs.8493	ESTs	8.00
407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	8.00
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
418036	Z37976	Hs.83337	latent transforming growth factor beta b	7.99
422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	7.96
421633	AF121860	Hs.106260	sorting nexin 10	7.92
432542	AW083920	Hs.16098	claudin 2	7.86
414869	AA157291	Hs.21479	ubinuclein 1	7.84
419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	7.80
406666	V00495	Hs.184411	albumin	7.78
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.78
439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	7.77
406360	NA		NA	7.76
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.76
431510	AA580082	Hs.112264	ESTs	7.76
414312	AA155694	Hs.191060	ESTs	7.71
443450	N66045	Hs.133529	ESTs	7.70
449870	AI672487	Hs.15423	hypothetical protein HDCMC04P	7.64
425681	AB018297	Hs.159183	KIAA0754 protein	7.63
408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	7.62
443285	AI301918	Hs.334264	ESTs	7.60
420807	AA280627	Hs.57846	ESTs	7.60
424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	7.60
410718	AI920783	Hs.191435	ESTs	7.60
430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo	7.60
434294	AJ271379	Hs.76194	ribosomal protein S5	7.60
445808	AV655234	Hs.298083	ESTs, Moderately similar to PC4259 ferri	7.56
438604	AA811896	Hs.44604	ESTs	7.54
458997	AW937420	Hs.69662	ESTs	7.54
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.54
409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	7.52
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	7.49
404996				7.48

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	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.48
	433859	AW896758	Hs.273789	ESTs	7.44
	423952	AW877787	Hs.136102	KIAA0853 protein	7.44
	431193	AW749505	Hs.296770	KIAA1719 protein	7.43
5	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	7.40
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	7.40
	424613	AL079850	Hs.151236	highly charged protein	7.37
	417720	AA205625	Hs.208067	ESTs	7.35
	449347	AV649748	Hs.295901	KIAA0493 protein	7.34
10	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.34
	447499	AW262580	Hs.147674	protocadherin beta 16	7.32
	426890	AA393167	Hs.41294	ESTs	7.31
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	7.28
	445019	AI205540	Hs.281295	ESTs	7.28
15	419474	AW968619	Hs.155849	ESTs	7.24
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	7.24
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	7.24
	448816	AB033052	Hs.22151	KIAA1226 protein	7.18
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	7.18
20	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.18
	420777	AA280223	Hs.130865	ESTs	7.16
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	7.14
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.14
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.14
25	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.13
	441124	T97717	Hs.119563	ESTs	7.12
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.10
	446432	AI377320	Hs.150058	ESTs	7.10
	439295	AW206091	Hs.253536	ESTs	7.08
30	436902	AW247145	Hs.192729	ESTs	7.08
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	7.08
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.08
	421373	AA808229	Hs.167771	ESTs	7.06
	432435	BE218886	Hs.282070	ESTs	7.05
35	427933	AW974643	Hs.190571	ESTs	7.04
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	7.04
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	7.01
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	6.98
	446322	N23033	Hs.155814	ESTs	6.98
40	442577	AA292998	Hs.163900	ESTs	6.96
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.94
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	6.92
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	6.90
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	6.90
45	453204	R10799	Hs.191990	ESTs	6.90
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.88
	427878	C05766	Hs.181022	CGI-07 protein	6.88
	454438	AA224053	Hs.172405	cell division cycle 27	6.86
	424402	M63108	Hs.1769	luteinizing hormone/choriogonadotropin r	6.86
50	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	6.84
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	419629	AB020695	Hs.91662	KIAA0888 protein	6.80
	451686	AA059246	Hs.110293	ESTs	6.80
55	430829	AW451999	Hs.194024	ESTs	6.78
	446501	AI302616	Hs.150819	ESTs	6.78
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.78
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.76
	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	6.73
60	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	6.72
	425478	AB007953	Hs.268840	ESTs	6.70
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	6.70
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	6.67
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.62
65	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.62
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.60
	450480	X82125	Hs.25040	zinc finger protein 239	6.58
	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.56
	414575	H11257	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	6.54
70	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	6.54
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	6.54
	449894	AK001578	Hs.24129	CLLL7 protein	6.53
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	6.53
	424745	AA214618	Hs.152759	activator of S phase kinase	6.52
75	441801	AW242799	Hs.86366	ESTs	6.52
	435542	AA687376	Hs.269533	ESTs	6.51
	427072	H38046	Hs.303193	ESTs	6.50
	418051	AW192535	Hs.19479	ESTs	6.46
	436217	T53925	Hs.107	fibrinogen-like 1	6.46
80	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.46
	430704	AW813091	Hs.335799	ESTs	6.44
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.43
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	6.41

	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	438202	AW169287	Hs.22588	ESTs	6.38
	458311	AF069478		gb:AF069478 Homo sapiens astrocytoma lib	6.36
5	451389	N73222	Hs.279009	matrix Gla protein	6.36
	427899	AA829286	Hs.332053	serum amyloid A1	6.35
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.34
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.34
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.32
10	433908	AW298141	Hs.157975	ESTs	6.32
	430114	AA847744	Hs.99640	ESTs	6.32
	434032	AW009951	Hs.206892	ESTs	6.31
	444656	AI277924	Hs.145199	ESTs	6.30
	433607	AA602004	Hs.23260	ESTs	6.26
15	440659	AF134160	Hs.7327	claudin 1	6.25
	435663	AI023707	Hs.134273	ESTs	6.24
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.24
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	6.24
	447500	AI381900	Hs.159212	ESTs	6.24
20	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.22
	417715	AW969587	Hs.86366	ESTs	6.22
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	6.20
	438138	R98299	Hs.177502	ESTs	6.20
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.20
25	416857	AA188775	Hs.292453	ESTs	6.20
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.18
	429598	AA811257	Hs.269710	ESTs	6.18
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.18
	438940	AF075045	Hs.271609	ESTs	6.18
30	400195	NA		NA	6.15
	430473	AW130690	Hs.59962	ESTs	6.12
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.10
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.10
	427513	AI476318	Hs.192480	ESTs	6.10
35	448934	AI598134	Hs.225592	ESTs, Highly similar to T51146 ring-box	6.10
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	6.08
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	6.08
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	6.08
	409048	H59990	Hs.37699	ESTs	6.08
40	427674	NM_003528	Hs.2178	H2B histone family, member Q	6.08
	452689	F33868	Hs.284176	transferrin	6.06
	453804	AA300204	Hs.35276	KIAA0852 protein	6.06
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	6.05
	408243	Y00787	Hs.624	interleukin 8	6.04
45	420721	AA927802	Hs.159471	ZAP3 protein	6.04
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	6.04
	435420	AI928513	Hs.59203	ESTs	6.04
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	6.04
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.02
50	442116	AI884570	Hs.128813	ESTs	6.00
	423568	NM_005256	Hs.129818	growth arrest-specific 2	6.00
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	5.99
	441794	AW197794	Hs.253338	ESTs	5.99
	434739	AA804487	Hs.144130	ESTs	5.98
55	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.96
	420218	AW958037	Hs.286	ribosomal protein L4	5.96
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.94
	445546	AW468821	Hs.156054	ESTs	5.94
	439096	AA830185	Hs.269680	ESTs	5.94
60	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.94
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.94
	417246	AI760098	Hs.21411	ESTs	5.94
	433190	M26901	Hs.3210	renin	5.92
	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	5.92
65	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.92
	434342	AI791138	Hs.116768	ESTs	5.92
	406668	T62745	Hs.184411	albumin	5.92
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.90
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	5.90
70	408867	AA437199	Hs.656	cell division cycle 25C	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.88
	450380	AI863675	Hs.114017	ESTs	5.88
	413026	AA809485	Hs.124219	hypothetical protein FLJ12934	5.88
	454653	AW812227		gb:RC2-ST0173-201099-011-g09 ST0173 Homo	5.87
75	457876	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	5.86
	437222	AL117588	Hs.12778	ESTs	5.86
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	5.86
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.84
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	5.84
80	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.84
	401352				5.84
	419088	AI538323	Hs.52620	integrin, beta 8	5.84
	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	5.83

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	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.82
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.82
	419220	AA811938	Hs.291759	ESTs	5.82
	439303	W00605	Hs.102784	ESTs	5.80
5	415954	AA171850	Hs.42251	ESTs	5.80
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	5.80
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	439527	AW298119	Hs.202536	ESTs	5.78
	435380	AA679001	Hs.192221	ESTs	5.78
10	424086	AI351010	Hs.102267	lysyl oxidase	5.76
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	5.76
	428460	AA428865	Hs.98563	ESTs	5.74
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	5.74
	413962	BE503035	Hs.279193	ESTs	5.74
15	453240	AI969564	Hs.166254	hypothetical protein DKFZp566I133	5.74
	410505	AW752139	Hs.314323	ESTs	5.72
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.72
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.72
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.71
20	433384	AI021992	Hs.124244	ESTs	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.68
	448666	NM_014953	Hs.323346	KIAA1008 protein	5.68
25	412246	AI160873	Hs.69233	zinc finger protein	5.68
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.66
	418269	AA806113	Hs.189025	ESTs	5.64
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	5.64
	422805	AA436989	Hs.121017	H2A histone family, member A	5.62
30	442252	AI733395	Hs.129124	ESTs	5.60
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.60
	435040	AI932350	Hs.152825	ESTs	5.59
	438777	AA825487	Hs.142179	ESTs	5.58
	433849	BE465884	Hs.280728	ESTs	5.58
35	438639	AI278360	Hs.31409	ESTs	5.58
	411274	NM_002776	Hs.69423	kallikrein 10	5.55
	435008	AF150262	Hs.162898	ESTs	5.55
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	5.54
	452881	AW135220	Hs.241921	ESTs	5.54
40	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.54
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.54
	418971	AA360392	Hs.87113	ESTs	5.52
	453716	AA037675	Hs.152675	ESTs	5.52
	406972	M32053		gb:Human H19 RNA gene, complete cds.	5.51
45	417543	AA203620	Hs.110153	ESTs	5.51
	419423	D26488	Hs.90315	KIAA0007 protein	5.51
	434674	AA831879	Hs.136985	ESTs	5.50
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	404227	NA		NA	5.49
	412766	BE544475	Hs.54347	ESTs	5.49
	441708	AI469911	Hs.26498	hypothetical protein FLJ21657	5.49
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	5.48
	437440	AA846804	Hs.123694	ESTs	5.48
55	410486	AW235094	Hs.69233	zinc finger protein	5.46
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.44
	437378	AI198823	Hs.160473	ESTs	5.44
	436907	AA737171	Hs.131809	ESTs	5.44
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.44
60	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.42
	441795	N58115	Hs.21137	AD024 protein	5.42
	452449	AW068658	Hs.20943	ESTs	5.42
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.40
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	5.40
65	441217	AI922183	Hs.213246	ESTs	5.40
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	5.40
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	5.40
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	5.40
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	5.39
70	446142	AI754693	Hs.145968	ESTs	5.38
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	5.36
	433929	AI375499	Hs.27379	ESTs	5.36
	421155	H87879	Hs.102267	lysyl oxidase	5.34
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.34
75	453931	AL121278	Hs.25144	ESTs	5.34
	409091	AW970386	Hs.269423	ESTs	5.33
	416057	AI927382	Hs.29857	ESTs	5.33
	438647	AA813118	Hs.163230	ESTs	5.32
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.32
80	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.30
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.30
	403432				5.29
	435820	AA700580	Hs.189000	ESTs	5.28

401714	NA		NA	5.28
449508	AK001566	Hs.23618	hypothetical protein FLJ10704	5.28
413151	H47969	Hs.141971	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.28
414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	5.28
417372	T99755	Hs.334728	ESTs	5.28
443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	5.28
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	5.27
408943	NM_007070	Hs.49105	FKBP-associated protein	5.26
415139	AW975942	Hs.48524	ESTs	5.26
447982	H22953	Hs.137551	ESTs	5.26
430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	5.24
453921	AI824009	Hs.44577	ESTs	5.24
409582	R27430	Hs.271565	ESTs	5.24
420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	5.23
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	5.23
418661	NM_001949	Hs.1189	E2F transcription factor 3	5.22
446271	D82484	Hs.330994	ESTs	5.22
435905	AW997484	Hs.5003	KIAA0456 protein	5.21
434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.21
415245	N59650	Hs.27252	ESTs	5.20
436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.20
431242	AA987742	Hs.251278	KIAA1201 protein	5.20
439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	5.20
424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	5.20
449138	AW294215	Hs.195631	ESTs	5.20
449416	AI651016	Hs.246311	ESTs	5.20
430092	AI821399	Hs.16514	ESTs	5.20
436574	AW293527	Hs.126465	ESTs	5.18
433377	AI752713	Hs.43845	ESTs	5.18
440987	AA911705	Hs.130229	ESTs	5.18
426116	AA868729	Hs.144694	ESTs	5.18
441928	AI370188	Hs.211454	ESTs	5.17
432657	AA831815	Hs.270940	ESTs, Weakly similar to I78885 serine/th	5.17
438011	BE466173	Hs.145696	splicing factor (CC1.3)	5.16
437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.16
423926	X03833	Hs.1722	interleukin 1, alpha	5.16
433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	5.15
415757	AA830854	Hs.187810	ESTs	5.14
420170	U43374	Hs.95631	Human normal keratinocyte mRNA	5.14
420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	5.12
425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.12
440652	AI216751	Hs.143977	ESTs	5.12
419706	C04649	Hs.77899	tropomyosin 1 (alpha)	5.12
427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.12
416113	AA173525	Hs.118758	ESTs, Weakly similar to RLF [H.sapiens]	5.12
446223	BE300091	Hs.119699	hypothetical protein FLJ12969	5.11
407624	AW157431	Hs.248941	ESTs	5.11
447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.11
452465	AA610211	Hs.34244	ESTs	5.10
442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	5.10
448952	AI609595	Hs.208038	ESTs	5.10
408170	AW204516	Hs.31835	ESTs	5.08
424238	AA337401	Hs.137635	ESTs	5.07
421072	AI215069	Hs.89113	ESTs	5.06
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.06
423654	AI674253	Hs.35828	ESTs	5.06
436862	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	5.06
436554	AI985810	Hs.301173	ESTs	5.05
433264	D85782	Hs.3229	cysteine dioxygenase, type I	5.04
452387	AI680772	Hs.306094	trinucleotide repeat containing 12	5.04
412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	5.03
430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.03
413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.00
418217	AI910647	Hs.13442	ESTs	5.00
401480	NA		NA	5.00
456179	H75490	Hs.271930	ESTs	5.00

TABLE 7B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
408432	1058667_1	AW195262 R27868 AW811262
408690	107490_1	AW864542 AA056567 AW882724
411765	125700_1	H43346 AA248302 AA095182
414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
424281	237742_1	AA766243 AA338252 AA338213

424492	240008_1	AI133482 AI207619 AA341626
428679	294049_1	AA431765 AA432015
430848	324621_1	AW021726 AA487752 AA488085
432340	345248_1	AA534222 AA632632 T81234
432363	345469_1	AA534489 AW970240 AW970323
432639	351744_1	AW973785 H60163 AA557608
434609	38950_1	R76593 AF147390 R76594
439518	47334_1	W76326 AF086341 W72300
443613	575391_1	AI079356 W23287
447197	711623_1	R36075 AI366546 R36167
447974	745643_1	R76886 AI453674 R77049
452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
454653	1228081_1	AW812227 AW812294 AW812092
458311	543550_1	AF069478 AF069479 AF069480

TABLE 7C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400534	6981826	Minus	278637-279292
401352	9931258	Minus	26064-26208
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401714	6715702	Plus	96484-96681
401742	2911728	Plus	64003-64147
403432	9719611	Minus	68204-68392
403776	7770611	Minus	1414-1513,1624-1756
404227	7838233	Minus	93110-93259
404567	7249169	Minus	101320-101501
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
406360	9256107	Minus	7513-7673

Table 8A shows 538 genes significantly down-regulated in colon cancer compared to normal colon. These were selected as for Table 7A and the ratio was equal to or less than than 0.33.

TABLE 8A: 538 GENES SIGNIFICANTLY DOWN-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal colon

Pkey	ExAccn	UnigeneID	Unigene Title	R1
421996	AW583807	Hs.1460	glucagon	0.0233
429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	0.0307
457407	AA505035	Hs.195651	ESTs	0.0416
423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	0.0564
426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.0567
425920	AL049977	Hs.162209	claudin 8	0.0601
431436	AA505035	Hs.195651	ESTs	0.0607
433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.0629
442009	AI733281	Hs.128320	ESTs	0.0634
416889	AW250318	Hs.80395	mal, T-cell differentiation protein	0.0707
429050	X81333	Hs.194777	meprin A, beta	0.0714
427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.0735
446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	0.0739
429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	0.0769
443506	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypotheti	0.0838
415314	N88802	Hs.5422	glycoprotein M6B	0.0853
451181	AI796330	Hs.207461	ESTs	0.0873
429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.0888
426635	BE395109	Hs.129327	hypothetical protein MGC13057	0.0900
429350	AI754634	Hs.131987	ESTs	0.0927
432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.0931

	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	0.0951
	441066	AW205427	Hs.190726	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.0957
	431252	NM_005478	Hs.251380	insulin-like 5	0.0985
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	0.0987
5	433546	AI075877	Hs.125461	hypothetical protein FLJ11539	0.1007
	415154	D63175		gb:HUM501B09B Clontech human placenta po	0.1032
	409921	AW600239		gb:EST00009 pGEM-T library Homo sapiens	0.1067
	432440	X63597	Hs.2996	sucrase-isomaltase	0.1107
	430468	NM_004673	Hs.241519	angiopoietin-like 1	0.1114
10	427167	AI239607	Hs.99196	hypothetical protein MGC11324	0.1147
	441212	AW242447	Hs.146182	cytosolic beta-glucosidase	0.1167
	423605	AF047826	Hs.129887	cadherin 19, type 2	0.1190
	411381	AW841862	Hs.306831	Homo sapiens cDNA: FLJ22549 fis, clone H	0.1211
	412639	AW961284	Hs.296235	ESTs	0.1239
15	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.1240
	403548				0.1248
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	0.1274
	457982	AW856093	Hs.183617	ESTs	0.1277
	448835	BE277929	Hs.11081	UBX domain-containing 2	0.1277
20	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	0.1291
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	0.1309
	407639	AW205369	Hs.312830	ESTs	0.1315
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	0.1325
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.1328
25	451742	T77609	Hs.117970	ankyrin 2, neuronal	0.1335
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.1379
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	0.1393
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.1395
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	0.1456
30	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.1459
	404767				0.1460
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	0.1462
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	0.1463
	452768	AW069459	Hs.61539	ESTs	0.1466
35	418692	AK000268	Hs.87383	hypothetical protein	0.1471
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	0.1471
	407551	Y10516		gb:H.sapiens mRNA for CD58 T3 protein.	0.1486
	402076				0.1487
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.1500
40	442080	AW444761	Hs.44565	ESTs	0.1500
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.1513
	429545	AI824164	Hs.77667	lymphocyte antigen 6 complex, locus E	0.1523
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	0.1529
	435056	AW023337	Hs.5422	glycoprotein M6B	0.1532
45	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	0.1538
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.1542
	408221	AA912183	Hs.47447	ESTs	0.1552
	425220	AW975317	Hs.162987	ESTs	0.1558
	445200	AA084460	Hs.12409	somatostatin	0.1558
50	443238	T78886	Hs.284450	ESTs	0.1563
	456064	AA256213	Hs.72010	ESTs	0.1582
	428133	AW167727	Hs.11873	ESTs	0.1605
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.1615
	437734	AA693951	Hs.180284	ESTs	0.1637
55	414290	AI568801	Hs.71721	ESTs	0.1638
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.1656
	411939	AI365585	Hs.146246	ESTs	0.1660
	442496	R55073	Hs.124130	ESTs	0.1676
	450693	AW450461	Hs.203965	ESTs	0.1698
60	420736	AI263022	Hs.82204	ESTs	0.1718
	405385				0.1745
	404638				0.1751
	427333	AF067797	Hs.176658	aquaporin 8	0.1757
	404246				0.1763
65	433785	BE044593	Hs.112704	ESTs	0.1767
	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	0.1769
	406980	S69265		(NONE)	0.1781
	421666	AL035250	Hs.1408	endothelin 3	0.1784
	452854	AA437061	Hs.14060	prokineticin 1 precursor	0.1795
70	400514				0.1805
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	0.1808
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	0.1812
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	0.1812
	412474	AI791451		gb:nl50c09.y5 NCI_CGAP_Ov2 Homo sapiens	0.1812
75	436008	AI078428	Hs.58785	ESTs	0.1820
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	0.1828
	431728	NM_007351	Hs.268107	multimerin	0.1832
	419746	AW867943	Hs.127216	hypothetical protein FLJ13465	0.1835
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.1838
80	415672	N53097	Hs.193579	ESTs	0.1838
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	0.1838
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	0.1842
	413714	AI560944	Hs.71428	ESTs	0.1845

427061	AB032971	Hs.173392	KIAA1145 protein	0.1847
405282				0.1848
400163				0.1855
412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.1863
447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	0.1876
407891	AA486620	Hs.41135	endomucin-2	0.1895
437140	AA312799	Hs.283689	activator of CREM in testis	0.1901
431544	AK000770	Hs.299329	Homo sapiens cDNA FLJ20763 fis, clone CO	0.1904
436659	AI217900	Hs.144464	ESTs	0.1905
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	0.1926
453698	AA037615	Hs.42746	ESTs	0.1928
423743	AB023148	Hs.173373	KIAA0931 protein	0.1941
428412	AA428240	Hs.126083	ESTs	0.1942
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.1944
434683	AW298724	Hs.202639	ESTs	0.1957
421865	AA609911	Hs.109012	MAX dimerization protein	0.1957
452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	0.1969
407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.1981
419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	0.2004
437740	AA810265	Hs.122915	ESTs	0.2016
405610				0.2017
437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.2025
416961	BE391476	Hs.80617	ribosomal protein S16	0.2041
401465				0.2045
437425	AW183714	Hs.20981	hypothetical protein DKFZp547M236	0.2049
416231	H30333	Hs.165062	ESTs	0.2049
401753				0.2050
433430	AI863735	Hs.186755	ESTs	0.2051
432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.2052
411644	H92064	Hs.278626	Arg/Abl-interacting protein ArgBP2	0.2059
403957				0.2063
435900	AI243036	Hs.16094	ESTs	0.2070
424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.2075
445500	AW451938	Hs.257512	ESTs	0.2075
419956	AL137939	Hs.40096	ESTs	0.2090
418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.2093
423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.2118
401381				0.2120
426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	0.2122
433476	AA594394	Hs.152616	ESTs	0.2125
423405	NM_014151	Hs.128155	HSPC053 protein	0.2130
442826	AI018777	Hs.131241	ESTs	0.2132
427060	AW378993	Hs.90286	ESTs	0.2137
437354	AA749215	Hs.291886	ESTs	0.2137
447734	AI421412	Hs.163659	ESTs	0.2144
424585	AA464840	Hs.131987	ESTs	0.2146
458016	AW188099	Hs.131813	ESTs	0.2151
423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	0.2151
401521				0.2157
430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	0.2165
401024				0.2171
414802	AI793107	Hs.27018	Ris	0.2179
441083	BE562611		gb:601336446F1 NIH_MGC_44 Homo sapiens c	0.2185
417355	D13168	Hs.82002	endothelin receptor type B	0.2186
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.2188
442930	AW881975	Hs.213923	ESTs	0.2193
431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	0.2209
444567	AV654020	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	0.2212
405654				0.2217
415471	F09747	Hs.268707	ESTs	0.2222
449243	AW295031	Hs.198671	ESTs	0.2229
436088	AA704687	Hs.191294	ESTs	0.2232
434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi	0.2242
427552	NM_005771	Hs.179608	retinol dehydrogenase homolog	0.2243
416439	AA180363	Hs.118769	ESTs	0.2244
459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	0.2254
459395	Z30300	Hs.281935	ESTs	0.2257
439039	AI656707	Hs.48713	ESTs	0.2268
433575	AA600175	Hs.39720	ESTs	0.2268
416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.2273
428415	AA337211	Hs.184222	Down syndrome critical region gene 1	0.2283
441899	AI372588	Hs.8022	TU3A protein	0.2283
437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	0.2290
434839	AI743069	Hs.134736	ESTs	0.2294
435731	AA699581	Hs.186811	ESTs	0.2299
400865				0.2304
446294	AI284935		gb:qk55g09.x1 NCI_CGAP_Co8 Homo sapiens	0.2305
414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens c	0.2309
411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	0.2315
453098	Z25935	Hs.86379	ESTs	0.2315
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	0.2319
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	0.2320
443482	AW188093	Hs.250385	ESTs	0.2326

	432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.2329
	421539	AA292747	Hs.97296	ESTs	0.2330
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	0.2344
	408001	AA046458	Hs.95296	ESTs	0.2347
5	409331	M36634	Hs.53973	vasoactive intestinal peptide	0.2351
	431094	AW972276	Hs.116195	ESTs	0.2354
	429575	AA706003	Hs.99387	ESTs	0.2358
	404958				0.2361
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	0.2364
10	452742	AW589945	Hs.97876	hypothetical protein DKFZp564K0322	0.2380
	417511	AL049176	Hs.82223	chordin-like	0.2381
	404927				0.2387
	430297	AW243166	Hs.129806	ESTs	0.2412
	447482	AB033059	Hs.18705	KIAA1233 protein	0.2415
15	418332	R34976	Hs.78293	ESTs	0.2416
	454145	AA046872	Hs.62798	ESTs	0.2421
	422472	R59096	Hs.279939	mitochondrial carrier homolog 1	0.2424
	404070				0.2427
	421232	AA989220	Hs.292100	ESTs	0.2427
20	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	0.2432
	412622	AW664708	Hs.171959	ESTs	0.2433
	454430	AI082777	Hs.61384	sema domain, seven thrombospondin repeat	0.2437
	416694	AW161284	Hs.79564	neuronal PAS domain protein 1	0.2443
	426724	AA383623	Hs.293616	ESTs	0.2444
25	405073				0.2445
	401236	H24185	Hs.92918	hypothetical protein	0.2445
	414203	BE262170	Hs.78629	ATPase, Na+/K+ transporting, beta 1 poly	0.2451
	401776				0.2452
	404696				0.2462
30	426666	AW500131	Hs.171763	CD22 antigen	0.2471
	427078	AI676062	Hs.111902	ESTs	0.2474
	424682	AW604804	Hs.151717	KIAA0437 protein	0.2478
	440383	AA884208	Hs.30484	ESTs	0.2481
	419118	AA234223	Hs.139204	ESTs	0.2494
35	443515	AV657547	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	0.2495
	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	0.2499
	404605				0.2500
	446066	AI343931	Hs.149383	ESTs	0.2505
	408345	R93851	Hs.63063	ESTs	0.2506
40	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	0.2508
	416950	AL049798	Hs.80552	dermatopontin	0.2510
	423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.2513
	449833	R82252	Hs.106106	protein kinase (cAMP-dependent, catalyti	0.2515
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	0.2519
45	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.2523
	422743	BE304678	Hs.119598	ribosomal protein L3	0.2526
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telen	0.2532
	450880	AK002183	Hs.285885	Homo sapiens cDNA FLJ11321 fis, clone PL	0.2536
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	0.2536
50	451979	F06972	Hs.27372	BMX non-receptor tyrosine kinase	0.2549
	440274	R24595	Hs.7122	scrapie responsive protein 1	0.2553
	430097	AI523245	Hs.127638	ESTs	0.2558
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	0.2564
	402695				0.2565
55	453992	AW014995	Hs.281080	ESTs	0.2569
	453888	AW450670	Hs.252819	ESTs	0.2569
	401371				0.2574
	456145	BE299427	Hs.21446	KIAA1716 protein	0.2579
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodieste	0.2580
60	422591	L07648	Hs.118630	MAX-interacting protein 1	0.2582
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	0.2584
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.2586
	405880				0.2588
	420321	D78761	Hs.96657	hyothetical protein	0.2595
65	454415	AK000846	Hs.58679	solute carrier family 7, (cationic amino	0.2602
	437032	AW867372	Hs.302063	immunoglobulin heavy constant mu	0.2604
	448025	BE502965	Hs.170426	ESTs	0.2605
	444304	AW628433	Hs.271296	ESTs, Weakly similar to I54374 gene NF2	0.2605
	424885	AI333771	Hs.82204	ESTs	0.2608
70	425381	D84371	Hs.1898	paraoxonase 1	0.2611
	457413	AA743462	Hs.165337	ESTs	0.2618
	452078	AA022620	Hs.52170	ESTs	0.2624
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	0.2628
	401974				0.2639
75	411319	BE537094		gb:601063333F1 NIH_MGC_10 Homo sapiens c	0.2646
	417761	R13727	Hs.21435	ESTs	0.2648
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	0.2653
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	0.2653
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	0.2660
80	402182				0.2660
	402610				0.2661
	444814	BE010749	Hs.255097	ESTs	0.2663
	450017	W56434	Hs.201608	ESTs	0.2663

	408684	R61377	Hs.12727	hypothetical protein FLJ21610	0.2667
	444209	AI753134	Hs.146494	ESTs	0.2668
	415022	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid	0.2677
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	0.2681
5	422909	AA533356		gb:nj67f10.s1 NCI_CGAP_Pr10 Homo sapiens	0.2681
	412047	AA934589	Hs.49696	ESTs	0.2693
	426356	BE536836	Hs.98682	hypothetical protein FKSG32	0.2703
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	0.2709
	402425				0.2710
10	450545	AW135582	Hs.201767	ESTs	0.2710
	417118	U38654	Hs.50477	RAB27A, member RAS oncogene family	0.2725
	419850	F06844		gb:HSC1ME091 normalized infant brain cDN	0.2727
	428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	0.2730
	441493	AW070446	Hs.127037	ESTs	0.2733
15	413541	BE147036		gb:QV4-HT0222-091199-024-e10 HT0222 Homo	0.2733
	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.2734
	455597	BE008545	Hs.156110	immunoglobulin kappa constant	0.2740
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	0.2740
	444195	AB002351	Hs.10587	KIAA0353 protein	0.2743
20	415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen	0.2747
	421823	N40850	Hs.28625	ESTs	0.2755
	434464	BE063921	Hs.295971	ESTs	0.2755
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	0.2756
	430073	U86136	Hs.232070	telomerase-associated protein 1	0.2762
25	432018	AA524447	Hs.152377	ESTs	0.2763
	422954	AW998605		gb:PM0-BN0065-100300-001-b10 BN0065 Homo	0.2768
	416397	H53035	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	0.2775
	442420	AI024834	Hs.131729	ESTs	0.2775
	410950	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	0.2778
30	427114	AI219896	Hs.97592	ESTs	0.2778
	448466	AI522109	Hs.171066	ESTs	0.2778
	434445	AI349306	Hs.11782	ESTs	0.2784
	457115	AA420712		gb:nc63c07.s1 NCI_CGAP_Pr1 Homo sapiens	0.2785
	459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	0.2786
35	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	0.2794
	433633	AI880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	0.2799
	440236	AW996722	Hs.125297	ESTs	0.2799
	405691				0.2804
	405334				0.2804
40	403047				0.2809
	412506	AW957159		gb:EST369229 MAGE resequences, MAGD Homo	0.2809
	441042	AA077736		gb:7B48A07 Chromosome 7 Fetal Brain cDNA	0.2815
	434660	AA764768	Hs.121158	hypothetical protein DKFZp434J0113	0.2816
	444453	AW379394	Hs.145126	ESTs	0.2817
45	457736	AK000390	Hs.4205	hypothetical protein FLJ20124	0.2820
	454012	M76424	Hs.37014	carbonic anhydrase VII	0.2821
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	0.2822
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	0.2827
	435021	AA922192	Hs.54709	ESTs	0.2828
50	413344	U46024	Hs.75302	myotubular myopathy 1	0.2837
	447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo sapiens c	0.2840
	457290	AA465293	Hs.105069	ESTs	0.2841
	458244	AI929453	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OV	0.2841
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	0.2842
55	407938	AA905097	Hs.85050	phospholamban	0.2845
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.2846
	428212	AW444451	Hs.134812	ESTs	0.2853
	424433	H04607	Hs.9218	ESTs	0.2857
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	0.2857
60	404769				0.2863
	411620	AW854536		gb:RC3-CT0255-200100-024-a08 CT0255 Homo	0.2868
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	0.2870
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens	0.2872
	441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.2874
65	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	0.2877
	421935	AA131632	Hs.109672	CMP-NeuAC:(beta)-N-acetylgalactosaminide	0.2878
	447955	BE544271	Hs.288390	hypothetical protein FLJ22795	0.2880
	405364				0.2881
	422165	AL041199	Hs.1481	histidine decarboxylase	0.2882
70	431087	H12723	Hs.290791	ESTs	0.2882
	450610	AA010370	Hs.60386	nuclear RNA export factor 3	0.2882
	445627	AW818475	Hs.7363	ESTs	0.2883
	436144	AW881250	Hs.148367	ESTs	0.2886
	445152	AI214667	Hs.283597	ESTs	0.2891
75	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.2891
	455614	AI693369	Hs.202274	ESTs	0.2899
	419683	AA248897	Hs.48784	ESTs	0.2900
	411886	AL046810	Hs.20021	vesicle-associated membrane protein 1 (s	0.2904
	430770	AA765694	Hs.123296	ESTs	0.2913
80	444459	AI680624	Hs.148676	ESTs	0.2913
	444918	AI202262	Hs.283362	ESTs	0.2915
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	0.2915
	435598	AA689470	Hs.163026	ESTs	0.2921

413056	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	0.2922
443998	AI620661	Hs.296276	ESTs	0.2924
424412	H15512	Hs.10043	hypothetical protein FLJ13074	0.2925
421204	AW081587	Hs.155051	ESTs	0.2928
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	0.2938
440507	H06994		gb:yl81b07.r1 Soares infant brain 1NIB H	0.2943
445555	AW974013	Hs.260809	ESTs	0.2945
438570	AW888554	Hs.84298	CD74 antigen (invariant polypeptide of m	0.2948
447195	T73745	Hs.279870	ESTs, Weakly similar to A46010 X-linked	0.2950
423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (fr	0.2956
421920	BE551245	Hs.1438	gamma-aminobutyric acid (GABA) receptor,	0.2956
412177	Z23091	Hs.73734	glycoprotein V (platelet)	0.2959
428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	0.2959
433745	AF075320	Hs.28980	hypothetical protein FLJ14540	0.2969
417935	R53697	Hs.170044	ESTs	0.2970
420674	NM_000055	Hs.1327	butyrylcholinesterase	0.2973
413537	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	0.2973
445194	AI215667	Hs.175044	ESTs	0.2974
454135	AW135965	Hs.246783	ESTs	0.2976
403418				0.2986
457605	AV657778	Hs.3314	selenoprotein P, plasma, 1	0.2989
408896	AI610447	Hs.48778	niban protein	0.2993
448542	BE256176	Hs.278712	eukaryotic translation initiation factor	0.2994
417945	R29072		gb:F1-101D 22 week old human fetal liver	0.2994
412518	BE047637	Hs.173739	hypothetical protein FLJ10297	0.2996
424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.2997
430778	D90337	Hs.247916	natriuretic peptide precursor C	0.3000
451531	AA018311	Hs.114762	ESTs	0.3003
444926	AI202492	Hs.212933	ESTs, Weakly similar to CLD4_HUMAN CLAUD	0.3003
407366	AF026942		gb:Homo sapiens clg33 mRNA, partial sequ	0.3012
459456	AA486036	Hs.190124	ESTs	0.3012
417111	AW016321	Hs.82306	destrin (actin depolymerizing factor)	0.3012
452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	0.3012
451959	AA056203	Hs.27337	hypothetical protein FLJ20623	0.3012
410482	AW772187	Hs.191859	ESTs	0.3013
417700	M36542	Hs.1101	POU domain, class 2, transcription facto	0.3018
404414				0.3019
432247	AA531287	Hs.105805	ESTs	0.3023
453471	AL037887	Hs.208179	ESTs	0.3028
417481	AA203281	Hs.21798	ESTs	0.3029
432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	0.3032
448744	AL135424	Hs.9469	pleckstrin homology domain-containing, f	0.3033
429223	BE264152	Hs.221994	ESTs	0.3034
404501	AW247252	Hs.75514	nucleoside phosphorylase	0.3037
406829	AW419128	Hs.84298	CD74 antigen (invariant polypeptide of m	0.3039
438839	AW297945	Hs.128490	ESTs	0.3039
431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.3042
456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	0.3045
458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	0.3048
443294	AI733625	Hs.133053	ESTs	0.3050
447023	AA356764	Hs.17109	integral membrane protein 2A	0.3052
458583	AI479646	Hs.157081	hypothetical protein MGC4170	0.3056
414567	BE281057	Hs.184519	hypothetical protein FLJ12949	0.3057
445123	AI762911	Hs.145369	ESTs	0.3064
412682	AW983772		gb:RC3-HN0002-060400-012-h09 HN0002 Homo	0.3065
434361	AF129755	Hs.117772	ESTs	0.3071
414026	BE241713		gb:TCAAP1E0472 Pediatric acute myelogeno	0.3072
432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	0.3073
408350	AW183350	Hs.250127	ESTs	0.3074
401042				0.3077
422586	AA312704	Hs.59457	hypothetical protein FLJ22127	0.3077
438692	AB007950	Hs.6360	KIAA0481 gene product	0.3077
447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3869590, mRNA,	0.3083
444414	AW293214	Hs.8752	transmembrane protein 4	0.3085
422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	0.3088
430410	AF099144	Hs.250700	tryptase beta 1	0.3090
419299	AI311085	Hs.62406	hypothetical protein FLJ22573	0.3091
400672				0.3094
444010	AW976457	Hs.282887	ESTs	0.3096
451699	AL118571	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPO	0.3096
432471	BE244667	Hs.296155	CGI-100 protein	0.3105
405277				0.3106
456765	AI497900	Hs.33067	ESTs	0.3106
452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	0.3106
426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	0.3106
406592				0.3106
423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo	0.3107
417919	AI928203	Hs.86379	ESTs	0.3110
414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	0.3110
457439	AW410408	Hs.271167	L-pipecolic acid oxidase	0.3116
426449	AL134009	Hs.169936	Homo sapiens mRNA; cDNA DKFZp586N1918 (f	0.3116
419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.3119
458544	AI631036	Hs.196843	ESTs	0.3119

	447778	BE620592	Hs.71190	ESTs, Weakly similar to S16506 hypotheti	0.3121
	449097	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	0.3125
	429338	AW170591	Hs.13967	ESTs, Weakly similar to PSM_HUMAN PROSTA	0.3125
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	0.3125
5	446404	AA019961	Hs.26216	LOC50627	0.3130
	446616	R65964	Hs.241569	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.3132
	409404	BE220053	Hs.129056	ESTs	0.3135
	417318	AW953937	Hs.12891	ESTs	0.3139
	443980	AI459140	Hs.299087	ESTs	0.3140
10	459138	AI903291		gb:RC-BT029-080199-047 BT029 Homo sapien	0.3142
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.3143
	434704	AW135276	Hs.192311	ESTs	0.3143
	414214	D49958	Hs.75819	glycoprotein M6A	0.3145
	446378	AI905699	Hs.239760	citrate synthase	0.3145
15	459233	AI939966		gb:MR0-CT0015-160799-002-b06 CT0015 Homo	0.3146
	428193	NM_004235	Hs.7934	Kruppel-like factor 4 (gut)	0.3148
	426515	BE394222	Hs.231444	Homo sapiens, Similar to hypothetical pr	0.3150
	426597	AA382250	Hs.145601	ESTs	0.3153
	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	0.3157
20	405071				0.3160
	407457	AJ242724		gb:Homo sapiens mRNA for partial putativ	0.3162
	409922	AW505582	Hs.130732	KIAA1575 protein	0.3172
	438219	AI916151	Hs.257194	ESTs	0.3173
	412944	AA384110	Hs.197143	ESTs	0.3175
25	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.3178
	426662	AA879474	Hs.122710	ESTs	0.3178
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	0.3179
	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	0.3181
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	0.3183
30	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	0.3185
	448812	H30775	Hs.22140	BM88 antigen	0.3188
	411288	AW835511		gb:QV0-LT0015-180200-127-d02 LT0015 Homo	0.3189
	422884	AW860975	Hs.13256	ESTs	0.3190
	405535				0.3195
35	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	0.3195
	455353	W26786		gb:15d7 Human retina cDNA randomly prime	0.3195
	414540	BE379050	Hs.306969	Homo sapiens, clone MGC:10782, mRNA, com	0.3195
	428568	AC004755	Hs.184922	Homo sapiens chromosome 19, fosmid 37502	0.3195
	428106	BE620016	Hs.182470	PTD010 protein	0.3198
40	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	0.3202
	445682	AW378397		gb:RC3-HT0220-031299-012-g06 HT0220 Homo	0.3205
	437568	AI954795	Hs.156135	ESTs	0.3205
	448943	AI608810	Hs.193288	ESTs	0.3205
	431999	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	0.3207
45	419279	AA235900	Hs.87500	ESTs	0.3208
	405913				0.3209
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.3212
	424729	AF063012	Hs.152531	heart and neural crest derivatives expre	0.3212
	440020	AI480204	Hs.177131	ESTs	0.3213
50	429082	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	0.3215
	433663	AF083131	Hs.229535	CATX-15 protein	0.3215
	400641				0.3216
	406140				0.3216
	415280	R56473	Hs.268715	ESTs	0.3217
55	447635	AI669669	Hs.195362	ESTs	0.3217
	401867				0.3217
	400767				0.3221
	457713	H47495	Hs.13810	hypothetical protein MGC15504	0.3221
	448758	AB018311	Hs.21917	KIAA0768 protein	0.3222
60	444750	AW242684	Hs.243623	ESTs	0.3223
	411466	AW847669		gb:IL3-CT0213-280100-056-G10 CT0213 Homo	0.3226
	432749	NM_014438	Hs.278909	interleukin 1, eta	0.3231
	408112	AW451982	Hs.248613	ESTs	0.3231
	433234	AB040928	Hs.65366	KIAA1495 protein	0.3231
65	422831	R02504	Hs.332943	ESTs	0.3234
	403215				0.3236
	451868	R85962	Hs.221926	ESTs, Weakly similar to I38022 hypotheti	0.3236
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	0.3242
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	0.3254
70	445848	AA774824	Hs.13377	Homo sapiens clone 23649 and 23755 unkno	0.3257
	441143	AI027604	Hs.159650	ESTs	0.3257
	405138				0.3262
	412888	M86151		gb:EST02679 Hippocampus, Stratagene (cat	0.3262
	409662	AW452320	Hs.279726	ESTs	0.3262
75	425438	T62216	Hs.270840	ESTs	0.3263
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	0.3263
	423512	AW844694	Hs.306752	Homo sapiens cDNA: FLJ21391 fis, clone C	0.3264
	436777	AA731199	Hs.293130	ESTs	0.3267
	431651	BE250915	Hs.266914	hypothetical protein FLJ10355	0.3267
80	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	0.3268
	426048	AI768853	Hs.134478	ESTs	0.3269
	451096	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	0.3270
	426942	AA393551	Hs.97450	ESTs	0.3271

454947	AW846590		gb:QV0-CT0180-011099-025-d07 CT0180 Homo	0.3275
413814	BE169692		gb:PM1-HT0527-290200-006-a05 HT0527 Homo	0.3275
422818	AA404290	Hs.97848	ESTs	0.3277
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.3278
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	0.3278
452164	AI863171		gb:tz44b02.x1 NCI_CGAP_Bm52 Homo sapien	0.3279
458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated	0.3279
433197	AB040889	Hs.281022	KIAA1456 protein	0.3280
405701				0.3282
437782	AI370876	Hs.79090	exportin 1 (CRM1, yeast, homolog)	0.3284
459001	AI761313	Hs.204605	ESTs	0.3286
422783	AA598956	Hs.120439	ethanolamine kinase	0.3289
417036	AF039918	Hs.80975	ectonucleoside triphosphate diphospholyd	0.3290
456041	BE270795	Hs.268864	ESTs	0.3295
423310	AA325225	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	0.3296
427530	AA405093	Hs.126519	ESTs	0.3296
420172	AA601122	Hs.95655	secreted and transmembrane 1	0.3297
445610	AI831648	Hs.143993	ESTs	0.3297
411328	AW837063		gb:QV1-LT0037-150200-069-g08 LT0037 Homo	0.3300

Table 8B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT number	Accession
409921	1159516_1	AW600239 AW600255 AW505332
410626	1212621_-1	BE407727
410845	1223881_1	AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283
410950	1227728_1	AW811633 AW811652 AW811898
411288	1237709_1	AW835511 AW835517 AW835513
411319	1238595_1	BE537094 AW836542
411328	1238987_1	AW837063 AW935882 AW935957
411466	1246771_1	AW847669 AW847667 BE145799
411514	1248638_1	AW850178 AW850233 AW850445 AW850446
411620	1252014_1	AW854536 AW854417 AW854495 AW854355
411880	1263110_1	AW872477 BE088101 T05990
412474	129869_1	AI791451 AI791288 BE019234 BE296601 AA111939
412506	1301336_1	AW957159 H09937 T75143
412682	1321572_1	AW983772 AW983730 AW983769 AW983836 AW983835 AW983837
412888	1334784_1	M86151 BE061884 BE061883 BE061898 BE061882 BE061887 BE061891 BE061890 BE061896 BE061893 BE061895 BE061894 BE061885 BE007474 BE007481 BE007553
413056	1347545_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
413537	1375441_1	BE146866 BE146865 BE146867
413541	1375499_1	BE147036 BE146951 BE146958 BE146966 BE146976 BE146955
413814	1391574_1	BE169692 BE169421
414026	1411109_1	BE241713 BE241912
414193	1424706_-2	BE260069
414349	1437515_-1	BE512968
414484	1452830_-1	BE314385
414539	1460320_1	BE379046 BE395459
415154	1525577_1	D63175 D78984 D63269
415160	1525766_1	T82802 D78670 R08505
416035	1567254_1	H42314 H43080 H45217 H15384
417945	1711126_1	R29072 R29717 R29699 R29709 R29751 R29609 R29060 R29718 R29057 R29591 R29683 R29575 R28913 R28910
419850	188485_1	F06844 F06845 Z45488 AW748501 AW748591 AW752021 AW748545 AW853362 AW853363 AW853427 AA251253
422909	222858_1	AA533356 AW468427 R67736 AA779031 AA614088 AI823404 AA318991 AA720986
422954	223239_1	AW998605 AW993131 BE514709 AA319445
423621	230314_1	BE002904 H64880 AA328679
424648	241947_1	AA344576 AA732430 AA344601
426132	261431_1	AA370501 AW962784 AA370727
426497	268121_1	AA379913 AA379981 AW963523
430553	319868_1	AW392821 AW392809 AW843258 AW843049 AW603156 BE165656 AW821728
431822	338082_1	AA516049 AW004922
434098	360006_1	AA625499 AA625269 AA625184
437483	43756_1	AL390174 AW898817
440507	495677_1	H06994 BE147898
441042	50823_1	AA077736 AA078505 BE562497 Z17859
441083	50904_1	BE562611 AA436054
445682	647580_1	AW378397 AW378390 AW378358 AI247957
446294	670076_1	AI284935 AW409822 BE408182
446901	697809_1	AI347274 AW844024
447787	73719_1	BE620108 BE312062 AW896316 BE262546
451385	86787_1	AA017656 AA017374 AA019761
452164	902091_1	AI863171 BE047919
454186	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 BE141749 AW177598

454790	1234752_1	AW820852 AW820773 AW821088
454947	1245953_1	AW846590 AW846615 AW846584 AW846592 AW846621 AW846610
455353	1284269_1	W26786 AW998612 AW902272
457115	286601_1	AA420712 AA469165 AA420737
459138	918860_1	AI903291 AI903455 AI903367 AI903403 AI903447 AI903405 AI903364 AI903229 AI903240 AI903346
459233	944881_1	AI939966 AI939988 AI939951 AI939981 AI939976 AI939959

Table 8C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400641	8117693	Plus	4786-4992
400672	8118724	Minus	148067-148503
400767	8131627	Minus	80531-80629,82169-82278
400865	1945037	Minus	44482-45526
401024	8117489	Plus	60551-60802
401042	8117611	Plus	151364-151606
401371	9650602	Plus	80901-81283
401381	8570226	Minus	118629-119146,119392-119657
401465	6682292	Plus	25676-25800
401521	7705251	Plus	9127-9234
401753	9838183	Minus	155287-155529,159719-159997
401776	9966323	Plus	115535-115743,117746-117839,120290-120455
401887	7229981	Plus	93973-94120
401974	3126777	Plus	85330-85683
402076	8117410	Plus	128316-128627
402182	8575917	Minus	98298-98439
402425	9796347	Minus	50224-50395
402610	9926549	Minus	22955-23124
402695	8569871	Minus	159927-160055
403047	3540153	Minus	59793-59968
403215	7630945	Minus	177270-177971
403418	6862692	Minus	176202-176395
403548	8081591	Minus	38760-39352
403957	8076835	Minus	81649-81754
404070	2996642	Plus	7210-7414,10043-10195
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,83149-83387
404414	7382165	Plus	143127-143398
404605	9212566	Plus	125032-125291
404638	9796751	Minus	99433-99526,100035-100161
404696	9800109	Minus	60037-60144,62675-63081
404767	7882827	Minus	23244-23759
404769	8099713	Minus	175801-176823
404927	7342002	Plus	68690-69563
404958	7407941	Minus	2731-4531
405071	7708797	Minus	11115-11552
405073	7769921	Plus	31419-31774
405138	8576241	Plus	90303-90516
405277	3980473	Plus	23471-23572
405282	3810573	Minus	10482-10689
405334	3135285	Plus	139386-139856
405364	2281075	Minus	48325-48491,49136-49252
405385	6552772	Plus	48332-48454
405535	9795658	Plus	63384-63545
405610	5757553	Minus	71907-72080
405654	4895155	Minus	53624-53759
405691	4508112	Plus	171350-171739
405701	4263751	Plus	93243-93364
405880	6758747	Minus	55673-56267
405913	7712139	Minus	7484-7678
406140	9168231	Minus	49887-50219
406592	4567182	Plus	352560-352963

Table 9A lists about 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metatases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific

background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of tumor samples divided by the 70th percentile of normal body tissue samples, where the 15th percentile of normal body tissues was subtracted from the numerator and denominator

Pkey	ExAccn	UnigeneID	Unigene Title	R1
436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	29.34
406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	25.56
406667	M12523			20.28
414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	18.84
428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	17.38
416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	16.61
431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	16.42
437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	15.92
407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	15.64
423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	15.59
441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	14.54
422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	13.68
432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.23
421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	13.21
453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	12.35
436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.11
422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	11.99
418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, Li c	11.87
407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	11.61
424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	11.27
414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	10.82
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	10.73
450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.10
423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
421964	X73079	Hs.288579	NM_002544:Homo sapiens polymeric immunog	9.68
447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	9.44
421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	9.38
406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.34
427563	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (	9.18
422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.06
406667	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.02
409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	8.89
424667	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.53
422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32671	8.23
452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	8.10
430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	8.05
413881	L00190	Hs.75599	(locuslink)NM_000486:Homo sapiens serine	7.96
406399				7.73
422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	7.71
428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	7.43
417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	7.40
435536	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	7.29
430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.25
451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	7.19
452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	7.18
452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	7.03
424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	7.00
443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	6.92
452194	AI694413	Hs.373599	Hs.373599:EST	6.88
411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.59
422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	6.55
431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	6.49
422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	6.33
412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	6.31
451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I isof	6.30
428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.29
430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	6.28
422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	6.27
444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	6.26
409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	6.23

417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.23
413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	6.23
422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	6.17
446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	6.17
415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.17
414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.16
422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	6.14
423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	6.13
452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	6.09
447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	6.02
443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	5.95
403220				5.90
408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
449722	BE280074	Hs.23960	Hs.23960:cyclin B1	5.87
425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	5.79
414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	5.79
408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	5.77
423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.77
421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
431301	AA502384	Hs.151529	Hs.151529:ESTs	5.71
418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	5.71
415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	5.68
436972	AA284679	Hs.25640	Hs.25640:claudin 3	5.66
414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	5.61
431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	5.57
424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	5.55
413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.54
409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.50
426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	5.38
420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	5.33
414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	5.32
414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.32
410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	5.28
414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.28
444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.27
438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.26
408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	5.25
414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	5.25
436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	5.25
414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.23
428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	5.22
443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interme	5.20
432978	AF125743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.18
425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.13
432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	5.12
408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	5.11
430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	5.08
426174	AA547959	Hs.115838	Hs.115838:ESTs	5.07
403218				5.07
411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.00
449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.98
433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	4.96
431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	4.91
430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.91
422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.90
422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	4.86
426953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	4.83
425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	4.81
428289	M26301	Hs.2253	Hs.2253:complement component 2	4.79
418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	4.78
409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.77
447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	4.72
429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	4.72
430680	AW136724	Hs.168974	Hs.168974:ESTs	4.69
414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.69
417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.67
403221				4.65
415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	4.65
433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	4.64
414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	4.64
406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.64
418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	4.60
422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.60
410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.60
411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.59
431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.57
428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.56

425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	4.56
422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	4.55
445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.55
422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	4.55
422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	4.54
431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.53
429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.53
432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	4.53
408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.49
420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	4.48
432378	AI493046	Hs.146133	Hs.146133:ESTs	4.48
431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	4.47
415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.47
437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.47
422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	4.46
436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.46
445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
426024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.44
415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.43
441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	4.43
426479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	4.40
407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	4.38
414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.37
447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	4.36
410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.36
439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.35
409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	4.33
432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	4.33
427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	4.33
439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.32
418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.32
428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.30
424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.30
429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.30
411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	4.30
413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.29
422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	4.28
425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	4.28
441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.27
439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.27
414361	AI086138	Hs.204044	Hs.204044:ESTs	4.26
417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.26
415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	4.24
409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.22
420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	4.19
421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.18
407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.18
418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.18
409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	4.18
419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	4.17
426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.17
408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.16
425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.15
453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.15
435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3-)-glycoprote	4.14
403219				4.14
407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.14
411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.14
424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (	4.12
439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.12
425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	4.12
413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (	4.11
428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	4.10
427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	4.09
441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.07
417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.07
442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.06
425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.05
412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (	4.04
425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	4.03
411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.03
452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.03
452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.02
450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.01
456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.01
412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.01
426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.01

	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.99
	403739				3.99
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.98
	405484				3.98
5	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.98
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.97
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.97
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.97
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.96
10	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.96
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.96
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.95
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	3.95
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.93
15	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.93
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	3.93
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	3.92
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.92
	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.91
20	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.90
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.89
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	3.89
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	3.88
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.88
25	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.88
	409453	AI885516	Hs.95612	Hs.95612:ESTs	3.87
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.86
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	3.86
	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	3.85
30	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	3.85
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	3.84
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	3.84
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.84
	422616	BE300330	Hs.116725	NM_012246:Homo sapiens selenophosphate s	3.83
35	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.83
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.83
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (	3.82
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	3.82
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	3.81
40	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	3.81
	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	3.81
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.80
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.79
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	3.79
45	405556				3.79
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.79
	400529				3.79
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.78
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	3.78
50	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	3.77
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	3.77
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.77
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	3.76
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.76
55	431350	AI192528	Hs.164537	Hs.164537:ESTs	3.76
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.75
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	3.75
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	3.74
	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.74
60	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.72
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.72
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.72
65	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.71
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	3.71
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	3.71
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.70
70	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.70
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.70
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.69
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.69
	437016	AU076916	Hs.5398	Hs.5398:guanine monphosphate synthetase	3.69
75	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	3.69
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	3.69
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.68
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.68
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	3.67
80	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	3.67
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	3.67
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	3.67
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	3.67

	452679	Z42387	Hs.83883	(locuslink)NM_020162:Homo sapiens transm	3.66
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	3.66
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.66
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	3.66
5	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.66
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.65
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.64
	404826				3.63
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	3.63
10	409964	AW368226	Hs.67928	Hs.67928:ESTs	3.63
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.63
	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	3.61
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding prot	3.60
15	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.59
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	3.59
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	3.59
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.59
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.58
20	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	3.58
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	3.58
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.57
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosp	3.57
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	3.57
25	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.56
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.55
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 ope	3.55
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	3.55
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.55
30	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.55
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.55
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	3.55
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.54
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.54
35	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	3.54
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	3.54
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.53
	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	3.53
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	3.53
40	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.53
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.53
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	3.52
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.52
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.51
45	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.51
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	3.51
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.51
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.51
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	3.51
50	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	3.51
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	3.51
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidas	3.51
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.51
	419693	AA133749	Hs.301350	Hs.301350:FXYD domain-containing ion tra	3.51
55	407971	AI469117	Hs.62918	Hs.62918:CDC91 cell division cycle 91-li	3.50
	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antige	3.50
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.50
	436014	AF281134	Hs.283741	NM_020156:Homo sapiens exosome component	3.50
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	3.50
60	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.50
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	3.50
	424909	S76187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	3.49
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	3.49
65	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	3.48
	407137	T97307			3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.48
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.47
70	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.47
	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.46
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.46
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.45
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.45
75	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.44
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.44
	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	3.44
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.44
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.43
80	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.43
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	3.43
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens mel transforming	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43

414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.43
400750				3.42
413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	3.41
425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	3.40
453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.40
428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.39
410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.39
428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	3.39
450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.39
413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.38
440676	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.38
400847				3.37
431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	3.37
410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	3.37
432633	AI796390	Hs.210667	Hs.210667:ESTs	3.36
429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (	3.36
424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.36
456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	3.35
418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.35
453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.35
400448				3.35
424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.35
430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.35
416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.35
429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.35
412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.34
451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.34
425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.34
446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.34
431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.34
448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.34
414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.34
421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	3.34
419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.33
435975	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.33
418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.33
433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.33
441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.33
432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.33
444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
432660	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	3.32
410219	T98226	Hs.171952	Hs.171952:occludin	3.32
410663	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.32
402829				3.32
445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.32
414198	AW505308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	3.32
443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.31
410268	AA316181	Hs.61635	NM_012449:Homo sapiens six transmembrane	3.30
425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.30
420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.30
421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	3.30
432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.30
409402	AF208234	Hs.695	Hs.695:cystatin B (stefin B)	3.30
421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.29
424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.29
448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.29
442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.29
459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.28
400846				3.28
422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.28
408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.28
432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.27
435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.27
456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.27
447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	3.27
414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.27
422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	3.26
437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	3.26
431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.26
457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.26
432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.25
417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.25
440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-ral simian leuk	3.25
401179				3.25
411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.25
453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.25
407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.25
447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.25
452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.24
428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.24
425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.24

446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.24
419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.24
426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.23
418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.23
444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.23
444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.23
424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.23
438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-li	3.23
409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multid	3.23
418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.23
419705	AW368634	Hs.154331	Hs.154331:ESTs	3.22
420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.22
413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	3.22
448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.22
425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.21
435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.21
451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.21
420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.21
412006	AW451618	Hs.290216	Hs.290216:ESTs	3.21
424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.21
437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.21
414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.20
400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.20
434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.20
452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.20
413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.19
437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.19
408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.19
433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfeit 4 (SURF4)	3.19
430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.19
417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.18
434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.18
428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	3.18
445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.18
420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.18
417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.18
412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.18
452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.18
433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.18
414883	AA926960	Hs.348669	Hs.348669:CDC28 protein kinase 1	3.18
421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.18
447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.17
424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-l	3.17
442315	AA173992	Hs.7956	Hs.7956:ESTs	3.17
449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.17
425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
428484	AF104032	Hs.184601	(locuslink)NM_003486:Homo sapiens solute	3.16
418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.16
436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.15
447151	AI022813	Hs.92679	(locuslink)NM_145754:Homo sapiens kinesi	3.15
418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.15
410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.15
423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.15
435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.15
458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (	3.14
420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.14
428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.14
450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXYD d	3.14
413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.13
407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.13
426841	AI052358	Hs.131741	Hs.131741:ESTs	3.13
418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.12
420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.12
438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.12
412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.12
428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.11
421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.11
400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.11
418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.11
449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.11
421532	AW136207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.11
432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.11
433179	AW362945	Hs.162459	Hs.162459:ESTs	3.11
452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.11
418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.10
421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.10
427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.10
457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.10

	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.10
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neutr	3.10
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
5	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.10
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.09
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.09
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.08
	404240				3.08
10	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	3.08
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.08
	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.08
	402260				3.08
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.08
15	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.08
	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.07
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.07
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.07
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.07
20	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.07
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.07
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.07
25	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.07
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.06
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.06
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.06
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.06
30	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.06
	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.06
	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.06
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.06
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.06
35	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.05
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.05
	408806	AW847814	Hs.75608	Hs.75608:tight junction protein 2 (zona	3.05
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.05
	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.05
40	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.05
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.05
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.05
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.05
	406363				3.05
45	439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannose-P-dolicho	3.05
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-li	3.04
	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	3.04
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.04
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.04
50	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.04
	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.04
	446620	AA128608	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.04
	452865	AI924046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	3.04
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.04
55	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.04
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.03
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.03
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.03
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.03
60	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	3.03
	440659	AF134160	Hs.7327	NM_021101:Homo sapiens claudin 1 (CLDN1)	3.03
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.03
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.02
65	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.02
	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.02
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.02
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.02
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.02
70	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.02
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.02
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.01
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.01
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.01
75	410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.01
	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.01
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.00
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.00
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.00
80	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.00
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.00
	419452	U33635	Hs.90572	Hs.90572:PTK7 protein tyrosine kinase 7	3.00
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.00

	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.00
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.00
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.00
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	2.99
5	437763	AA469369	Hs.5831	Hs.5831:tissue inhibitor of metalloprote	2.99
	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, ribo	2.99
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.99
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	2.98
	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	2.98
10	432396	AW295956	Hs.11900	(locuslink)NM_032527:Homo sapiens hypoth	2.98
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	2.98
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	2.98
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.98
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	2.98
15	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	2.98
	452124	AA454220	Hs.61170	Hs.61170:ESTs	2.98
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	2.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	2.97
	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	2.97
20	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	2.97
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	2.97
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.97
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	2.97
	430354	AA954810	Hs.239784	Hs.239784:scribble	2.97
25	417079	U65590	Hs.81134	(locuslink)NM_000577:Homo sapiens interl	2.97
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.97
	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostasin)	2.97
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	2.96
	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinesi	2.96
30	412429	AV650262	Hs.75765	NM_002089:Homo sapiens GRO2 oncogene (GR	2.96
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	2.96
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	2.96
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.96
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.96
35	428781	AF164799	Hs.193384	Hs.193384:putatative 28 kDa protein	2.96
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	2.96
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	2.96
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	2.95
	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	2.95
40	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.95
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	2.95
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alph	2.95
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	2.95
	443883	AA114212,	Hs.9930	Hs.9930:serine (or cysteine) proteinase	2.95
45	445720	AL040482	Hs.286173	Hs.286173:KIAA1595 protein	2.95
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	2.95
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	2.94
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.94
	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	2.94
50	444824	AA843575	Hs.12056	NM_001671:Homo sapiens asialoglycoprotei	2.94
	431629	AU077025	Hs.265827	NM_022873:Homo sapiens interferon, alpha	2.94
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	2.94
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.93
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.93
55	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	2.93
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	2.93
	412088	AI689496	Hs.108932	Hs.108932:ESTs	2.93
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.92
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	2.92
60	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.92
	417944	AU077196	Hs.82985	NM_000393:Homo sapiens collagen, type V,	2.92
	428343	AL043021	Hs.12705	(locuslink)NM_145294:Homo sapiens simila	2.92
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	2.92
	451608	AA384525	Hs.26745	NM_016499:Homo sapiens HSPC244 (MGC:1337	2.92
65	434608	AA805443	Hs.179909	NM_024831:Homo sapiens nuclear receptor	2.92
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	2.91
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	2.91
	438549	BE386801	Hs.21858	Hs.21858:serine (or cysteine) proteinase	2.91
	440246	W52010	Hs.191379	Hs.191379:ESTs	2.91
70	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	2.91
	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	2.91
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	2.91
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	2.91
	450167	AA446404	Hs.24563	NM_013248:Homo sapiens NTF2-like export	2.91
75	408815	AW957974	Hs.25485	(locuslink)NM_024599:Homo sapiens hypoth	2.91
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	2.91
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	2.91
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	2.91
	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	2.90
80	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	2.90
	405203				2.90
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	2.90
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	2.90

	455967	L12535	Hs.75551	(locuslink)NM_012425:Homo sapiens Ras su	2.90
	402104				2.90
	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	2.90
	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cytoso	2.90
5	456157	AW979153	Hs.336881	Hs.336881:ESTs	2.90
	429505	AW820035	Hs.278679	NM_033274:Homo sapiens a disintegrin and	2.89
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	2.89
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	2.89
	438543	AA810141	Hs.192182	Hs.192182:ESTs	2.89
10	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythrob	2.89
	441455	AJ271671	Hs.7854	NM_014437:Homo sapiens solute carrier fa	2.89
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	2.89
	415674	BE394784	Hs.78596	NM_002797:Homo sapiens proteasome (proso	2.89
	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.89
15	418062	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (	2.89
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	2.89
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	2.89
	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yamaguchi sarcoma viral	2.89
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	2.88
20	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	2.88
	411030	BE387193	Hs.67896	(locuslink)NM_007346:Homo sapiens opioid	2.88
	413822	R08950	Hs.272044	Hs.272044:ESTs, Weakly similar to hypoth	2.88
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	2.88
	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	2.88
25	440490	AW513684	Hs.7218	Hs.7218:acetyl-Coenzyme A synthetase 2 (	2.87
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	2.87
	423570	AW838306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	2.87
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	2.87
	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	2.87
30	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	2.87
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	2.87
	421178	BE267994	Hs.102419	Hs.102419:zinc finger protein	2.87
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	2.87
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	2.87
35	453145	R63438	Hs.183454	Hs.183454:Homo sapiens cDNA FLJ14883 fis	2.86
	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	2.86
	424732	D80001	Hs.152629	Hs.152629:KIAA0179 protein	2.86
	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	2.86
	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	2.86
40	407082	Z47055			2.86
	450038	AA005159	Hs.188489	Hs.188489:ESTs	2.86
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.85
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rh-related antige	2.85
	417824	AA084798	Hs.82646	NM_006145:Homo sapiens DnaJ (Hsp40) homo	2.85
45	426989	AI815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (	2.85
	434916	AF161383	Hs.284207	Hs.284207:hypothetical protein BC003515	2.85
	412664	AA421404	Hs.346868	NM_006824:Homo sapiens EBNA1 binding pro	2.85
	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	2.85
	409504	AA304961	Hs.699	Hs.699:peptidylprolyl isomerase B (cyclo	2.84
50	439920	H05430	Hs.288433	NM_016522:Homo sapiens neurotrimin (HNT)	2.84
	418462	BE001596	Hs.85266	Hs.85266:Integrin, beta 4	2.84
	442199	BE277633	Hs.372542	NM_004879:Homo sapiens etoposide-induced	2.84
	406710	AI708347	Hs.184014	Hs.184014:ribosomal protein L31	2.84
	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	2.84
55	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3-)-glycopro	2.84
	448730	AB032983	Hs.21894	Hs.21894:KIAA1157 protein	2.84
	433027	AF191018	Hs.279923	(locuslink)NM_014366:Homo sapiens putati	2.84
	449090	AK001735	Hs.22983	NM_020121:Homo sapiens UDP-glucose ceram	2.84
	439737	AI751438	Hs.41271	Hs.41271:Homo sapiens mRNA full length i	2.84
60	403912				2.84
	423225	AA852604	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.84
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	2.84
	429211	AF052693	Hs.198249	NM_005268:Homo sapiens gap junction prot	2.84
	452518	AA280722	Hs.24758	Hs.24758:Homo sapiens cDNA FLJ32068 fis,	2.84
65	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	2.83
	448489	AI523875		R45782:Ha616-f Adult heart, Clontech Hom	2.83
	426194	T50872	Hs.2001	NM_001061:Homo sapiens thromboxane A syn	2.83
	422129	AU076635	Hs.1478	NM_000185:Homo sapiens serine (or cystei	2.83
	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	2.83
70	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	2.83
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	2.83
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	2.83
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	2.83
	439720	AI935202	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.83
75	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.83
	425907	AA365752	Hs.155965	Hs.155965:ESTs	2.83
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	2.82
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	2.82
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.82
80	415697	AI365603	Hs.279696	Hs.279696:DKFZP566I1024 protein	2.82
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	2.82
	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.82
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	2.82

	427022	AW245839	Hs.173255	NM_004596:Homo sapiens small nuclear rib	2.82
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	2.82
	400845				2.81
	419501	AW843822	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.81
5	418140	BE613836	Hs.83551	(locuslink)NM_002403:Homo sapiens microf	2.81
	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	2.81
	419768	T72104	Hs.93194	Hs.93194:apolipoprotein A-I	2.81
	436673	AF201931	Hs.5268	Hs.5268:zinc finger, DHHC domain contain	2.81
	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	2.81
10	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	2.81
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	2.81
	433061	AW068033	Hs.296422	(locuslink)NM_025233:Homo sapiens nucleo	2.81
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.81
	407338	AA773213	Hs.91202	Hs.91202:Homo sapiens cDNA FLJ25946 fis,	2.81
15	410240	AL157424	Hs.61289	Hs.61289:synaptojanin 2	2.80
	423880	BE278111	Hs.134200	Hs.134200:DKFZP564C186 protein	2.80
	422098	H03117	Hs.111497	Hs.111497:neuronal protein 17.3	2.80
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	2.80
	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	2.80
20	456602	AA411607	Hs.118964	NM_017660:Homo sapiens hypothetical prot	2.80
	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	2.80
	426437	BE076537	Hs.169895	Hs.169895:ubiquitin-conjugating enzyme E	2.79
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	2.79
	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	2.79
25	409531	BE384319	Hs.54702	(locuslink)NM_007255:Homo sapiens xylosy	2.79
	448988	Y09763	Hs.22785	NM_021987:Homo sapiens gamma-aminobutyri	2.79
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	2.79
	419846	NM_015977	Hs.285681	NM_032951:Homo sapiens Williams Beuren s	2.79
	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	2.79
30	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	2.79
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	2.79
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	2.79
	407844	AW073716	Hs.8037	(locuslink)NM_005723:Homo sapiens tetras	2.79
	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	2.79
35	419235	AW470411	Hs.288433	NM_016522:Homo sapiens neurotrimin (HNT)	2.78
	407754	AA527348	Hs.288967	Hs.288967:Homo sapiens, similar to RIKEN	2.78
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	2.78
	414181	AK000476	Hs.75798	NM_016470:Homo sapiens chromosome 20 ope	2.78
	418869	AW516565		AA229762:nc49f01.r1 NCI_CGAP_Pr3 Homo sa	2.78
40	419444	NM_002496	Hs.90443	NM_002496:Homo sapiens NADH dehydrogenas	2.78
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	2.78
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.78
	423013	AW875443	Hs.22209	Hs.22209:secreted modular calcium-bindin	2.78
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.78
45	447402	H54520	Hs.351327	(locuslink)NM_017828:Homo sapiens hypoth	2.78
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	2.78
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	2.78
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	2.78
	419757	AA773820	Hs.63970	Hs.63970:ESTs	2.77
50	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	2.77
	408044	BE206939	Hs.42287	NM_001952:Homo sapiens E2F transcription	2.77
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	2.77
	451690	AW451469	Hs.209990	Hs.209990:ESTs	2.77
	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	2.77
55	444207	AI565004	Hs.374415	Hs.374415:ESTs	2.77
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cDNA: FLJ21909 fis	2.77
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	2.77
	425978	BE253927	Hs.24983	Hs.24983:hypothetical protein from EUROI	2.77
	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	2.77
60	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	2.77
	450701	H39960	Hs.288467	Hs.288467:Homo sapiens cDNA FLJ12280 fis	2.77
	412890	T85247	Hs.351875	NM_004374:Homo sapiens cytochrome c oxid	2.77
	415752	BE314524	Hs.78776	NM_012342:Homo sapiens putative transmem	2.76
	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	2.76
65	450770	AA019924	Hs.28803	Hs.28803:ESTs	2.76
	419594	AA013051	Hs.91417	(locuslink)NM_007027:Homo sapiens topois	2.76
	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 l	2.76
	417767	BE242241	Hs.82542	NM_001637:Homo sapiens acyloxyacyl hydro	2.76
	439968	AA224760	Hs.153	NM_000971:Homo sapiens ribosomal protein	2.76
70	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	2.75
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.75
	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	2.75
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.75
	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	2.75
75	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	2.75
	435025	T08990	Hs.4742	Hs.4742:GPAA1P anchor attachment protein	2.75
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.75
	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	2.75
	408196	AL034548	Hs.43627	NM_006943:Homo sapiens SRY (sex determin	2.75
80	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	2.75
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.75
	451356	AA748418	Hs.33368	Hs.33368:hypothetical protein FLJ11175	2.75
	421643	BE281170	Hs.106357	NM_007126:Homo sapiens velosin-containin	2.74

	423527	AI206965	Hs.105861	(locuslink)NM_024712:Homo sapiens engulf	2.74
	428000	R35145	Hs.291904	Hs.291904:accessory protein BAP31	2.74
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	2.74
	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	2.74
5	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	2.74
	440457	BE387593	Hs.21321	(locuslink)NM_145808:Homo sapiens granul	2.74
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.74
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	2.73
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	2.73
10	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	2.73
	421921	H83363	Hs.355993	NM_012456:Homo sapiens translocase of in	2.73
	403217				2.73
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	2.73
	418733	AA227714	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.73
15	400275		Hs.4888	NM_006513:Homo sapiens seryl-tRNA synthe	2.73
	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cDNA FLJ14761 fis	2.73
	411872	AW327356	Hs.90918	Hs.90918:chromosome 11 open reading fram	2.73
	403483				2.73
	438119	AW963217	Hs.203961	Hs.203961:ESTs, Weakly similar to hypoth	2.73
20	422009	AI742845	Hs.110713	NM_003472:Homo sapiens DEK oncogene (DNA	2.73
	436995	AI160015	Hs.125489	Hs.125489:KIAA1961 protein	2.73
	400509				2.73
	429305	AF095727	Hs.287832	Hs.287832:myelin protein zero-like 1	2.73
	445899	AI263736	Hs.145626	Hs.145626:Homo sapiens, Similar to hypot	2.72
25	453557	AA522464	Hs.285996	NM_024956:Homo sapiens hypothetical prot	2.72
	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.72
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	2.72
	437809	AL137723	Hs.5855	Hs.5855:Homo sapiens mRNA; cDNA DKFZp434	2.72
	428466	AF151063	Hs.184456	NM_016486:Homo sapiens hypothetical prot	2.71
30	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	2.71
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	2.71
	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.71
	427782	AI956052	Hs.115960	NM_024036:Homo sapiens hypothetical prot	2.71
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.71
35	400277		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.71
	426263	AI908774	Hs.259785	Hs.259785:carnitine palmitoyltransferase	2.71
	445515	BE388665	Hs.179999	Hs.179999:Homo sapiens, clone IMAGE:3457	2.71
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.71
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	2.71
40	420511	AF052692	Hs.98485	NM_024009:Homo sapiens gap junction prot	2.71
	424965	AW956282	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.71
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	2.71
	412973	L37368	Hs.75104	Hs.75104:RNA binding protein S1, serine-	2.70
	410113	AW996564	Hs.250824	Hs.250824:Homo sapiens cDNA: FLJ23435 fi	2.70
45	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.70
	447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	2.70
	450493	M93718	Hs.166373	Hs.166373:nitric oxide synthase 3 (endot	2.70
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.70
	450747	AI064821	Hs.129953	Hs.129953:Ewing sarcoma breakpoint regio	2.70
50	436042	AF284422	Hs.119178	(locuslink)NM_020246:Homo sapiens cation	2.70
	432981	NM_002733	Hs.3136	Hs.3136:protein kinase, AMP-activated, g	2.70
	431341	AA307211	Hs.251531	NM_002789:Homo sapiens proteasome (proso	2.70
	408204	AA454501	Hs.43666	NM_007079:Homo sapiens protein tyrosine	2.70
	416770	AW163570	Hs.79768	NM_014740:Homo sapiens KIAA0111 gene pro	2.70
55	447507	H59696	Hs.18747	NM_005837:Homo sapiens POP7 (processing	2.70
	424500	AF040704	Hs.149443	(locuslink)NM_007022:Homo sapiens putati	2.69
	414237	BE536554	Hs.278270	Hs.278270:unactive progesterone receptor	2.69
	400231		Hs.169476	NM_002046:Homo sapiens glyceraldehyde-3-	2.69
	431209	NM_001533	Hs.2730	Hs.2730:heterogeneous nuclear ribonucleo	2.69
60	444118	AA458542	Hs.10326	NM_007263:Homo sapiens coatomer protein	2.69
	424608	X80695	Hs.151134	Hs.151134:oxidase (cytochrome c) assembl	2.69
	418546	AA224827		AA224827:nc32g04.s1 NCI_CGAP_Pr2 Homo sa	2.69
	440002	AW769844	Hs.111222	Hs.111222:hypothetical protein FLJ22875	2.69
	449957	D31365	Hs.24220	(locuslink)NM_016479:Homo sapiens scotin	2.69
65	432920	U37689	Hs.3128	NM_006232:Homo sapiens polymerase (RNA)	2.69
	450306	AL080080	Hs.24766	NM_030755:Homo sapiens thioredoxin domai	2.69
	429544	BE299343	Hs.2430	NM_005997:Homo sapiens transcription fac	2.68
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	2.68
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	2.68
70	453905	NM_002314	Hs.36566	NM_016735:Homo sapiens LIM domain kinase	2.68
	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	2.68
	420957	X98743	Hs.100555	Hs.100555:DEAD/H (Asp-Glu-Ala-Asp/His) b	2.68
	418187	NM_004604	Hs.83734	NM_004604:Homo sapiens syntaxin 4A (plac	2.68
	409533	AW969543	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.68
75	433184	AA147979	Hs.285005	NM_020243:Homo sapiens translocase of ou	2.68
	455303	AW892049		BE066891:PM3-BT0338-211299-002-e12 BT033	2.68
	452600	AI910842	Hs.103381	Hs.103381:ESTs, Weakly similar to hypoth	2.68
	415410	AF037332	Hs.278569	NM_014748:Homo sapiens KIAA0064 gene pro	2.67
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxonase 2 (PO	2.67
80	435049	AL122067	Hs.4746	NM_021941:Homo sapiens hypothetical prot	2.67
	450528	NM_014072	Hs.25063	NM_031268:Homo sapiens PRO0461 protein (	2.67
	433339	AF019226	Hs.8036	NM_004283:Homo sapiens RAB3D, member RAS	2.67
	408783	AF192522	Hs.47701	NM_013389:Homo sapiens NPC1 (Niemann-Pic	2.67

451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	2.67
427716	L38951	Hs.180446	Hs.180446:karyopherin (importin) beta 1	2.67
436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	2.67
415116	AA160363	Hs.269956	Hs.269956:ESTs	2.67
425838	NM_014071	Hs.159613	NM_014071:Homo sapiens nuclear receptor	2.66
418706	U73524	Hs.87465	NM_006831:Homo sapiens ATP/GTP-binding p	2.66
410165	BE560228	Hs.71869	NM_013258:Homo sapiens apoptosis-associa	2.66
410134	U68140	Hs.58927	(locuslink)NM_002533:Homo sapiens nuclea	2.66
430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	2.66
425910	AA830797	Hs.184760	NM_005760:Homo sapiens CCAAT-box-binding	2.66
427954	J03060	Hs.247551	NM_002455:Homo sapiens metaxin 1 (MTX1),	2.66
439971	W32474	Hs.301746	Hs.301746:Homo sapiens cDNA FLJ37267 fis	2.66
438449	AK001333	Hs.6216	Hs.6216:DnaJ (Hsp40) homolog, subfamily	2.66
435906	AI686379	Hs.110796	(locuslink)NM_020150:Homo sapiens SAR1 p	2.66
433387	L76528	Hs.3260	NM_000021:Homo sapiens presenilin 1 (Alz	2.66
447191	NM_014521	Hs.17667	(locuslink)NM_014521:Homo sapiens SH3-do	2.66
444099	D87432	Hs.10315	NM_003983:Homo sapiens solute carrier fa	2.66
417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	2.66
418529	AW005695	Hs.250897	Hs.250897:TRK-fused gene	2.65
426025	AW138330	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.65
420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	2.65
408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	2.65
444395	N66148	Hs.11125	(locuslink)NM_014041:Homo sapiens signal	2.65
431222	X56777	Hs.273790	NM_007155:Homo sapiens zona pellucida gl	2.65
406790	AA293303	Hs.356342	Hs.356342:ESTs, Highly similar to 211320	2.65
440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	2.65
416526	H61082	Hs.14743	Hs.14743:ESTs	2.65
413995	BE048146	Hs.75671	NM_004603:Homo sapiens syntaxin 1A (brai	2.65
424908	AW513963	Hs.39143	Hs.39143:hypothetical protein MGC13125	2.65
442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.65
452882	AW972990	Hs.196270	NM_030780:Homo sapiens folate transporte	2.65
406862	AW150807	Hs.356262	Hs.356262:ESTs, Highly similar to A31233	2.64
451295	AI557212	Hs.17132	Hs.17132:ESTs	2.64
448428	AF282874	Hs.21201	NM_015480:Homo sapiens nectin 3 (DKFZP56	2.64
426611	BE178050	Hs.171271	NM_001904:Homo sapiens catenin (cadherin	2.64
426216	N77630	Hs.13895	Hs.13895:Homo sapiens cDNA FLJ11654 fis,	2.64
407223	H96850		H96850:yw03b12.s1 Soares melanocyte 2NbH	2.64
427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	2.64
420157	AA857991	Hs.123106	Hs.123106:ESTs	2.64
428471	X57348	Hs.184510	Hs.184510:stratifin	2.64
451544	AK000429	Hs.26570	NM_017814:Homo sapiens hypothetical prot	2.64
413245	BE244334	Hs.75249	Hs.75249:ADP-ribosylation factor-like 6	2.64
415020	BE249915	Hs.293533	Hs.293533:Homo sapiens cDNA FLJ37093 fis	2.64
437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.64
418684	U82987	Hs.87246	NM_014417:Homo sapiens BCL2 binding comp	2.64
410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	2.64
436183	AI146327	Hs.334802	(locuslink)NM_024718:Homo sapiens hypoth	2.64
441226	BE563042	Hs.118820	Hs.118820:hypothetical protein BC007882	2.64
432788	AA521091	Hs.178499	Hs.178499:HSPC063 protein	2.64
432746	AA564512	Hs.372775	Hs.372775:Homo sapiens, clone IMAGE:3946	2.64
450377	AB033091	Hs.355925	Hs.355925:KIAA1265 protein	2.64
434633	AI189587	Hs.120915	Hs.120915:ESTs	2.64
424707	BE061914	Hs.10844	Hs.10844:leucine-rich alpha-2-glycoprote	2.64
427600	AW630918	Hs.179774	Hs.179774:proteasome (prosome, macropain	2.63
446522	NM_003876	Hs.15196	NM_003876:Homo sapiens putative receptor	2.63
436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	2.63
410701	AF198620	Hs.10283	NM_005105:Homo sapiens RNA binding motif	2.63
410182	NM_001983	Hs.59544	NM_001983:Homo sapiens excision repair c	2.63
406716	AW148546	Hs.169476	Hs.169476:glyceraldehyde-3-phosphate deh	2.63
430308	BE540865	Hs.238990	NM_004064:Homo sapiens cyclin-dependent	2.63
431074	BE072772	Hs.8997	Hs.8997:Sad1 unc-84 domain protein 1	2.63
412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	2.63
440524	R71264	Hs.16798	Hs.16798:Homo sapiens mRNA; cDNA DKFZp56	2.63
435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	2.63
422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	2.63
447528	AI612027	Hs.76277	NM_138393:Homo sapiens hypothetical prot	2.63
406774	AW518383	Hs.177592	Hs.177592:ribosomal protein, large, P1	2.63
439755	AW748482	Hs.77873	Hs.77873:B7 homolog 3	2.63
435311	W86610	Hs.185736	Hs.185736:ESTs	2.63
428699	AW578252	Hs.190161	Hs.190161:LR8 protein	2.62
410678	BE540516	Hs.378825	Hs.378825:Homo sapiens cDNA FLJ37850 fis	2.62
414839	X63692	Hs.77462	(locuslink)NM_001379:Homo sapiens DNA (c	2.62
443217	NM_001545	Hs.9078	Hs.9078:immature colon carcinoma transcr	2.62
448749	AW859679	Hs.21902	Hs.21902:Homo sapiens clone 25237 mRNA s	2.62
450009	AI399947	Hs.166486	Hs.166486:Homo sapiens cDNA FLJ11432 fis	2.62
407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	2.62
442232	AI357813	Hs.337460	Hs.337460:ESTs, Highly similar to HYEP_H	2.62
419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.62
416114	AI695549	Hs.183868	Hs.183868:glucuronidase, beta	2.62
439437	AI207788	Hs.343628	Hs.343628:sialyltransferase 4B (beta-gal	2.61
408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	2.61
443142	AI696513	Hs.108705	Hs.108705:protein phosphatase 2 (formerl	2.61
426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.61

	419667	AU077005	Hs.92208	NM_003815:Homo sapiens a disintegrin and	2.61
	415072	BE253687	Hs.77876	Hs.77876:hypothetical gene MGC19595	2.61
	406670	W79632	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.61
	403399				2.61
5	419579	W49529	Hs.296200	NM_023948:Homo sapiens hypothetical prot	2.61
	437202	AA326110	Hs.374481	Hs.374481:ESTs, Weakly similar to T34549	2.61
	414020	NM_002984	Hs.75703	NM_002984:Homo sapiens small inducible c	2.61
	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.61
	446488	AB037782	Hs.15119	Hs.15119:KIAA1361 protein	2.61
10	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	2.60
	448204	AI475124	Hs.170561	Hs.170561:ESTs	2.60
	449175	AJ005892	Hs.23170	(locuslink)NM_012280:Homo sapiens FtsJ h	2.60
	411201	T74588	Hs.8509	Hs.8509:ESTs, Weakly similar to C3HU com	2.60
	424805	AF230904	Hs.153260	NM_031892:Homo sapiens SH3-domain kinase	2.60
15	425421	L11669	Hs.157145	Hs.157145:tetracycline transporter-like	2.60
	422739	H20106	Hs.119591	(locuslink)NM_004069:Homo sapiens adapto	2.60
	450858	C18458	Hs.25597	Hs.25597:elongation of very long chain f	2.59
	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cDNA FLJ14201 fis	2.59
	430504	H52761	Hs.44095	Hs.44095:cyclin M3	2.59
20	439578	AW263124	Hs.350547	NM_024665:Homo sapiens nuclear receptor	2.59
	416041	AA345547	Hs.53263	(locuslink)NM_024647:Homo sapiens nucleo	2.59
	451920	AA224483	Hs.27239	Hs.27239:zinc finger, DHHC domain contai	2.59
	414163	BE262310	Hs.75782	NM_001521:Homo sapiens general transcrip	2.59
	422140	BE295918	Hs.112193	(locuslink)NM_025259:Homo sapiens chromo	2.59
25	452817	AA322859	Hs.284275	Hs.284275:p21 (CDKN1A)-activated kinase	2.59
	413353	AW293542	Hs.75309	Hs.75309:eukaryotic translation elongati	2.59
	421700	BE515018	Hs.107014	NM_016641:Homo sapiens membrane interact	2.59
	410801	BE275469	Hs.66493	NM_016430:Homo sapiens Down syndrome cri	2.59
	440511	AF132959	Hs.7236	NM_015953:Homo sapiens eNOS interacting	2.59
30	407887	AA579668	Hs.41072	(locuslink)NM_004568:Homo sapiens serine	2.59
	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.59
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	2.59
	417952	AI192838	Hs.173135	Hs.173135:dual-specificity tyrosine-(Y)-	2.59
	433053	BE301909	Hs.279952	NM_015917:Homo sapiens glutathione S-tra	2.59
35	450935	BE514743	Hs.379039	NM_005851:Homo sapiens tumor suppressor	2.59
	417891	W79410	Hs.82887	(locuslink)NM_021959:Homo sapiens protei	2.59
	438364	AK000860	Hs.6191	NM_020441:Homo sapiens coronin, actin-bi	2.59
	430976	AA505112	Hs.282990	NM_033550:Homo sapiens chromosome 20 ope	2.58
	444838	AV651680	Hs.208558	Hs.208558:ESTs	2.58
40	416435	AI431301	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.58
	415444	BE247295	Hs.78452	Hs.78452:solute carrier family 20 (phosp	2.58
	452222	AW806287	Hs.21432	Hs.21432:SEX gene	2.58
	400541				2.58
	444309	U83236	Hs.10803	Hs.10803:calcium and integrin binding 1	2.58
45	416116	H51847	Hs.99858	Hs.99858:ribosomal protein L7a	2.58
	418629	BE247550	Hs.86859	(locuslink)NM_005310:Homo sapiens growth	2.58
	432996	AF105025	Hs.279901	Hs.279901:PTD009 protein	2.57
	426781	AL048967	Hs.172207	(locuslink)NM_007363:Homo sapiens non-PO	2.57
	452636	BE615074	Hs.145279	Hs.145279:SET translocation (myeloid leu	2.57
50	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	2.57
	447674	BE270640	Hs.19192	NM_001798:Homo sapiens cyclin-dependent	2.57
	445647	AV654627	Hs.271808	Hs.271808:Homo sapiens cDNA FLJ38018 fis	2.57
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	2.57
	402861				2.57
55	450069	AI698139	Hs.202093	Hs.202093:ESTs	2.57
	414029	BE297731	Hs.75709	NM_002355:Homo sapiens mannose-6-phospha	2.57
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.57
	449961	AW265634	Hs.133100	Hs.133100:ESTs	2.56
	449378	AW664026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 5	2.56
60	442599	AF078037	Hs.324051	(locuslink)NM_006663:Homo sapiens RelA-a	2.56
	448633	AA311426	Hs.21635	NM_001070:Homo sapiens tubulin, gamma 1	2.56
	416078	AL034349	Hs.79005	NM_002844:Homo sapiens protein tyrosine	2.56
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	2.56
	451564	AU076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	2.56
65	457601	AF041429	Hs.284265	(locuslink)NM_145169:Homo sapiens simila	2.56
	439630	AA313607	Hs.58633	Hs.58633:Homo sapiens cDNA: FLJ22145 fis	2.55
	419587	S62907	Hs.91343	NM_000807:Homo sapiens gamma-aminobutyri	2.55
	448279	BE250564	Hs.283655	Hs.283655:lysophospholipase II	2.55
	453350	AI917771	Hs.61790	(locuslink)NM_024658:Homo sapiens import	2.55
70	423720	AL044191	Hs.23388	NM_030817:Homo sapiens hypothetical prot	2.55
	400237		Hs.83347	NM_001087:Homo sapiens angio-associated,	2.55
	420856	BE513294	Hs.205736	Hs.205736:KIAA1978 protein	2.55
	421541	NM_003942	Hs.105584	Hs.105584:ribosomal protein S6 kinase, 9	2.55
	434848	BE256304	Hs.32148	NM_018445:Homo sapiens AD-015 protein (L	2.55
75	424488	AK000413	Hs.149227	(locuslink)NM_017806:Homo sapiens hypoth	2.55
	449089	D78850	Hs.250465	Hs.250465:Homo sapiens mRNA; cDNA DKFZp4	2.55
	430053	AF052155	Hs.227949	NM_030673:Homo sapiens SEC13-like 1 (S.	2.55
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	2.55
	407755	AI151353	Hs.29742	Hs.29742:Homo sapiens cDNA FLJ32147 fis,	2.55
80	446673	NM_016361	Hs.15871	NM_016361:Homo sapiens LPAP for lysophos	2.55
	411766	AA399671	Hs.71969	Hs.71969:Homo sapiens mRNA; cDNA DKFZp66	2.55
	415198	AW009480	Hs.943	Hs.943:natural killer cell transcript 4	2.55
	436495	BE258948	Hs.290874	Hs.290874:Homo sapiens, clone MGC:31984	2.55

	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.55
	443358	H65417	Hs.17757	(locuslink)NM_021622:Homo sapiens plecks	2.55
	452349	AB028944	Hs.29189	Hs.29189:ATPase, Class VI, type 11A	2.55
	427721	AI582843	Hs.180455	NM_005053:Homo sapiens RAD23 homolog A (	2.54
5	407559	AA313352	Hs.280858	Hs.280858:Homo sapiens cDNA FLJ32370 fis	2.54
	413426	U88837	Hs.75354	Hs.75354:GCN1 general control of amino-a	2.54
	425465	L18964	Hs.1904	Hs.1904:protein kinase C, iota	2.54
	444152	AI125694	Hs.149305	Hs.149305:hypothetical protein MGC2603	2.54
	451820	AW058357	Hs.199248	NM_000958:Homo sapiens prostaglandin E r	2.54
10	441356	BE384361	Hs.182885	(locuslink)NM_004556:Homo sapiens nuclea	2.54
	444410	BE387360	Hs.33719	Hs.33719:Homo sapiens, similar to data s	2.54
	415200	AL040328	Hs.78202	NM_003072:Homo sapiens SWI/SNF related,	2.54
	403955				2.54
	430361	AI033965	Hs.239926	Hs.239926:sterol-C4-methyl oxidase-like	2.54
15	432401	NM_013330	Hs.274479	NM_013330:Homo sapiens NME7 (NME7), mRNA	2.54
	446719	W39500	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.54
	439941	AI392640	Hs.18272	NM_030674:Homo sapiens solute carrier fa	2.54
	436685	W28661	Hs.5288	Hs.5288:Homo sapiens mRNA; cDNA DKFZp434	2.54
	424522	AL134847	Hs.149957	Hs.149957:ribosomal protein S6 kinase, 9	2.54
20	442904	AW575008	Hs.11355	Hs.11355:thymopoietin	2.54
	422605	H16646	Hs.118666	Hs.118666:hypothetical protein PP591	2.54
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cDNA FLJ32174 fis	2.54
	447362	AW176120	Hs.9061	NM_024099:Homo sapiens hypothetical prot	2.53
	416305	AU076628	Hs.79187	NM_001338:Homo sapiens coxsackie virus a	2.53
25	422624	BE616678	Hs.76152	NM_006854:Homo sapiens KDEL (Lys-Asp-Glu	2.53
	447298	BE617527	Hs.239818	NM_006219:Homo sapiens phosphoinositide-	2.53
	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.53
	404854				2.53
	415761	AA132666	Hs.78802	(locuslink)NM_002093:Homo sapiens glycog	2.53
30	431104	AW970859	Hs.313503	Hs.313503:ESTs	2.53
	439180	AI393742	Hs.199067	Hs.199067:v-erb-b2 erythroblastic leukem	2.53
	424250	AF073310	Hs.143648	NM_003749:Homo sapiens insulin receptor	2.53
	452878	AW081128	Hs.246374	Hs.246374:Homo sapiens cDNA FLJ31250 fis	2.53
	415742	BE410243	Hs.78769	NM_003249:Homo sapiens thimet oligopepti	2.53
35	404140				2.53
	407255	AA012992	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.53
	422509	AA258513	Hs.117865	Hs.117865:solute carrier family 17 (anio	2.53
	434866	AW002565	Hs.355460	Hs.355460:Homo sapiens cDNA: FLJ21763 fi	2.53
	429743	AA804398	Hs.288995	(locuslink)NM_017961:Homo sapiens hypoth	2.53
40	433047	M86135	Hs.279946	NM_004990:Homo sapiens methionine-tRNA s	2.53
	418945	BE246762	Hs.89499	Hs.89499:arachidonate 5-lipoxygenase	2.52
	445926	AF054284	Hs.334826	NM_012433:Homo sapiens splicing factor 3	2.52
	411353	BE383533	Hs.279784	Hs.279784:prolactin regulatory element b	2.52
	448252	BE622791	Hs.12199	NM_030577:Homo sapiens hypothetical prot	2.52
45	447365	BE383676	Hs.334	(locuslink)NM_005435:Homo sapiens Rho gu	2.52
	414844	AA296874	Hs.77494	NM_080916:Homo sapiens deoxyguanosine ki	2.52
	444025	AA578364	Hs.349093	NM_015945:Homo sapiens ovarian cancer ov	2.52
	416149	AA311965	Hs.79058	NM_003168:Homo sapiens suppressor of Ty	2.52
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	2.52
50	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.52
	445625	BE246743	Hs.353181	(locuslink)NM_025092:Homo sapiens hypoth	2.52
	431565	AF161470	Hs.260622	Hs.260622:butyrate-induced transcript 1	2.52
	410179	W27723	Hs.59498	(locuslink)NM_003718:Homo sapiens cell d	2.52
	431476	BE612705	Hs.256697	(locuslink)NM_005340:Homo sapiens histid	2.52
55	406672	M26041	Hs.198253	(locuslink)NM_002122:Homo sapiens major	2.52
	418180	BE618087	Hs.83724	Hs.83724:hypothetical protein MGC5466	2.52
	428248	AI126772	Hs.40479	Hs.40479:Homo sapiens cDNA FLJ25802 fis,	2.52
	419935	AB020980	Hs.93832	Hs.93832:putative membrane protein	2.52
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.52
60	426691	NM_006201	Hs.171834	(locuslink)NM_006201:Homo sapiens PCTAIR	2.51
	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	2.51
	456266	L29073	Hs.198726	NM_003651:Homo sapiens cold shock domain	2.51
	428921	Z43809	Hs.194638	Hs.194638:polymerase (RNA) II (DNA direc	2.51
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.51
65	422607	Z45471	Hs.118684	NM_006923:Homo sapiens stromal cell-deri	2.51
	421846	AA017707	Hs.1432	NM_002743:Homo sapiens protein kinase C	2.51
	414874	D26351	Hs.77515	NM_002224:Homo sapiens inositol 1,4,5-tr	2.51
	432956	AL037895	Hs.279861	NM_015959:Homo sapiens CGI-31 protein (L	2.51
	438393	AA351815	Hs.50740	Hs.50740:Homo sapiens mRNA; cDNA DKFZp76	2.51
70	418360	AW296974	Hs.84264	NM_006401:Homo sapiens acidic (leucine-r	2.50
	401061				2.50
	426559	AB001914	Hs.170414	Hs.170414:paired basic amino acid cleavi	2.50
	412204	AI125507	Hs.24937	Hs.24937:transformer-2 alpha (htra-2 alp	2.50
	448950	AF288687	Hs.9275	NM_020410:Homo sapiens CGI-152 protein (	2.50
75	409936	AK001691	Hs.57655	(locuslink)NM_018234:Homo sapiens duduli	2.50
	414675	R79015	Hs.288968	Hs.288968:RAB22A, member RAS oncogene fa	2.50
	409983	D50922	Hs.57729	(locuslink)NM_012289:Homo sapiens Kelch-	2.50
	450914	AI743761	Hs.142528	Hs.142528:ESTs	2.50
	444630	AI753230	Hs.323562	(locuslink)NM_032121:Homo sapiens hypoth	2.50
80	401353				2.50
	441680	AW444598	Hs.7940	(locuslink)NM_021159:Homo sapiens RAP1,	2.50
	406860	AA876469		AA876469:oe48b04.s1 NCI_CGAP_Pr25 Homo s	2.50
	449163	AW161356	Hs.23119	NM_003492:Homo sapiens chromosome X open	2.50

432975	AA331517	Hs.286055	Hs.286055:chimerin (chimaerin) 2	2.50
430600	AW950967	Hs.274348	NM_004639:Homo sapiens HLA-B associated	2.50
407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	2.50

TABLE 9B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183
451129	1495511_1	BE072881 AI762181 BE072946
459306	223120_-4	AW578452
448489	2189115_1	R45782 R45781
418869	12789_14	AA229762 AA230035
418546	242836_1	T59708 AA224827 T59843 BE156903
455303	1152492_1	BE066891 BE066895 AW892049 BE066897 BE903884
406860	0_0	AA876469

TABLE 9C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406399	9256288	Minus	63448-63554
403220	7630969	Plus	64338-64517
403218	7630969	Plus	58039-58149
403221	7630969	Plus	66294-66438,66936-67124
403219	7630969	Plus	61858-61995
403739	7630882	Plus	44563-44766,48209-48483,52255-52495
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
400529	9796988	Plus	138232-138423
404826	6572184	Plus	47726-48046
400750	8119067	Plus	198991-199168,199316-199548
400847	9188605	Plus	44643-44835
400448	9887687	Minus	177372-177674
402829	8918414	Plus	101532-101852,102006-102263
400846	9188605	Plus	39310-39474
401179	9438647	Plus	113477-113893
404240	5002624	Minus	116132-116407,116653-116922
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
406363	9256114	Plus	14403-14602,17000-17147,17241-17368
405203	7230116	Plus	125295-125463
402104	8119072	Plus	122409-122600
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
400845	9188605	Plus	34428-34612
403217	7630969	Plus	54089-54163,55427-55623
403483	9966188	Minus	144546-144854
400509	9796539	Minus	157909-158430
403399	6684178	Plus	61841-62145,62367-62756
400541	7574902	Plus	126235-126380,126478-126597
402861	2814366	Minus	14933-15231,15387-15627
403955	7770475	Minus	54527-54740
404854	7143420	Plus	14260-14537
404140	9843520	Plus	37761-38147
401061	3242744	Minus	99468-99549,100707-100848,100918-101107,
401353	9931296	Minus	50831-51352

Table 10A lists about 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium). These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metatases, the "average" normal adult tissue level was set to the 85th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 10A: 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	15.54
428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	14.52
446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	14.04
431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	14.02
423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	13.72
406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	13.44
418406	X73501	Hs.84905	Hs.84905:cytokeratin 20	12.70
406667	M12523			12.42
416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	11.98
437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	11.58
422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	11.50
418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	10.16
418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.11
422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	10.01
421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	9.77
441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	9.69
424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	9.48
453863	X02544	Hs.572	Hs.572:orosomucoid 1	9.20
407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.18
436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	9.04
423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	8.69
430178	AW449612	Hs.152475	Hs.152475:ESTs	8.51
423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	8.43
447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	8.17
409683	U33317	Hs.711	NM_001926:Homo sapiens defensin, alpha 6	8.12
431777	AA570296	Hs.307047	NM_032579:Homo sapiens colon and small i	8.08
450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	8.06
427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (	7.95
436624	T64297	Hs.351719	NM_001443:Homo sapiens fatty acid bindin	7.74
410407	X66839	Hs.63287	NM_001216:Homo sapiens carbonic anhydras	7.46
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	7.41
407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	7.40
412374	X01388	Hs.73849	NM_000040:Homo sapiens apolipoprotein C-	7.34
407244	M10014			7.31
419741	NM_007019	Hs.93002	Hs.93002:ubiquitin-conjugating enzyme E2	7.31
406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	7.26
414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	7.21
404519				7.18
413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	7.13
422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	7.10
414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	7.02
430828	AI763257	Hs.86327	Hs.86327:homeo box B9	6.83
433927	AI557019	Hs.116467	NM_032391:Homo sapiens small nuclear pro	6.81
406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	6.78
423538	AW603823	Hs.146268	Hs.146268:ESTs, Weakly similar to C71400	6.53
434206	AW136973	Hs.362915	Hs.362915:Homo sapiens cDNA FLJ34876 fis	6.37
409041	AB033025	Hs.50081	Hs.50081:KIAA1199 protein	6.33
432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	6.19
422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.19
436330	NM_004413	Hs.109	NM_004413:Homo sapiens dipeptidase 1 (re	6.01
421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	6.00
430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	5.97
413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	5.94
420923	AF097021	Hs.273321	NM_006418:Homo sapiens differentially ex	5.94
428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homof	5.90
420802	U22376	Hs.1334	NM_005375:Homo sapiens v-myb myeloblasto	5.89
452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	5.89
431727	AW293464	Hs.162031	Hs.162031:ESTs	5.85
421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	5.84
432023	AW273128	Hs.300268	Hs.300268:EST	5.75
447033	AI357412	Hs.157601	Hs.157601:ESTs	5.69
411734	AW374954	Hs.71779	Hs.71779:ESTs, Weakly similar to S24C_AR	5.69
406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	5.55
428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	5.48
443247	BE614387	Hs.333893	Hs.333893:cell division cycle associated	5.45
409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	5.44
449388	H53191	Hs.36723	Hs.36723:ESTs, Weakly similar to C05G5.5	5.38
428046	AW812795	Hs.337534	Hs.337534:Homo sapiens cDNA FLJ25241 fis	5.38
433013	AI697890	Hs.127337	(locuslink)NM_004655:Homo sapiens axin 2	5.38
419079	AW014836	Hs.18844	Hs.18844:ESTs	5.37
428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	5.35
422956	BE545072	Hs.122579	(locuslink)NM_018098:Homo sapiens epithe	5.34
424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	5.30
450543	AI394037	Hs.170296	Hs.170296:Homo sapiens cDNA: FLJ22090 fi	5.30
428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	5.30
435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	5.28
411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	5.28
427722	AK000123	Hs.180479	NM_017671:Homo sapiens chromosome 20 ope	5.26
430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	5.26
414816	Y13709	Hs.77399	NM_001255:Homo sapiens caudal type homeo	5.21
430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	5.16

	447208	BE315291	Hs.237971	NM_024096:Homo sapiens hypothetical prot	5.14
	430207	AW079559	Hs.152258	Hs.152258:ESTs	5.12
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	5.12
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.07
5	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	5.06
	452194	AI694413	Hs.373599	Hs.373599:EST	5.01
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	4.99
	406399				4.98
	403220				4.94
10	408380	AF123050	Hs.44532	NM_006398:Homo sapiens ubiquitin D (UBD)	4.92
	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	4.92
	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	4.85
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	4.84
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	4.81
15	441377	BE218239	Hs.202656	Hs.202656:ESTs	4.81
	444666	BE293347	Hs.11638	(locuslink)NM_016234:Homo sapiens fatty-	4.80
	415701	NM_003878	Hs.78619	(locuslink)NM_003878:Homo sapiens gamma-	4.80
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	4.80
	455630	AV655701	Hs.75183	NM_000773:Homo sapiens cytochrome P450,	4.78
20	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	4.78
	423337	NM_004655	Hs.127337	NM_004655:Homo sapiens axin 2 (conductin	4.75
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	4.73
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	4.70
	423936	U77629	Hs.135639	NM_005170:Homo sapiens achaete-scute com	4.70
25	404661				4.68
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	4.67
	420005	AW271106	Hs.133294	Hs.133294:ESTs	4.66
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I isof	4.61
	427506	AK000134	Hs.179100	NM_017678:Homo sapiens hypothetical prot	4.60
30	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	4.59
	453884	AA355925	Hs.36232	NM_021067:Homo sapiens KIAA0186 gene pro	4.55
	431301	AA502384	Hs.151529	Hs.151529:ESTs	4.54
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	4.54
	449032	AA045573	Hs.22900	NM_004289:Homo sapiens nuclear factor (e	4.54
35	434540	NM_016045	Hs.3945	NM_016045:Homo sapiens chromosome 20 ope	4.54
	407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	4.53
	458748	AI381530	Hs.371132	Hs.371132:ESTs	4.53
	408298	AI745325	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.51
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	4.50
40	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	4.49
	425371	D49441	Hs.155981	NM_005823:Homo sapiens mesothelin (MSLN)	4.49
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	4.46
	432867	AW016936	Hs.233364	Hs.233364:ESTs	4.44
	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif-	4.44
45	430294	AI538226	Hs.32976	(locuslink)NM_004485:Homo sapiens guanin	4.42
	411248	AA551538	Hs.69321	Hs.69321:KIAA1359 protein	4.39
	402496				4.38
	430937	X53463	Hs.2704	NM_002083:Homo sapiens glutathione perox	4.37
	434414	AI798376		AF134163:Homo sapiens Human endogenous r	4.36
50	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	4.35
	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.33
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	4.33
	450531	AW301032	Hs.203800	Hs.203800:ESTs	4.33
	403055				4.31
55	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	4.31
	400965				4.30
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	4.29
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	4.29
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	4.28
60	430832	AI073913	Hs.100686	Hs.100686:anterior gradient protein 3	4.28
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	4.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	4.27
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	4.27
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	4.27
65	439211	AI890347	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.27
	459299	BE094291	Hs.155651	NM_021784:Homo sapiens hepatocyte nuclea	4.25
	449720	AA311152	Hs.288708	(locuslink)NM_025113:Homo sapiens hypoth	4.24
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	4.24
	421777	BE562088	Hs.108196	NM_016095:Homo sapiens HSPC037 protein (	4.21
70	419395	BE268326	Hs.90280	Hs.90280:5-aminoimidazole-4-carboxamide	4.20
	443211	AI128388	Hs.143655	Hs.143655:ESTs	4.20
	403218				4.20
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.19
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	4.19
75	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	4.19
	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	4.18
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	4.18
	440869	NM_014297	Hs.7486	NM_014297:Homo sapiens protein expressed	4.17
	414075	U11862	Hs.75741	NM_001091:Homo sapiens amiloride binding	4.17
80	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	4.16
	440409	AW294316	Hs.125608	Hs.125608:ESTs	4.16
	445564	AB028957	Hs.12896	Hs.12896:KIAA1034 protein	4.16
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	4.12

401866				4.11
431611	U58766	Hs.264428	Hs.264428:tissue specific transplantatio	4.10
430187	AI799909	Hs.158989	Hs.158989:Homo sapiens cDNA FLJ37936 fis	4.10
414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	4.08
449281	AI808699	Hs.162717	NM_032756:Homo sapiens hypothetical prot	4.08
449722	BE280074	Hs.23960	Hs.23960:cyclin B1	4.08
418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	4.06
435066	BE261750	Hs.4747	NM_001363:Homo sapiens dyskeratosis cong	4.05
414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	4.04
403221				4.04
409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.03
449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.03
431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	4.01
439759	AL359055	Hs.67709	Hs.67709:Homo sapiens mRNA full length i	4.00
441362	BE614410	Hs.23044	NM_080668:Homo sapiens similar to RIKEN	3.99
417900	BE250127	Hs.82906	Hs.82906:CDC20 cell division cycle 20 ho	3.99
428987	NM_004751	Hs.194710	NM_004751:Homo sapiens glucosaminyl (N-a	3.99
456977	AK000252	Hs.169758	NM_017723:Homo sapiens hypothetical prot	3.99
445919	T53519	Hs.334692	Hs.334692:hypothetical protein MGC14141	3.98
423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	3.98
422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	3.97
422363	T55979	Hs.115474	NM_002915:Homo sapiens replication facto	3.97
433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	3.97
415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	3.96
425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	3.96
415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.95
432407	AA221036		AF134164:Homo sapiens Human endogenous r	3.95
408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	3.94
408494	AA554714	Hs.187578	Hs.187578:Homo sapiens cDNA FLJ11639 fis	3.94
412610	X90908	Hs.74126	NM_001445:Homo sapiens fatty acid bindin	3.94
433323	AA805132	Hs.159142	Hs.159142:lunatic fringe homolog (Drosop	3.94
422515	AW500470	Hs.117950	Hs.117950:phosphoribosylaminoimidazole c	3.92
436543	NM_002212	Hs.5215	Hs.5215:integrin beta 4 binding protein	3.91
418113	AI272141	Hs.83484	Hs.83484:SRY (sex determining region Y)-	3.91
433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	3.90
431939	AW008061	Hs.231994	Hs.231994:Homo sapiens, clone IMAGE:4341	3.90
453439	AI572438	Hs.32976	NM_004485:Homo sapiens guanine nucleotid	3.89
441888	AI733306	Hs.128071	NM_022901:Homo sapiens hypothetical prot	3.89
432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	3.89
425234	AW152225	Hs.165909	Hs.165909:ESTs, Weakly similar to hypoth	3.89
423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	3.87
410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	3.85
436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	3.85
422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	3.84
432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	3.84
424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	3.84
416209	AA236776	Hs.79078	NM_002358:Homo sapiens MAD2 mitotic arre	3.83
430680	AW138724	Hs.168974	Hs.168974:ESTs	3.83
434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	3.82
436481	AA379597	Hs.5199	NM_014176:Homo sapiens HSPC150 protein s	3.82
453700	AB009426	Hs.560	NM_001644:Homo sapiens apolipoprotein B	3.81
410619	BE512730	Hs.65114	Hs.65114:keratin 18	3.81
409420	Z15008	Hs.54451	NM_005562:Homo sapiens laminin, gamma 2	3.79
422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	3.79
432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	3.78
453967	AW009077	Hs.232947	Hs.232947:ESTs	3.78
426106	AI678765	Hs.21812	Hs.21812:ESTs	3.78
434170	AA626509	Hs.159642	(locuslink)NM_001490:Homo sapiens glucos	3.78
418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	3.78
444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	3.74
419229	AI827237	Hs.362919	Hs.362919:ESTs	3.74
437156	AI916600	Hs.121194	Hs.121194:Homo sapiens cDNA: FLJ21569 fi	3.74
452833	BE559681	Hs.30736	(locuslink)NM_015201:Homo sapiens block	3.73
426831	BE296216	Hs.172673	NM_000687:Homo sapiens S-adenosylhomocys	3.73
428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	3.72
443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	3.71
408832	AW085690	Hs.63428	Hs.63428:Homo sapiens cDNA FLJ34457 fis,	3.71
440300	N39760	Hs.8859	NM_138793:Homo sapiens apyrase (SHAPY),	3.71
425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	3.71
432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	3.71
412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	3.71
417001	AU076648	Hs.80741	NM_000282:Homo sapiens propionyl Coenzym	3.69
421225	AA463798	Hs.102696	Hs.102696:MCT-1 protein	3.69
445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	3.69
428330	L22524	Hs.2256	NM_002423:Homo sapiens matrix metallopro	3.67
447472	AW207347	Hs.211101	Hs.211101:ESTs	3.67
423349	AF010258	Hs.127428	NM_002142:Homo sapiens homeo box A9 (HOX	3.67
422026	U80736	Hs.110826	Hs.110826:trinucleotide repeat containin	3.66
419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	3.66
417720	AA205625	Hs.208067	Hs.208067:ESTs	3.66
411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	3.66
421515	Y11339	Hs.105352	(locuslink)NM_018414:Homo sapiens GalNAc	3.65
433675	AW977653	Hs.75319	Hs.75319:ribonucleotide reductase M2 pol	3.65

437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	3.65
445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	3.64
412140	AA219691	Hs.73625	NM_005733:Homo sapiens RAB6 interacting,	3.64
420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	3.63
439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	3.63
414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	3.62
428862	NM_000346	Hs.2316	Hs.2316:SRY (sex determining region Y)-b	3.62
414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	3.62
412056	T28160	Hs.778	Hs.778:guanylate cyclase activator 2A (g	3.61
401519				3.60
428011	BE387514	Hs.181418	NM_014730:Homo sapiens KIAA0152 gene pro	3.60
450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	3.60
421903	AW079940	Hs.15951	(locuslink)NM_145202:Homo sapiens prolin	3.58
413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystel	3.58
424544	M88700	Hs.150403	NM_000790:Homo sapiens dopa decarboxylas	3.58
431563	AI027643	Hs.120912	Hs.120912:ESTs	3.57
435602	AF217515	Hs.283532	NM_018455:Homo sapiens uncharacterized b	3.57
434369	AI650363	Hs.116462	Hs.116462:ESTs	3.57
439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	3.56
447334	AA515032	Hs.91109	Hs.91109:ESTs, Weakly similar to putativ	3.56
422150	AI867118	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	3.56
450663	H43540	Hs.25292	Hs.25292:ribonuclease H2, large subunit	3.56
424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	3.56
422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	3.55
422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	3.55
422532	AL008726	Hs.118126	(locuslink)NM_000308:Homo sapiens protec	3.55
425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	3.55
442053	R35343	Hs.24968	Hs.24968:hypothetical protein BC016683	3.55
437386	W52452	Hs.356766	Hs.356766:Homo sapiens mRNA; cDNA DKFZp7	3.54
415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	3.53
446372	AB020644	Hs.14945	Hs.14945:fatty-acid-Coenzyme A ligase, l	3.53
432378	AI493046	Hs.146133	Hs.146133:ESTs	3.53
434171	BE247688	Hs.347349	(locuslink)NM_004749:Homo sapiens cell c	3.52
428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	3.52
415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	3.51
414918	AI219207	Hs.72222	Hs.72222:fer-1-like 4 (C. elegans)	3.51
440340	AW895503	Hs.125276	Hs.125276:Homo sapiens cDNA FLJ25833 fis	3.51
418384	AW149266	Hs.25130	Hs.25130:Homo sapiens cDNA FLJ14923 fis,	3.51
418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	3.51
429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	3.51
409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	3.50
431567	N51357	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (	3.50
453883	AI638516	Hs.347524	Hs.347524:Homo sapiens, clone MGC:24665	3.50
442700	AA377618	Hs.103834	NM_024056:Homo sapiens hypothetical prot	3.50
410237	AI750589	Hs.61258	Hs.61258:argininosuccinate lyase	3.50
428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	3.49
436213	AA325512	Hs.71472	NM_024662:Homo sapiens hypothetical prot	3.49
442923	AW248322	Hs.95835		3.49
431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	3.48
452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	3.48
448993	AI471630	Hs.355952	Hs.355952:ESTs, Weakly similar to 090320	3.48
447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	3.48
414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	3.47
420996	AK001927	Hs.100895	(locuslink)NM_018099:Homo sapiens hypoth	3.47
439580	AF086401	Hs.293847	Hs.293847:ESTs	3.46
422158	L10343	Hs.112341	NM_002638:Homo sapiens protease inhibito	3.46
418256	AW845318	Hs.12271	(locuslink)NM_012162:Homo sapiens F-box	3.46
400157		Hs.356473	NM_006713:Homo sapiens activated RNA pol	3.46
406709	AI355761	Hs.242463	Hs.242463:keratin 8	3.46
453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.46
421526	AL080121	Hs.105460	NM_015393:Homo sapiens DKFZP564O0823 pro	3.45
415164	AW084352	Hs.157123	Hs.157123:ESTs	3.45
405451				3.44
414361	AI086138	Hs.204044	Hs.204044:ESTs	3.44
422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	3.44
417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.44
457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	3.43
450983	AA305384	Hs.25740	NM_014584:Homo sapiens ERO1-like (S. cer	3.43
421828	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.42
418588	BE387040	Hs.182476	NM_031295:Homo sapiens Williams Beuren s	3.42
417348	AI940507	Hs.318526	NM_025138:Homo sapiens hypothetical prot	3.42
423554	M90516	Hs.1674	NM_002056:Homo sapiens glutamine-fructos	3.42
451310	AW250651	Hs.26213	NM_052951:Homo sapiens chromosome 20 ope	3.41
425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	3.41
429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	3.40
437575	AW954355	Hs.36529	NM_024320:Homo sapiens hypothetical prot	3.40
432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	3.40
439955	AW203959	Hs.149532	Hs.149532:ESTs	3.40
443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interme	3.40
435745	AW967059	Hs.374342	Hs.374342:Homo sapiens clone 24711 mRNA	3.40
403532				3.39
413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.39
425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	3.39

	424996	AF006005	Hs.154104	NM_002657:Homo sapiens pleiomorphic aden	3.38
	402944				3.37
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.37
	427528	AU077143	Hs.179565	NM_002388:Homo sapiens MCM3 minichromoso	3.37
5	426711	AA383471	Hs.343800	(locuslink)NM_033255:Homo sapiens epithe	3.37
	439186	AI697274	Hs.105435	Hs.105435:GDP-mannose 4,6-dehydratase	3.36
	444783	AK001468	Hs.62180	NM_018685:Homo sapiens anillin, actin bi	3.36
	426174	AA547959	Hs.115838	Hs.115838:ESTs	3.36
	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	3.36
10	421605	BE440108	Hs.106127	NM_015972:Homo sapiens RNA polymerase I	3.36
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	3.36
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	3.36
	403219				3.36
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	3.34
15	456946	T29678	Hs.166068	Hs.166068:villin 1	3.33
	425580	L11144	Hs.1907	Hs.1907:galanin	3.33
	412605	AW410734	Hs.74111	Hs.74111:RNA binding protein (autoantige	3.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	3.33
	416782	L35035	Hs.79886	(locuslink)NM_144563:Homo sapiens ribose	3.33
20	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	3.33
	441633	AW958544	Hs.112242	NM_032413:Homo sapiens normal mucosa of	3.32
	416975	NM_004131	Hs.1051	NM_004131:Homo sapiens granzyme B (granz	3.31
	428874	W32133	Hs.194366	Hs.194366:transthyretin (prealbumin, amy	3.31
	431192	AI670056	Hs.137274	Hs.137274:ESTs, Weakly similar to hypoth	3.30
25	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	3.30
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	3.29
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	3.29
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.29
30	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	3.29
	437810	BE246399	Hs.367646	NM_016617:Homo sapiens hypothetical prot	3.29
	403381				3.28
	434031	BE384165	Hs.23723	(locuslink)NM_025215:Homo sapiens pseudo	3.28
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.28
35	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.28
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	3.28
	412994	D32257	Hs.75113	Hs.75113:general transcription factor II	3.28
	443162	T49951	Hs.9029	(locuslink)NM_015515:Homo sapiens type I	3.28
	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3-)-glycoprote	3.28
40	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	3.28
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	3.27
	419359	AL043202	Hs.90073	Hs.90073:CSE1 chromosome segregation 1-l	3.27
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.27
	444371	BE540274	Hs.239	Hs.239:forkhead box M1	3.27
45	450221	AA328102	Hs.24641	NM_018204:Homo sapiens cytoskeleton asso	3.27
	449207	AL044222	Hs.23255	NM_004298:Homo sapiens nucleoporin 155kD	3.27
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	3.27
	403485				3.27
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	3.26
50	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.26
	405484				3.26
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	3.26
	449139	BE268315	Hs.23111	NM_004461:Homo sapiens phenylalanine-tRN	3.26
	404684				3.25
55	447188	H65423	Hs.17631	NM_030804:Homo sapiens hypothetical prot	3.25
	423226	AA323414	Hs.146109	Hs.146109:ESTs, Weakly similar to T28937	3.24
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.24
	424243	AI949359	Hs.143600	Hs.143600:golgi phosphoprotein 4	3.24
	435014	BE560898	Hs.10026	NM_022061:Homo sapiens ribosomal protein	3.24
60	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	3.24
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.23
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.23
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	3.23
	432035	AA524725	Hs.162108	Hs.162108:ESTs	3.23
65	408868	AW292286	Hs.255058	Hs.255058:ESTs	3.23
	429504	X99133	Hs.204238	Hs.204238:lipocalin 2 (oncogene 24p3)	3.22
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	3.22
	426991	AK001536	Hs.214410	Hs.214410:Homo sapiens cDNA FLJ31573 fis	3.22
	408901	AK001330	Hs.48855	(locuslink)NM_018101:Homo sapiens hypoth	3.22
70	439979	AW600291	Hs.6823	NM_018092:Homo sapiens neuropilin (NRP)	3.22
	453968	AA847843	Hs.62711	Hs.62711:Homo sapiens, clone IMAGE:33512	3.22
	457465	AW301344	Hs.122908	NM_030928:Homo sapiens DNA replication f	3.22
	426317	AA312350	Hs.169294	NM_003202:Homo sapiens transcription fac	3.21
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	3.21
75	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	3.20
	444261	AA298958	Hs.10724	Hs.10724:mitochondrial ribosomal protein	3.20
	454033	AF107457	Hs.37035	NM_005515:Homo sapiens homeo box HB9 (HL	3.20
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	3.20
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	3.20
80	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	3.19
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.19
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.19
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.18

	419239	AA468183	Hs.335798	(locuslink)NM_033103:Homo sapiens rhophl	3.18
	426215	AW963419	Hs.155223	NM_003714:Homo sapiens stanniocalcin 2 (	3.18
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	3.17
	413313	NM_002047	Hs.293885	NM_002047:Homo sapiens glycyl-tRNA synth	3.17
5	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	3.17
	408353	BE439838	Hs.44298	NM_015969:Homo sapiens mitochondrial rib	3.17
	400203		Hs.1390	NM_002794:Homo sapiens proteasome (proso	3.16
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.16
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	3.16
10	416984	H38765	Hs.80706	NM_000903:Homo sapiens NAD(P)H dehydroge	3.16
	450635	AW403954	Hs.25237	NM_016647:Homo sapiens mesenchymal stem	3.16
	406708	AI282759		AI282759:qt84a01.x1 NCI_CGAP_Co14 Homo s	3.16
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.16
	430127	AA219498	Hs.233952	Hs.233952:proteasome (prosome, macropain	3.16
15	417308	H60720	Hs.81892	NM_014736:Homo sapiens KIAA0101 gene pro	3.15
	408116	AA251393	Hs.289052	NM_052842:Homo sapiens BCL2-like 12 (pro	3.15
	402474				3.15
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.15
	446595	T57448	Hs.15467	NM_017943:Homo sapiens hypothetical prot	3.15
20	444954	AW247076	Hs.12163	NM_003908:Homo sapiens eukaryotic transl	3.15
	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	3.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.15
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.15
	436391	AJ227892	Hs.146274	Hs.146274:ESTs	3.15
25	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	3.14
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.14
	432370	AA308334	Hs.274424	NM_018946:Homo sapiens N-acetylneuramini	3.14
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.14
	417791	AW965339	Hs.44269	Hs.44269:Homo sapiens cDNA FLJ37972 fis,	3.14
30	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	3.13
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	3.13
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	3.13
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	3.13
	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.13
35	446386	AI032108	Hs.54424	Hs.54424:hepatocyte nuclear factor 4, al	3.12
	407804	AF228603	Hs.39957	NM_016445:Homo sapiens pleckstrin 2 (mou	3.12
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	3.12
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.11
	407168	R45175	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	3.11
40	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	3.11
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	3.11
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.10
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (	3.10
	434861	AA206153	Hs.4209	NM_016491:Homo sapiens mitochondrial rib	3.10
45	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	3.10
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.09
	454464	AW811606	Hs.271819	Hs.271819:mucin 17	3.09
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	3.09
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.09
50	421470	R27496	Hs.1378	NM_005139:Homo sapiens annexin A3 (ANXA3	3.09
	419551	AW582256	Hs.91011	NM_006408:Homo sapiens anterior gradient	3.09
	418691	AW752389	Hs.87296	Hs.87296:Homo sapiens cDNA FLJ20269 fis,	3.08
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	3.08
	447760	AI431328	Hs.348605	NM_052963:Homo sapiens mitochondrial top	3.08
55	405506				3.08
	429957	AW204530	Hs.99500	Hs.99500:ESTs	3.08
	410166	AK001376	Hs.59346	NM_018122:Homo sapiens hypothetical prot	3.08
	422880	AF228704	Hs.193974	Hs.193974:glutathione reductase	3.08
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	3.08
60	431722	AF161528	Hs.268049	(locuslink)NM_016101:Homo sapiens hypoth	3.08
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	3.08
	433659	AK001301	Hs.3487	NM_018093:Homo sapiens hypothetical prot	3.07
	439492	AF086310	Hs.103159	Hs.103159:ESTs, Weakly similar to T06291	3.07
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	3.07
65	412530	AA766268	Hs.266273	(locuslink)NM_024918:Homo sapiens chromo	3.07
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.06
	453132	AW951952	Hs.293724	Hs.293724:Homo sapiens cDNA FLJ12683 fis	3.06
	424971	AA479005	Hs.154036	NM_003311:Homo sapiens tumor suppressing	3.06
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	3.05
70	439273	AW139099	Hs.367692	Hs.367692:Homo sapiens cDNA FLJ25668 fis	3.05
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.05
	435703	AW630133	Hs.83313	(locuslink)NM_020192:Homo sapiens GK003	3.05
	407289	AA135159	Hs.203349	Hs.203349:Homo sapiens cDNA FLJ12149 fis	3.04
	403739				3.04
75	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.04
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.04
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.04
	406545				3.03
	450553	AW850613	Hs.8715	Hs.8715:hypothetical protein MGC3232	3.03
80	418867	D31771	Hs.89404	NM_002449:Homo sapiens msh homeo box hom	3.03
	422976	AU076657	Hs.1600	Hs.1600:chaperonin containing TCP1, subu	3.03
	434523	AA703709	Hs.23410	(locuslink)NM_016539:Homo sapiens sirtui	3.03
	440088	BE559877	Hs.183232	NM_024839:Homo sapiens hypothetical prot	3.02

414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.02
407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	3.02
434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.02
422283	AW411307	Hs.114311	NM_003504:Homo sapiens CDC45 cell divisi	3.02
412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.02
450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.02
417975	AA641836	Hs.30085	NM_024616:Homo sapiens hypothetical prot	3.02
420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.01
436561	BE560135	Hs.5232	NM_014165:Homo sapiens HSPC125 protein (	3.01
426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	3.01
417678	X06560	Hs.82396	(locuslink)NM_002534:Homo sapiens 2',5'-	3.01
417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.00
429983	W92620	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (	3.00
417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.00
414732	AW410976	Hs.77152	Hs.77152:MCM7 minichromosome maintenance	3.00
409614	BE297412	Hs.55189	NM_016489:Homo sapiens 5'-nucleotidase,	3.00
439053	BE244588	Hs.6456	Hs.6456:chaperonin containing TCP1, subu	3.00
411096	U80034	Hs.68583	NM_005932:Homo sapiens mitochondrial int	2.99
433312	AI241331	Hs.131765	Hs.131765:ESTs, Moderately similar to I3	2.99
420767	AF072711	Hs.99918	Hs.99918:carboxyl ester lipase (bile sal	2.99
429523	AK000788	Hs.205280	Hs.205280:Homo sapiens cDNA FLJ20781 fis	2.99
423242	AL039402	Hs.125783	Hs.125783:chromosome 1 open reading fram	2.99
420552	AK000492	Hs.98806	Hs.98806:hypothetical protein FLJ20485	2.99
413380	AI904232	Hs.75323	Hs.75323:prohibitin	2.99
421533	N71826	Hs.105465	NM_003095:Homo sapiens small nuclear rib	2.99
439352	BE614347	Hs.169615	NM_023080:Homo sapiens hypothetical prot	2.98
428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	2.98
431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.98
457211	AW972565	Hs.32399	(locuslink)NM_145240:Homo sapiens simila	2.98
410467	AF102546	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.97
422066	AW249275	Hs.343521	Hs.343521:malate dehydrogenase 2, NAD (m	2.97
418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	2.97
453012	T95804	Hs.31334	NM_012469:Homo sapiens chromosome 20 ope	2.97
412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	2.97
413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	2.97
418362	AL031714	Hs.84285	NM_003345:Homo sapiens ubiquitin-conjuga	2.97
431350	AI192528	Hs.164537	Hs.164537:ESTs	2.96
417911	AA333387	Hs.82916	Hs.82916:chaperonin containing TCP1, sub	2.96
413597	AW302885	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	2.96
409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (	2.96
445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	2.96
418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	2.96
408194	AA601038	Hs.191797	Hs.191797:ESTs	2.96
421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	2.96
459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	2.96
425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	2.96
439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	2.95
408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.95
432843	BE250865	Hs.279529	NM_013237:Homo sapiens px19-like protein	2.95
406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	2.95
410006	AW732308	Hs.57783	NM_003751:Homo sapiens eukaryotic transl	2.94
442577	AA292998	Hs.163900	Hs.163900:ESTs, Highly similar to winged	2.94
425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	2.94
449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	2.94
427779	AA906997	Hs.180780	NM_021238:Homo sapiens TERA protein (TER	2.94
446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	2.94
414549	BE393069	Hs.183506	NM_024841:Homo sapiens hypothetical prot	2.93
410817	AI262789	Hs.93659	(locuslink)NM_004911:Homo sapiens protei	2.93
419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.93
428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	2.93
414416	AW409985	Hs.76084	(locuslink)NM_032737:Homo sapiens hypoth	2.93
434094	AA305599	Hs.238205	Hs.238205:hypothetical protein PRO2013	2.93
409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.93
429048	AI372949	Hs.44241	Hs.44241:Homo sapiens cDNA: FLJ21447 fis	2.93
426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	2.92
422397	AJ223366	Hs.116051	(locuslink)NM_138768:Homo sapiens myelom	2.92
426715	AB037855	Hs.171917	Hs.171917:hypothetical protein FLJ11085	2.92
429539	AK001839	Hs.206501	(locuslink)NM_020467:Homo sapiens hypoth	2.92
443715	AI583187	Hs.9700	NM_001238:Homo sapiens cyclin E1 (CCNE1)	2.92
453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	2.92
433888	BE176078	Hs.30819	Hs.30819:hypothetical protein C40	2.92
424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	2.92
422558	NM_006420	Hs.118249	Hs.118249:ADP-ribosylation factor guanin	2.92
407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	2.92
429626	U36787	Hs.211571	NM_005333:Homo sapiens holocytochrome c	2.92
413374	NM_001034	Hs.75319	NM_001034:Homo sapiens ribonucleotide re	2.92
442159	AW163390	Hs.278554	NM_007276:Homo sapiens chromobox homolog	2.92
400133		Hs.184693	NM_005648:Homo sapiens transcription elo	2.91
419381	AB023420	Hs.90093	Hs.90093:heat shock 70kD protein 4	2.91
436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	2.91
426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	2.91
436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	2.91
425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	2.91

433487	U31814	Hs.3352	NM_001527:Homo sapiens histone deacetyla	2.91
416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	2.90
430287	AW182459	Hs.125759	Hs.125759:likely ortholog of mouse RING	2.90
434026	R15486	Hs.285218	(locuslink)NM_021213:Homo sapiens phosph	2.90
447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	2.90
411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	2.90
432754	BE241691	Hs.3100	Hs.3100:lysyl-tRNA synthetase	2.90
437016	AU076916	Hs.5398	Hs.5398:guanine monphosphate synthetase	2.90
446228	NM_016046	Hs.14415	NM_016046:Homo sapiens exosomal core pro	2.90
420421	AF281133	Hs.343589	Hs.343589:exosome component Rrp41	2.89
428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	2.89
414420	AA043424	Hs.76095	NM_052815:Homo sapiens immediate early r	2.89
457264	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	2.89
401405				2.89
453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	2.89
400247		Hs.356473	NM_006713:Homo sapiens activated RNA pol	2.89
421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	2.89
413610	AL117554	Hs.119908	NM_015934:Homo sapiens nucleolar protein	2.89
413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	2.89
418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	2.88
427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	2.88
417634	W27202	Hs.82327	NM_000178:Homo sapiens glutathione synth	2.88
435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	2.88
425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	2.88
446849	AU076617	Hs.16251	(locuslink)NM_016207:Homo sapiens cleava	2.88
412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	2.88
413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	2.88
407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	2.88
408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	2.87
448250	NM_016034	Hs.20776	(locuslink)NM_016034:Homo sapiens mitoch	2.87
428810	AF068236	Hs.193788	NM_000625:Homo sapiens nitric oxide synt	2.87
427505	AA361562	Hs.178761	Hs.178761:26S proteasome-associated pad1	2.87
418443	NM_005239	Hs.85146	Hs.85146:v-ets erythroblastosis virus E2	2.87
447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	2.87
409262	AK000631	Hs.52256	Hs.52256:hypothetical protein FLJ20624	2.87
443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	2.87
450378	AW249181	Hs.154796	Hs.154796:Homo sapiens cDNA FLJ37976 fis	2.86
411761	AI733848	Hs.71935	NM_021220:Homo sapiens zinc finger prote	2.86
415691	AW963979	Hs.24723	Hs.24723:ESTs	2.86
417715	AW969587	Hs.86366	Hs.86366:ESTs	2.86
452099	BE612992	Hs.27931	Hs.27931:hypothetical protein FLJ10607 s	2.86
436138	H53323	Hs.25717	Hs.25717:Homo sapiens cDNA: FLJ23454 fis	2.86
432858	BE618609	Hs.279591	Hs.279591:Homo sapiens, Similar to RNA p	2.86
434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	2.86
444237	AA336878	Hs.9842	Hs.9842:ESTs	2.85
456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	2.85
411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	2.85
424270	AK001818	Hs.144407	NM_018283:Homo sapiens hypothetical prot	2.85
414396	BE548266	Hs.76057	(locuslink)NM_000403:Homo sapiens galact	2.85
426120	AA325243	Hs.166887	Hs.166887:copine I	2.85
448663	BE614599	Hs.356501	(locuslink)NM_032335:Homo sapiens hypoth	2.85
443802	AW504924	Hs.9805	Hs.9805:exportin 5	2.85
445863	R12234	Hs.13396	Hs.13396:Homo sapiens clone 25028 mRNA s	2.85
434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	2.85
440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	2.85
449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	2.85
432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	2.84
446421	BE297434	Hs.15071	Hs.15071:chaperonin containing TCP1, sub	2.84
427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	2.84
425649	U30930	Hs.158540	(locuslink)NM_003360:Homo sapiens UDP gl	2.84
429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	2.84
435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	2.84
424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	2.84
407833	AW955632	Hs.66666	Hs.66666:chromosome 7 open reading frame	2.84
415083	AI632683	Hs.27179	Hs.27179:Homo sapiens cDNA FLJ12933 fis,	2.83
421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	2.83
443572	AA025610	Hs.9605	Hs.9605:cleavage and polyadenylation spe	2.83
443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	2.83
413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (	2.83
453028	AB006532	Hs.31442	NM_004260:Homo sapiens RecQ protein-like	2.83
425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	2.83
432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	2.83
410197	NM_005518	Hs.59889	(locuslink)NM_005518:Homo sapiens 3-hydr	2.83
413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	2.83
417677	NM_016055	Hs.82389	NM_016055:Homo sapiens mitochondrial rib	2.83
425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	2.82
437430	W44671	Hs.124	NM_014628:Homo sapiens gene predicted fr	2.82
428289	M26301	Hs.2253	Hs.2253:complement component 2	2.82
407137	T97307			2.82
400750				2.82
428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	2.82
432633	AI796390	Hs.210667	Hs.210667:ESTs	2.82
432816	N38913	Hs.221575	Hs.221575:ESTs	2.82

410045	AA806930	Hs.58189	Hs.58189:eukaryotic translation initiati	2.82
454144	BE280478	Hs.182695	NM_024026:Homo sapiens mitochondrial rib	2.82
430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	2.81
434583	AA095761	Hs.349092	Hs.349092:ESTs, Weakly similar to A42442	2.81
431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	2.81
428093	AW594506	Hs.104830	Hs.104830:ESTs	2.81
416047	BE439894	Hs.78991	NM_012080:Homo sapiens DNA segment, nume	2.81
447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	2.81
452199	BE255643	Hs.110695	Hs.110695:hypothetical protein MGC3133	2.81
425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	2.80
445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	2.80
422809	AK001379	Hs.121028	NM_018136:Homo sapiens hypothetical prot	2.80
417869	BE076254	Hs.82793	Hs.82793:proteasome (prosome, macropain)	2.80
436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	2.80
418731	AI264688	Hs.1197	NM_002157:Homo sapiens heat shock 10kD p	2.80
432840	AK001403	Hs.279521	Hs.279521:hypothetical protein FLJ20530	2.80
428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	2.80
441181	AA416925	Hs.374811	Hs.374811:Homo sapiens, similar to 4-1BB	2.80
409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	2.79
450010	AW293801	Hs.255052	Hs.255052:ESTs	2.79
418960	NM_004494	Hs.89525	(locuslink)NM_004494:Homo sapiens hepato	2.79
401179				2.79
419252	AW138434	Hs.129805	Hs.129805:ESTs	2.79
434750	BE019254	Hs.4112	Hs.4112:t-complex 1	2.79
412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	2.79
400529				2.79
436414	BE264633	Hs.143638	NM_033661:Homo sapiens WD repeat domain	2.79
436291	BE568452	Hs.344037	(locuslink)NM_003981:Homo sapiens protei	2.79
427963	AI042582	Hs.181271	NM_016057:Homo sapiens CGI-120 protein (	2.79
426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	2.79
413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	2.79
442468	N77737	Hs.8349	NM_138933:Homo sapiens apobec-1 compleme	2.79
413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	2.79
413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	2.79
430120	AW675298	Hs.233694	(locuslink)NM_018396:Homo sapiens putati	2.79
452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	2.79
417164	AA338283	Hs.81361	Hs.81361:heterogeneous nuclear ribonucle	2.79
407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	2.79
409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	2.78
447619	AI174800	Hs.19054	(locuslink)NM_018530:Homo sapiens hypoth	2.78
434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.78
414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	2.78
443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	2.78
414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.78
430512	AF182294	Hs.241578	NM_016200:Homo sapiens U6 snRNA-associat	2.78
432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	2.78
414697	BE266134	Hs.76927	Hs.76927:translocase of outer mitochondr	2.78
420665	AW469240	Hs.371581	Hs.371581:ESTs	2.78
428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	2.78
448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	2.77
443343	BE409809	Hs.301005	Hs.301005:histone H2A.F/Z variant	2.77
418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	2.77
424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	2.77
456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	2.77
432543	AA552690	Hs.152423	Hs.152423:Homo sapiens cDNA: FLJ21274 fi	2.77
423271	W47225	Hs.126256	NM_000576:Homo sapiens interleukin 1, be	2.77
410595	AW629223	Hs.64794	NM_006978:Homo sapiens zinc finger prote	2.77
448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	2.77
457757	AA434109	Hs.12271	NM_012162:Homo sapiens F-box and leucine	2.77
420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	2.77
410094	BE147897	Hs.58593	NM_004128:Homo sapiens general transcrip	2.77
403817				2.77
459125	AA811363	Hs.29464	Hs.29464:Homo sapiens cDNA: FLJ23460 fis	2.77
432705	AI879473	Hs.157123	Hs.157123:ESTs	2.77
446658	AI440137	Hs.164989	NM_138492:Homo sapiens hypothetical prot	2.76
419485	AA489023	Hs.99807	Hs.99807:Homo sapiens mRNA; cDNA DKFZp31	2.76
432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	2.76
428438	NM_001955	Hs.2271	NM_001955:Homo sapiens endothelin 1 (EDN	2.76
414767	BE541381	Hs.178705	NM_033515:Homo sapiens MacGAP protein (M	2.76
406830	AI829848	Hs.342389	Hs.342389:peptidylprolyl isomerase A (cy	2.76
432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	2.76
430450	R23553	Hs.241489	(locuslink)NM_015913:Homo sapiens hypoth	2.76
433808	NM_014062	Hs.3566	Hs.3566:ART-4 protein	2.75
431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.75
433369	Z49254	Hs.3254	NM_021134:Homo sapiens mitochondrial rib	2.75
446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	2.75
432204	AI916132	Hs.121593	Hs.121593:Homo sapiens cDNA FLJ13123 fis	2.75
424438	AA340724	Hs.271912	Hs.271912:Homo sapiens cDNA FLJ38690 fis	2.75
433862	D86960	Hs.3610	NM_014873:Homo sapiens KIAA0205 gene pro	2.75
417080	BE392846	Hs.1063	Hs.1063:small nuclear ribonucleoprotein	2.75
428242	H55709	Hs.2250	Hs.2250:leukemia inhibitory factor (chol	2.75
416188	BE157260	Hs.79070	NM_002467:Homo sapiens v-myc myelocytoma	2.75
436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	2.75

	419489	AW411280	Hs.90693	NM_013400:Homo sapiens replication initi	2.75
	407971	AI469117	Hs.62918	Hs.62918:CDC91 cell division cycle 91-li	2.75
	432403	AA550815	Hs.124840	(locuslink)NM_138456:Homo sapiens hypoth	2.75
	410775	AB014460	Hs.66196	NM_002528:Homo sapiens nth endonuclease	2.75
5	444197	BE266947	Hs.10590	NM_018683:Homo sapiens zinc finger prote	2.75
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	2.75
	406806	AW088535	Hs.350108	Hs.350108:ribosomal protein, large, P0	2.75
	411580	AL080088	Hs.70877	NM_015421:Homo sapiens DKFZP564K2062 pro	2.75
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	2.74
10	426235	AI631964	Hs.34447	Hs.34447:Homo sapiens cDNA FLJ38512 fis,	2.74
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	2.74
	419713	AW968058	Hs.92381	NM_019094:Homo sapiens nudix (nucleoside	2.74
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	2.74
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	2.74
15	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	2.74
	452767	AW014195	Hs.61472	Hs.61472:Homo sapiens, clone IMAGE:51841	2.74
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	2.73
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	2.73
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	2.73
20	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	2.73
	423908	AJ006422	Hs.135183	NM_006369:Homo sapiens centaurin, alpha	2.73
	433412	AV653729	Hs.8185	NM_021199:Homo sapiens sulfide dehydroge	2.73
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	2.73
	452461	N78223	Hs.108106	Hs.108106:ubiquitin-like, containing PHD	2.73
25	407699	AA825974	Hs.32646	NM_024622:Homo sapiens hypothetical prot	2.73
	412258	AA376768	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.73
	450256	AA286887	Hs.24724	Hs.24724:Homo sapiens cDNA FLJ39185 fis,	2.72
	443905	AI215948	Hs.143969	Hs.143969:ESTs	2.72
	413274	NM_004893	Hs.75258	NM_004893:Homo sapiens H2A histone famil	2.72
30	408885	C02741	Hs.48712	NM_017948:Homo sapiens hypothetical prot	2.72
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	2.72
	424692	AA429834	Hs.151791	NM_014679:Homo sapiens KIAA0092 gene pro	2.72
	413762	AW411479	Hs.848	NM_002014:Homo sapiens FK506 binding pro	2.72
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	2.72
35	450164	AI239923	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.71
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.71
	450897	W16741	Hs.351629	NM_014017:Homo sapiens HSPC003 protein (	2.71
	447349	AI375546		BE743847:601577765F1 NIH_MGC_9 Homo sapi	2.71
	445413	AA151342	Hs.12677	(locuslink)NM_016077:Homo sapiens CGI-14	2.71
40	448826	AI580252	Hs.255565	Hs.255565:Homo sapiens cDNA FLJ33892 fis	2.71
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	2.71
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	2.71
	441020	W79283	Hs.35962	Hs.35962:Homo sapiens mRNA; cDNA DKFZp68	2.70
	458933	AI638429	Hs.24763	NM_002882:Homo sapiens RAN binding prote	2.70
45	423787	AJ295745	Hs.236204	Hs.236204:nuclear pore complex protein	2.70
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	2.70
	439656	AW138241	Hs.160602	Hs.160602:Homo sapiens cDNA FLJ36008 fis	2.70
	425236	AW067800	Hs.155223	NM_003714:Homo sapiens stanniocalcin 2 (	2.70
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	2.70
50	448296	BE622756	Hs.10949	Hs.10949:Homo sapiens cDNA FLJ14162 fis,	2.70
	430200	BE613337	Hs.234896	Hs.234896:geminin	2.70
	424308	AW975531	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.70
	423453	AW450737	Hs.128791	NM_015939:Homo sapiens CGI-09 protein (L	2.70
	421344	AW631030	Hs.103665	(locuslink)NM_015873:Homo sapiens villin	2.70
55	446607	AI691065	Hs.155780	Hs.155780:ESTs	2.70
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	2.70
	443835	AF016371	Hs.9880	NM_006347:Homo sapiens peptidyl prolyl i	2.70
	413794	AF234532	Hs.61638	NM_012334:Homo sapiens myosin X (MYO10),	2.70
	451481	AA300228	Hs.295866	(locuslink)NM_030974:Homo sapiens hypoth	2.70
60	458820	BE552151	Hs.108118	Hs.108118:hypothetical protein FLJ22474	2.70
	425905	AB032959	Hs.318584	NM_032173:Homo sapiens hypothetical prot	2.69
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	2.69
	431201	AA678405	Hs.8854	Hs.8854:Pvt1 oncogene homolog, MYC activ	2.69
	437897	AA770561	Hs.146170	Hs,146170:hypothetical protein FLJ22969	2.69
65	441703	AW390054	Hs.192843	NM_022145:Homo sapiens leucine zipper pr	2.69
	433916	AW732839	Hs.3631	NM_001551:Homo sapiens immunoglobulin (C	2.69
	422516	BE258862	Hs.117950	NM_006452:Homo sapiens phosphoribosylami	2.69
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.69
	427464	BE262956	Hs.178292	Hs.178292:protein O-fucosyltransferase 1	2.69
70	453876	AW021748	Hs.110406	Hs.110406:ESTs	2.69
	424373	AJ133798	Hs.146219	NM_014427:Homo sapiens copine VII (CPNE7	2.69
	411619	AI418609	Hs.71040	NM_017816:Homo sapiens hypothetical prot	2.69
	413004	T35901	Hs.75117	Hs.75117:interleukin enhancer binding fa	2.69
	420062	AW411096	Hs.94785	(locuslink)NM_021809:Homo sapiens TGFB-i	2.69
75	446077	BE251048	Hs.22579	Hs.22579:Homo sapiens clone CDABP0036 mR	2.68
	446269	AW263155	Hs.14559	NM_018131:Homo sapiens hypothetical prot	2.68
	428728	NM_016625	Hs.191381	Hs.191381:hypothetical protein LOC51319	2.68
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	2.68
	421933	R98881	Hs.109655	NM_006746:Homo sapiens sex comb on midle	2.68
80	417750	AI267720	Hs.260523	Hs.260523:neuroblastoma RAS viral (v-ras	2.68
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	2.68
	421720	AF155096	Hs.107213	Hs.107213:formin binding protein 3	2.68
	425601	AW629485	Hs.140720	NM_012083:Homo sapiens frequently rearra	2.68

	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	2.68
	433159	AB035898	Hs.150587	NM_020242:Homo sapiens kinesin-like 7 (K	2.68
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	2.68
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	2.68
5	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (	2.68
	427719	AI393122	Hs.134726	(locuslink)NM_145060:Homo sapiens hypoth	2.68
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	2.68
	457313	AF047002	Hs.241520	NM_005782:Homo sapiens transcriptional c	2.67
	413142	M81740	Hs.75212	(locuslink)NM_002539:Homo sapiens ornith	2.67
10	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	2.67
	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	2.67
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	2.67
	447913	AW438602	Hs.191179	Hs.191179:ESTs	2.67
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	2.67
15	439586	AA922936	Hs.110039	Hs.110039:ESTs	2.67
	427477	AW973119	Hs.178391	NM_021029:Homo sapiens ribosomal protein	2.67
	421839	BE258778	Hs.108809	NM_006429:Homo sapiens chaperonin contai	2.67
	400448				2.67
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	2.67
20	445304	BE613206	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	2.67
	417601	NM_014735	Hs.82292	NM_014735:Homo sapiens KIAA0215 gene pro	2.66
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	2.66
	431021	AI869664	Hs.351863	(locuslink)NM_003312:Homo sapiens thiosu	2.66
	453157	AF077036	Hs.31989	NM_015449:Homo sapiens NICE-3 protein (N	2.66
25	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	2.66
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	2.66
	456248	AL035786	Hs.82425	NM_005717:Homo sapiens actin related pro	2.66
	427691	AW194426	Hs.20726	Hs.20726:ESTs, Moderately similar to hyp	2.66
	419705	AW368634	Hs.154331	Hs.154331:ESTs	2.66
30	421254	AK001724	Hs.102950	NM_016128:Homo sapiens coat protein gamm	2.66
	422719	BE017985	Hs.102558	Hs.102558:Homo sapiens cDNA FLJ40369 fis	2.66
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	2.66
	432435	BE218886	Hs.282070	Hs.282070:ESTs	2.66
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.65
35	436106	AI050715	Hs.2331	Hs.2331:E2F transcription factor 5, p130	2.65
	431127	U66618	Hs.250581	Hs.250581:SWI/SNF related, matrix associ	2.65
	425568	AW963118	Hs.161784	Hs.161784:ESTs	2.65
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	2.65
	414761	AU077228	Hs.77256	NM_004456:Homo sapiens enhancer of zeste	2.65
40	412738	N34731	Hs.74562	NM_078480:Homo sapiens fuse-binding prot	2.65
	409893	AW247090	Hs.57101	Hs.57101:MCM2 minichromosome maintenance	2.65
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.64
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	2.64
	417957	H53497	Hs.83006	NM_016071:Homo sapiens mitochondrial rib	2.64
45	409119	AA531133	Hs.4253	Hs.4253:hypothetical protein MGC2574	2.64
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	2.64
	409214	AW405967	Hs.333388	Hs.333388:similar to CG3714 gene product	2.64
	414883	AA926960	Hs.348669	Hs.348669:CDC28 protein kinase 1	2.64
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	2.64
50	408633	AW963372	Hs.222088	NM_014109:Homo sapiens PRO2000 protein (	2.64
	447769	AW873704	Hs.320831	Hs.320831:chromosome 20 open reading fra	2.64
	432964	AF118395	Hs.279865	NM_014317:Homo sapiens trans-prenyltrans	2.63
	444855	BE409261	Hs.12084	Hs.12084:Tu translation elongation facto	2.63
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	2.63
55	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	2.63
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	2.63
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	2.63
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	2.63
	406122				2.63
60	420988	AW006352	Hs.159643	Hs.159643:ESTs, Weakly similar to putati	2.63
	436433	AW631437	Hs.5184	(locuslink)NM_016397:Homo sapiens TH1-li	2.63
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	2.63
	410397	AF217517	Hs.63042	NM_018457:Homo sapiens DKFZp564J157 prot	2.63
	419420	AA355435	Hs.30724	(locuslink)NM_001516:Homo sapiens genera	2.63
65	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	2.63
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	2.63
	436199	R38946	Hs.127951	Hs.127951:Homo sapiens cDNA FLJ14503 fis	2.63
	425081	X74794	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.63
	442025	AW887434	Hs.11810	NM_032026:Homo sapiens CDA11 protein (CD	2.62
70	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.62
	409703	NM_006187	Hs.56009	Hs.56009:2'-5'-oligoadenylate synthetase	2.62
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	2.62
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	2.62
	451926	AW134519	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.62
75	413781	J05272	Hs.850	(locuslink)NM_000683:Homo sapiens IMP (i	2.62
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	2.62
	421405	AA251944	Hs.104058	NM_015957:Homo sapiens CGI-29 protein (L	2.62
	429491	NM_012111	Hs.204041	NM_012111:Homo sapiens chromosome 14 ope	2.62
	453335	AW857376	Hs.169238	NM_000149:Homo sapiens fucosyltransferas	2.62
80	441126	NM_000429	Hs.323715	(locuslink)NM_000429:Homo sapiens methio	2.62
	417404	NM_007350	Hs.82101	(locuslink)NM_007350:Homo sapiens plecks	2.62
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.62
	446766	AF083208	Hs.16178	NM_012138:Homo sapiens apoptosis antagon	2.62

	437033	AW248364	Hs.5409	(locuslink)NM_004875:Homo sapiens RNA po	2.62
	412123	BE251328	Hs.73291	NM_018256:Homo sapiens WD repeat domain	2.62
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	2.61
	433037	NM_014158	Hs.279938	NM_014158:Homo sapiens HSPC067 protein (	2.61
5	414438	AI879277	Hs.76136	(locuslink)NM_003329:Homo sapiens thiore	2.61
	416221	BE513171	Hs.79086	(locuslink)NM_007208:Homo sapiens mitoch	2.61
	443898	AW804296	Hs.9950	NM_014302:Homo sapiens Sec61 gamma (SEC6	2.61
	410007	AW950887	Hs.57813	NM_014596:Homo sapiens zinc ribbon domai	2.61
	412715	NM_000947	Hs.74519	NM_000947:Homo sapiens primase, polypept	2.61
10	449864	BE276386	Hs.111429	NM_032486:Homo sapiens dynactin 4 (MGC32	2.61
	448625	AW970786	Hs.178470	NM_024829:Homo sapiens hypothetical prot	2.61
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	2.61
	410686	AI733735	Hs.114905	NM_033266:Homo sapiens ER to nucleus sig	2.60
	411400	AA311919	Hs.69851	NM_018983:Homo sapiens nucleolar protein	2.60
15	429770	AI766047	Hs.99736	Hs.99736:hypothetical protein MGC39350	2.60
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	2.60
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	2.60
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	2.60
	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	2.60
20	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	2.60
	457234	AW968360	Hs.14355	Hs.14355:Homo sapiens cDNA FLJ13207 fis,	2.60
	420911	U77413	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (	2.60
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.60
	438533	AI440266	Hs.170673	NM_138969:Homo sapiens retinal short cha	2.60
25	421699	AL161994	Hs.107003	NM_021178:Homo sapiens enhancer of inves	2.60
	452220	BE158006	Hs.212296	Hs.212296:ESTs	2.60
	439148	AA372280	Hs.178576	(locuslink)NM_030877:Homo sapiens cateni	2.60
	453949	AU077146	Hs.36927	(locuslink)NM_006644:Homo sapiens heat s	2.59
	451110	AI955040	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.59
30	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	2.59
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	2.59
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	2.59
	442990	AA197226	Hs.19347	NM_032351:Homo sapiens mitochondrial rib	2.59
	424197	AF096834	Hs.142989	NM_015982:Homo sapiens germ cell specifi	2.59
35	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	2.59
	410219	T98226	Hs.171952	Hs.171952:occludin	2.59
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	2.59
	441153	BE562826		BE562826:601336534F1 NIH_MGC_44 Homo sap	2.59
	410570	AI133096	Hs.64593	NM_006356:Homo sapiens ATP synthase, H+	2.58
40	430594	AK000790	Hs.246885	NM_017958:Homo sapiens hypothetical prot	2.58
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	2.58
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.58
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.58
	449019	AI949095	Hs.67776	Hs.67776:Homo sapiens, clone IMAGE:54556	2.58
45	410442	X73424	Hs.63788	Hs.63788:propionyl Coenzyme A carboxylas	2.58
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	2.58
	454417	AI244459	Hs.110826	Hs.110826:trinucleotide repeat containin	2.58
	416330	AU077101	Hs.79222	Hs.79222:galactosidase, beta 1	2.58
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	2.58
50	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	2.58
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	2.58
	406180				2.58
	416297	AA157634	Hs.79172	Hs.79172:solute carrier family 25 (mitoc	2.58
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	2.58
55	447532	AK000614	Hs.18791	NM_017899:Homo sapiens hypothetical prot	2.57
	420309	AW043637	Hs.21766	Hs.21766:ESTs, Weakly similar to hypothe	2.57
	447418	AA063074	Hs.18552	Hs.18552:E2IG2 protein	2.57
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	2.57
	428342	AI739168	Hs.349283	Hs.349283:Homo sapiens cDNA FLJ31753 fis	2.57
60	427254	AL121523	Hs.97774	Hs.97774:ESTs	2.57
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (	2.57
	425689	W16480	Hs.24283	Hs.24283:Homo sapiens cDNA FLJ25952 fis,	2.57
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	2.57
	427678	BE267756	Hs.180312	NM_016065:Homo sapiens mitochondrial rib	2.57
65	444656	AI277924	Hs.145199	Hs.145199:ESTs, Weakly similar to hypoth	2.57
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	2.57
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	2.56
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	2.56
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.56
70	409964	AW368226	Hs.67928	Hs.67928:ESTs	2.56
	431910	AK000142	Hs.101774	Hs.101774:hypothetical protein FLJ23045	2.56
	413010	AA393273	Hs.75133	NM_003201:Homo sapiens transcription fac	2.56
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	2.56
	419423	D26488	Hs.90315	Hs.90315:KIAA0007 protein	2.56
75	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.56
	437623	D63880	Hs.5719	NM_014865:Homo sapiens chromosome conden	2.56
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	2.56
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	2.56
	425368	AB014595	Hs.155976	(locuslink)NM_003588:Homo sapiens cullin	2.56
80	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	2.56
	427876	AI494291	Hs.369171	Hs.369171:ESTs	2.56
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	2.56
	416432	BE391767	Hs.79322	(locuslink)NM_005051:Homo sapiens glutam	2.55

	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	2.55
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	2.55
	454003	AA058944	Hs.116602	Hs.116602:hypothetical protein BC009115	2.55
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	2.55
5	457400	AF032906	Hs.252549	NM_001336:Homo sapiens cathepsin Z (CTSZ	2.55
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	2.55
	402829				2.55
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	2.55
	400995				2.55
10	452945	AW978187	Hs.79103	NM_030579:Homo sapiens cytochrome b5 out	2.55
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	2.55
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fls485 (LOC51066)	2.55
	424755	AB033094	Hs.152925	Hs.152925:KIAA1268 protein	2.55
	410012	AW015832	Hs.57898	(locuslink)NM_017819:Homo sapiens hypoth	2.55
15	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	2.55
	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	2.55
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	2.55
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	2.55
	406629	AW277078	Hs.181165	Hs.181165:eukaryotic translation elongat	2.55
20	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	2.54
	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	2.54
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	2.54
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	2.54
	427368	BE041451	Hs.177507	Hs.177507:hypothetical protein HSPC155	2.54
25	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	2.54
	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	2.54
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	2.54
	456031	AA335996	Hs.355907	Hs.355907:ESTs, Weakly similar to protei	2.54
	442432	BE093589	Hs.38178	NM_024629:Homo sapiens hypothetical prot	2.54
30	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	2.54
	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	2.54
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	2.54
	432876	AW248272	Hs.279652	NM_015956:Homo sapiens mitochondrial rib	2.53
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	2.53
35	425994	AK000207	Hs.165803	NM_017708:Homo sapiens hypothetical prot	2.53
	445982	BE410233	Hs.13501	(locuslink)NM_014303:Homo sapiens pescad	2.53
	444232	W56010	Hs.347297	(locuslink)NM_013397:Homo sapiens over-e	2.53
	435655	AW105663	Hs.6947	(locuslink)NM_014159:Homo sapiens Huntin	2.53
	417686	AA769155	Hs.235498	Hs.235498:hypothetical protein FLJ14075	2.53
40	417933	X02308	Hs.82962	NM_001071:Homo sapiens thymidylate synth	2.53
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	2.53
	452313	Y00486	Hs.28914	Hs.28914:adenine phosphoribosyltransfera	2.53
	438317	AA826401	Hs.122393	Hs.122393:ESTs	2.53
	409299	AA045650	Hs.53125	NM_004597:Homo sapiens small nuclear rib	2.53
45	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	2.53
	412525	AA581439	Hs.152328	Hs.152328:ESTs	2.53
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.53
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	2.53
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	2.53
50	434274	AA628539	Hs.57783	Hs.57783:eukaryotic translation initiati	2.53
	400282		Hs.289101	NM_005313:Homo sapiens glucose regulated	2.53
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	2.53
	453344	BE349075	Hs.44571	Hs.44571:ESTs	2.53
	449915	NM_004529	Hs.404	NM_004529:Homo sapiens myeloid/lymphoid	2.53
55	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.52
	439012	BE383814	Hs.6455	NM_006666:Homo sapiens RuvB-like 2 (E. c	2.52
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.52
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidas	2.52
	442315	AA173992	Hs.7956	Hs.7956:ESTs	2.52
60	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.52
	422385	BE549407	Hs.115823	(locuslink)NM_006638:Homo sapiens ribonu	2.52
	433517	AW022133	Hs.189838	Hs.189838:ESTs	2.52
	450230	AW016607	Hs.201582	Hs.201582:ESTs	2.52
	432866	BE395875	Hs.279609	NM_014342:Homo sapiens mitochondrial car	2.52
65	433001	AF217513	Hs.279905	NM_016359:Homo sapiens nucleolar protein	2.52
	440773	AA352702	Hs.37747	NM_022767:Homo sapiens hypothetical prot	2.52
	440587	AL138461	Hs.323084	(locuslink)NM_031209:Homo sapiens tRNA-g	2.52
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	2.52
	424259	AK001776	Hs.143954	(locuslink)NM_018270:Homo sapiens chromo	2.52
70	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.52
	453204	R10799	Hs.191990	Hs.191990:ESTs	2.52
	453665	AA626250	Hs.326184	Hs.326184:Homo sapiens nuclear protein p	2.52
	432353	NM_016558	Hs.274411	NM_016558:Homo sapiens SCAN domain conta	2.52
	433271	BE621697	Hs.14317	NM_018648:Homo sapiens nucleolar protein	2.51
75	431770	BE221880	Hs.268555	NM_012255:Homo sapiens 5'-3' exoribonucl	2.51
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	2.51
	428839	AI767756	Hs.82302	(locuslink)NM_147174:Homo sapiens hepara	2.51
	404826				2.51
	429669	BE185499	Hs.2471	NM_014878:Homo sapiens KIAA0020 gene pro	2.51
80	434474	AL042936	Hs.211571	(locuslink)NM_005333:Homo sapiens holocy	2.51
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	2.51
	450422	AA743525	Hs.60300	NM_033414:Homo sapiens hypothetical prot	2.51
	440214	AA247118	Hs.7049	(locuslink)NM_018386:Homo sapiens hypoth	2.51

421168	AF182277	Hs.330780	Hs.330780:cytochrome P450, subfamily IIB	2.51
435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.51
452101	T60298	Hs.10844	NM_052972:Homo sapiens leucine-rich alph	2.51
436043	AW963838	Hs.168830	Hs.168830:Homo sapiens cDNA FLJ12136 fis	2.51
424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	2.51
435677	AA694142	Hs.6685	Hs.6685:thyroid hormone receptor interac	2.51
406363				2.51
452018	AW102941	Hs.211265	Hs.211265:ESTs	2.51
409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.51
421937	AI878857	Hs.109706	NM_016185:Homo sapiens hematological and	2.51
416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.51
421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	2.50
434584	D57341	Hs.188361	Hs.188361:Homo sapiens cDNA FLJ12807 fis	2.50
428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	2.50
426053	U68105	Hs.172182	NM_002568:Homo sapiens poly(A) binding p	2.50
432642	BE297635	Hs.3069	NM_004134:Homo sapiens heat shock 70kD p	2.50
452390	AI864142	Hs.29288	(locuslink)NM_022759:Homo sapiens endo-b	2.50
429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	2.50
400076				2.50
420596	NM_002692	Hs.99185	NM_002692:Homo sapiens polymerase (DNA d	2.50
422244	Y08890	Hs.113503	NM_002271:Homo sapiens karyopherin (impo	2.50
410723	AA100683	Hs.372108	Hs.372108:ESTs	2.50
435496	AW840171	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.50
425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	2.50
433626	AF078859	Hs.86347	NM_013341:Homo sapiens hypothetical prot	2.50
448391	H71025	Hs.21075	NM_016328:Homo sapiens GTF2I repeat doma	2.50

TABLE 10B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
406708	0_0	AI282759
459306	223120_-4	AW578452
447349	1063443_1	BE743847 AW809603 BM469626 AI375546
441153	264480_3	BE562826 BE378727

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404519	8152000	Plus	12817-13000
406399	9256288	Minus	63448-63554
403220	7630969	Plus	64338-64517
404661	9797073	Plus	33374-33675,33769-34008
402496	9797769	Minus	8615-9103
403055	8748904	Minus	109532-110225
400965	7770576	Minus	173043-173564
403218	7630969	Plus	58039-58149
401866	8018106	Plus	73126-73623
403221	7630969	Plus	66294-66438,66936-67124
401519	6649315	Plus	157315-157950
405451	7622517	Minus	145949-146227
403532	8076842	Minus	81750-81901
402944	9368423	Plus	110411-110716,111173-111640
403219	7630969	Plus	61858-61995
403381	9438267	Minus	26009-26178
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
404684	9797403	Minus	110881-111020
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
405506	6466489	Plus	80014-80401,80593-81125
403739	7630882	Plus	44563-44766,48209-48483,52255-52495

406545	7711510	Plus	145662-145781,147854-147984,148098-14824
401405	7768126	Minus	69276-69452,69548-69958
400750	8119067	Plus	198991-199168,199316-199548
401179	9438647	Plus	113477-113893
400529	9796988	Plus	138232-138423
403817	8962065	Plus	110297-111052
400448	9887687	Minus	177372-177674
406122	9144087	Minus	30940-31386
406180	7283201	Minus	38923-39107
402829	8918414	Plus	101532-101852,102006-102263
400995	8099094	Plus	141186-141601
404826	6572184	Plus	47726-48046
406363	9256114	Plus	14403-14602,17000-17147,17241-17368

Table 11A lists about 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium) that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 3.0, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metatases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 11A: 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	37.18
406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	31.24
407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	24.81
406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	20.54
431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	20.38
428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	20.13
406667	M12523			19.89
437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	19.68
446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	19.55
423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	18.33
421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	17.47
414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	17.37
416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	15.15
441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	14.23
407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	14.12
422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	13.64
432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.48
424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	13.43
418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	13.20
453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	12.58
436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.34
421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	11.72
409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	11.72
452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	11.49
406399				11.25
414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	11.12
407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	11.01
423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.70
447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	10.69
450685	L15533	Hs.423	NM_138938:Homo sapiens pancrealitis-asso	10.57
427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (	10.48
418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	10.20
422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	10.19
423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	9.72
422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	9.70
430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	9.65
406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.52
428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	9.47
422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.41
413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	9.39
422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	9.31
417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	9.30

422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	9.01
413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	8.99
424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.80
420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	8.71
446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	8.67
428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	8.47
452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	8.47
422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	8.43
421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	8.34
424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	8.12
435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	8.09
413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	7.92
436972	AA284679	Hs.25640	Hs.25640:claudin 3	7.89
430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	7.87
409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	7.71
423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	7.58
430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.48
451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I isof	7.31
422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	7.31
425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	7.29
411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	7.23
451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	7.12
418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	7.12
414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	7.10
447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	7.06
452194	AI694413	Hs.373599	Hs.373599:EST	7.02
414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.97
417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.96
423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	6.96
403220				6.95
415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	6.87
449722	BE280074	Hs.23960	Hs.23960:cyclin B1	6.87
414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	6.80
415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.78
411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	6.66
408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	6.65
431301	AA502384	Hs.151529	Hs.151529:ESTs	6.62
428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	6.59
424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	6.56
431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	6.54
431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	6.50
408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.47
428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	6.46
408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	6.45
428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.41
426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	6.41
419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	6.27
414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	6.20
422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	6.19
414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	6.18
425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	6.16
432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	6.16
443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	6.15
426174	AA547969	Hs.115838	Hs.115838:ESTs	6.10
430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.07
420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	6.06
409453	AI885516	Hs.95612	Hs.95612:ESTs	6.06
408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	6.03
444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.99
444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	5.97
421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	5.95
430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.92
443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interme	5.90
428874	W32133	Hs.194366	Hs.194366:transthyretin (prealbumin, amy	5.88
408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.86
452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	5.82
412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	5.77
421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	5.75
403218				5.74
412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	5.72
449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	5.72
429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	5.72
414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.72
415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	5.71
425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	5.70
432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.70

	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	5.67
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	5.67
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.63
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	5.62
5	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	5.60
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	5.59
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.58
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.56
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	5.56
10	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	5.54
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	5.53
	403221				5.52
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	5.52
15	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.48
	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	5.44
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.42
	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	5.41
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	5.36
20	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	5.34
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	5.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	5.32
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.31
	430680	AW138724	Hs.168974	Hs.168974:ESTs	5.25
25	432378	AI493046	Hs.146133	Hs.146133:ESTs	5.25
	419693	AA133749	Hs.301350	Hs.301350:FXYD domain-containing ion tra	5.24
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	5.21
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	5.21
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	5.21
30	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	5.20
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	5.20
	428289	M26301	Hs.2253	Hs.2253:complement component 2	5.19
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	5.19
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	5.15
35	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	5.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	5.11
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.09
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	5.08
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	5.08
40	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	5.07
	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	5.07
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	5.07
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	5.06
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	5.06
45	414361	AI086138	Hs.204044	Hs.204044:ESTs	5.04
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	5.03
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	5.03
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	5.01
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	5.00
50	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.99
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	4.99
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.98
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.98
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.98
55	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.97
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	4.97
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.95
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	4.95
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.93
60	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	4.93
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.91
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.91
65	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.89
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.89
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.88
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	4.88
70	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	4.87
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (	4.87
	405484				4.87
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.87
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
75	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	4.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	4.81
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.79
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.79
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.79
80	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.78
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.77
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.76
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	4.76

	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	4.75
	400529				4.75
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	4.75
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
5	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	4.72
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.72
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.70
	405556				4.70
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.70
10	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.70
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.70
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.70
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	4.65
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.64
15	403739				4.61
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	4.61
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	4.61
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	4.60
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.60
20	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.59
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	4.59
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	4.59
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	4.59
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.58
25	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3-)-glycoprote	4.57
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.57
	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	4.55
	409964	AW368226	Hs.67928	Hs.67928:ESTs	4.54
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	4.54
30	432407	AA221036		AF134164:Homo sapiens Human endogenous r	4.54
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.53
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	4.53
	403219				4.53
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.52
35	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	4.51
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.51
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	4.51
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.50
40	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	4.50
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.49
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.48
	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	4.47
45	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	4.47
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	4.46
	452299	AW206330	Hs.355663	Hs.355663:ESTs	4.46
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.46
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	4.46
50	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.46
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	4.45
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	4.44
	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif-	4.44
55	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	4.43
	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.43
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	4.43
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.42
	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.41
60	431350	AI192528	Hs.164537	Hs.164537:ESTs	4.39
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	4.39
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	4.39
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	4.38
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	4.38
65	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	4.38
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	4.38
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.37
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	4.36
	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	4.36
70	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.35
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.34
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (	4.34
	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antige	4.34
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	4.33
75	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	4.32
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.32
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	4.32
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	4.31
	436391	AJ227892	Hs.146274	Hs.146274:ESTs	4.30
80	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.29
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.29
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	4.29

	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	4.29
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	4.29
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	4.28
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.27
5	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	4.27
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	4.27
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	4.27
	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	4.24
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	4.24
10	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (	4.24
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	4.23
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.23
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	4.23
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	4.23
15	426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	4.23
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.22
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	4.22
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	4.21
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	4.21
20	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	4.21
	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	4.20
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	4.19
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	4.19
25	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	4.19
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.19
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	4.18
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	4.17
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	4.17
30	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	4.17
	404826				4.17
	414198	AW505308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	4.17
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	4.17
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	4.16
35	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	4.16
	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	4.15
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	4.15
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	4.14
	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	4.14
40	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	4.13
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	4.13
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	4.13
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	4.12
45	428471	X57348	Hs.184510	Hs.184510:stratifin	4.12
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.11
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	4.10
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.10
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	4.10
50	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	4.10
	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	4.09
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	4.09
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	4.09
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	4.09
55	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	4.08
	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	4.08
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	4.08
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	4.06
	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	4.06
60	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	4.04
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	4.04
	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	4.04
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	4.04
65	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	4.02
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	4.02
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	4.02
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.02
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.01
70	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	4.00
	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	4.00
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.99
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	3.98
	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	3.98
75	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	3.98
	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	3.98
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.97
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.96
	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.96
80	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.95
	437016	AU076916	Hs.5398	Hs.5398:guanine monphosphate synthetase	3.94
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.94
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.94

	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.94
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.93
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	3.93
	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	3.92
5	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.92
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.91
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	3.90
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.89
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	3.89
10	407971	AI469117	Hs.62918	Hs.62918:CDC91 cell division cycle 91-li	3.89
	400750				3.89
	446140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	3.89
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.89
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.89
15	426788	AF062283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	3.88
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosp	3.88
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.88
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	3.87
	410268	AA316181	Hs.61635	NM_012449:Homo sapiens six transmembrane	3.87
20	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.87
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.86
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.86
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	3.85
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.85
25	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.85
	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.85
	452220	BE158006	Hs.212296	Hs.212296:ESTs	3.85
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.85
	433658	L03678	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.84
30	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.84
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.84
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.84
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens met transforming	3.84
	427318	AF186081	Hs.175783	NM_014579:Homo sapiens solute carrier fa	3.83
35	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.83
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.83
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.82
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.82
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (	3.82
40	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.82
	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.81
	421481	AW391972	Hs.104696	Hs.104696:KIAA1324 protein	3.81
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.80
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.80
45	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	3.80
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.80
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.80
	410219	T98226	Hs.171952	Hs.171952:occludin	3.80
	407137	T97307			3.78
50	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	3.78
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	3.78
	450010	AW293801	Hs.255052	Hs.255052:ESTs	3.78
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.78
	440676	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.77
55	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	3.77
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	3.77
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	3.77
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	3.76
	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.76
60	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.76
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	3.75
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.74
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.74
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.74
65	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.74
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.74
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.74
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.73
	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.73
70	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.73
	400419	AF084545		AF084545:Homo sapiens versican Vint isof	3.73
	421357	AK000809	Hs.103808	NM_017896:Homo sapiens chromosome 20 ope	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.73
75	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transm	3.72
	419743	AW408762	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.72
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.72
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
80	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	3.71
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.71
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.71
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.71

	406722	H27498	Hs.293441	Hs.293441:Homo sapiens SNC73 protein (SN	3.71
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.71
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.70
	409327	L41162	Hs.53563	NM_001853:Homo sapiens collagen, type IX	3.70
5	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.70
	400846				3.70
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.70
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.70
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.70
10	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.69
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	3.69
	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.69
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.69
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (	3.69
15	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.68
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.68
	401179				3.67
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.67
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.67
20	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-ral simian leuk	3.66
	409402	AF208234	Hs.695	Hs.695:cystatin B (stefin B)	3.66
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.66
	432633	AI796390	Hs.210667	Hs.210667:ESTs	3.66
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.66
25	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.65
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.65
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.65
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.64
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.64
30	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.64
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.64
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidas	3.63
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.62
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.62
35	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.62
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.61
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.61
	400847				3.60
40	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	3.60
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.60
	404854				3.60
	400448				3.60
	453331	AI240665	Hs.352537	Hs.352537:Homo sapiens cDNA FLJ31066 fis	3.60
45	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.60
	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.59
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.59
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.59
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.59
50	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.59
	426722	U53823	Hs.171952	NM_002538:Homo sapiens occludin (OCLN),	3.58
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.58
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	3.57
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.57
55	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.57
	424241	AW995948	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, i	3.57
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.57
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.56
	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.56
60	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.56
	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.56
	413859	AW992356	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, i	3.56
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.55
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.55
65	411704	AI499220	Hs.71573	(locuslink)NM_017988:Homo sapiens hypoth	3.55
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.54
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.54
	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.54
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.54
70	452488	N74921	Hs.184389	Hs.184389:ESTs, Moderately similar to S1	3.54
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.54
	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.53
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.53
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.53
75	428582	BE336699	Hs.185055	Hs.185055:BENE protein	3.53
	446147	AL133064	Hs.14051	(locuslink)NM_145698:Homo sapiens endoze	3.53
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.52
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.52
	442007	AA301116	Hs.142838	NM_032390:Homo sapiens MKI67 (FHA domain	3.52
80	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.52
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.51
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.51
	421340	F07783	Hs.1369	NM_000574:Homo sapiens decay acceleratin	3.50

429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.50
452862	AW378065	Hs.8687	Hs.8687:ESTs	3.50
442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.50
404240				3.50
424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	3.50
445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.49
424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.49
424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.49
428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	3.49
456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.49
424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.49
419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.49
439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannose-P-dolicho	3.49
428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.48
430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alph	3.48
431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.48
422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	3.48
457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.48
419705	AW368634	Hs.154331	Hs.154331:ESTs	3.48
454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
402829				3.47
451707	AW051061	Hs.60973	Hs.60973:Homo sapiens cDNA FLJ40829 fis,	3.47
433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.47
420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.47
437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.47
439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding prot	3.46
452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.46
450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	3.46
408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.46
446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	3.46
437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.45
427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	3.45
433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfeit 4 (SURF4)	3.45
400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.45
433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.45
410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.45
456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	3.44
432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.44
428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.44
417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.44
458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (	3.44
425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.44
448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	3.44
448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.44
420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	3.44
412420	AL035668	Hs.73853	NM_001200:Homo sapiens bone morphogeneti	3.43
424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.43
414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostasin)	3.43
422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	3.43
428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43
428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neutr	3.42
445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.42
442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.42
427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.42
427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.41
428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.41
453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	3.41
441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	3.41
414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.41
423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	3.41
443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	3.41
426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.40
422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.40
451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.40
400205		Hs.81848	NM_006265:Homo sapiens RAD21 homolog (S.	3.40
428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.39
448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.39
426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.39
417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.39
406363				3.39
444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	3.39
423309	BE006775	Hs.126782	NM_014467:Homo sapiens sushi-repeat prot	3.38
426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	3.38
452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.38
419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.38
457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.38
400125		Hs.125078	(locuslink)NM_004152:Homo sapiens ornith	3.38
429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	3.37
410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.37
434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.37
423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.37
427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.37

446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	3.36
426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.36
429747	M87507	Hs.2490	Hs.2490:caspase 1, apoptosis-related cys	3.36
406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.36
439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.36
418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.36
421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	3.36
451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.36
449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	3.36
426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	3.36
425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	3.35
444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.35
436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.35
457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	3.35
432169	Y00971	Hs.2910	NM_002765:Homo sapiens phosphoribosyl py	3.35
412525	AA581439	Hs.152328	Hs.152328:ESTs	3.35
416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	3.35
419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	3.35
432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	3.34
400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.34
423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	3.34
424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	3.34
450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.34
437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	3.34
431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.34
427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.34
439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.34
448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.34
407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.34
445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	3.34
444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.34
429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	3.33
427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.33
415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	3.33
414271	AK000275	Hs.75871	(locuslink)NM_012408:Homo sapiens protei	3.33
424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.33
437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	3.32
430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.32
444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	3.32
426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythrob	3.32
430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.32
402104				3.32
446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.32
443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
414883	AA926960	Hs.348669	Hs.348669:CDC28 protein kinase 1	3.31
413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.31
451564	AU076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	3.31
437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	3.31
441866	BE464341	Hs.21201	Hs.21201:nectin 3	3.31
438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.31
422192	AA305159	Hs.113019	NM_015931:Homo sapiens fis485 (LOC51066)	3.31
446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.31
415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytoso	3.31
449644	AW960707	Hs.148324	Hs.148324:ESTs	3.31
422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.31
417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.30
428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	3.30
447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.30
450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.30
422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	3.30
426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	3.30
449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.29
424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	3.29
442772	AW503680	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.29
430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.29
448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.29
420332	NM_001756	Hs.1305	NM_001756:Homo sapiens serine (or cystei	3.29
417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	3.29
412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	3.28
427308	D26067	Hs.174905	Hs.174905:KIAA0033 protein	3.28
432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.28
449199	AI990122	Hs.196988	Hs.196988:ESTs	3.28
442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cytoso	3.28
422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	3.28
452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	3.28
431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.28
402260				3.28
409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multid	3.28
409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.28
447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.27
426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.27

429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.27
434521	NM_002267	Hs.3886	Hs.3886:karyopherin alpha 3 (importin al	3.27
454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.27
445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	3.27
448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	3.26
425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	3.26
440286	U29589	Hs.7138	NM_000740:Homo sapiens cholinergic recep	3.26
413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	3.26
412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	3.26
426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	3.26
427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.26
440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	3.26
425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.25
416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	3.25
449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.25
424381	AA285249	Hs.146329	NM_007194:Homo sapiens CHK2 checkpoint h	3.25
426784	U03749	Hs.172216	NM_001275:Homo sapiens chromogranin A (p	3.25
420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.25
438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	3.24
419216	AU076718	Hs.164021	NM_002993:Homo sapiens small inducible c	3.24
430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.24
458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	3.24
410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	3.24
420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.24
435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	3.23
427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	3.23
412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	3.23
430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	3.23
432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.23
432731	R31178	Hs.287820	Hs.287820:fibronectin 1	3.23
410340	AW182833	Hs.112188	(locuslink)NM_021826:Homo sapiens hypoth	3.23
410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	3.23
430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	3.23
425907	AA365752	Hs.155965	Hs.155965:ESTs	3.23
436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	3.22
403912				3.22
429782	NM_005754	Hs.220689	Hs.220689:Ras-GTPase-activating protein	3.22
416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	3.22
445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.22
422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	3.22
409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	3.22
411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.22
414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	3.22
450770	AA019924	Hs.28803	Hs.28803:ESTs	3.22
433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	3.22
414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	3.21
428781	AF164799	Hs.193384	Hs.193384:putatative 28 kDa protein	3.21
432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.21
454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.21
447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	3.21
409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	3.21
400836				3.20
420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	3.20
414343	AL036166	Hs.75914	NM_006815:Homo sapiens coated vesicle me	3.20
447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	3.20
412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.20
425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.20
407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.20
400845				3.20
407082	Z47055			3.20
452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinesi	3.20
403217				3.20
414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.19
431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.19
417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.19
457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.19
445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	3.19
430280	AA361258	Hs.237868	Hs.237868:Homo sapiens mRNA; cDNA DKFZp6	3.19
422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	3.19
422938	NM_001809	Hs.1594	NM_001809:Homo sapiens centromere protei	3.18
435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.18
449704	AK000733	Hs.23900	Hs.23900:Rac GTPase activating protein 1	3.18
426925	NM_001196	Hs.172894	Hs.172894:BH3 interacting domain death a	3.18
414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	3.18
405387				3.18
444108	R55784	Hs.140942	Hs.140942:Homo sapiens cDNA FLJ38396 fis	3.18
424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-l	3.17
424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.17
451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	3.17
426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	3.17
447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.17
410663	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.17

	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3-)-glycopro	3.17
	451032	W03692	Hs.323079	Hs.323079:Homo sapiens mRNA; cDNA DKFZp5	3.17
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	3.17
	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yamaguchi sarcoma viral	3.16
5	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.16
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	3.16
	432728	NM_006979	Hs.278721	NM_006979:Homo sapiens HLA class II regi	3.16
	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	3.16
10	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	3.16
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	3.16
	429556	AW139399	Hs.314807	Hs.314807:hypothetical protein MGC2655	3.15
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	3.15
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	3.15
15	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	3.15
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.15
	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	3.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.14
	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	3.14
20	407961	AW672939	Hs.41694	Hs.41694:origin recognition complex, sub	3.14
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-li	3.14
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.14
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	3.14
	450295	AI766732	Hs.210628	Hs.210628:ESTs	3.14
25	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.13
	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (renal a	3.13
30	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	3.13
	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	3.12
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	3.12
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	3.12
	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
35	424727	AW590378	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.12
	435975	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.12
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	3.12
	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	3.12
40	428699	AW578252	Hs.190161	Hs.190161:LR8 protein	3.12
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	3.12
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.12
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	3.12
	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	3.12
45	410240	AL157424	Hs.61289	Hs.61289:synaptojanin 2	3.12
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	3.11
	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, ribo	3.11
	405203				3.11
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	3.11
50	417211	T97617	Hs.269092	Hs.269092:ESTs	3.11
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	3.11
	429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.11
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	3.11
	408805	H69912	Hs.48269	NM_003384:Homo sapiens vaccinia related	3.10
55	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	3.10
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	3.10
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	3.10
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	3.10
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.10
60	429238	NM_002849	Hs.198288	NM_002849:Homo sapiens protein tyrosine	3.10
	433409	AI278802	Hs.25661	Hs.25661:ESTs, Moderately similar to hyp	3.10
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.10
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.10
	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	3.10
65	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	3.10
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.10
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.10
70	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	3.09
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	3.09
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-li	3.09
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.09
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.09
75	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	3.09
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	3.09
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	3.09
	430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	3.09
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	3.09
80	426989	AI815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (	3.08
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	3.08
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	3.08
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	3.08

410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	3.08
415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.08
419757	AA773820	Hs.63970	Hs.63970:ESTs	3.08
427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	3.08
424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.08
453914	NM_000507	Hs.574	NM_000507:Homo sapiens fructose-1,6-bisp	3.08
420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	3.08
431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	3.07
411423	AW845987	Hs.68864	(locuslink)NM_139248:Homo sapiens membra	3.07
449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	3.07
423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	3.07
448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.07
450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 l	3.07
432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	3.07
421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	3.07
430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	3.07
436553	AW407157	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.06
458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	3.06
450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	3.06
418062	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (	3.06
407223	H96850		H96850:yw03b12.s1 Soares melanocyte 2NbH	3.06
418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.06
450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXYD d	3.06
408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	3.06
435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	3.06
421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.05
440246	W52010	Hs.191379	Hs.191379:ESTs	3.05
446770	AV660309	Hs.154986	Hs.154986:ESTs, Weakly similar to PLLP_H	3.05
440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	3.05
425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	3.05
453830	AA534296	Hs.20953	Hs.20953:hypothetical protein BC010003	3.05
412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	3.05
422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	3.05
441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	3.05
408524	D87942	Hs.46328	Hs.46328:fucosyltransferase 2 (secretor	3.05
408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	3.05
430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	3.04
432281	AK001239	Hs.274263	Hs.274263:hypothetical protein FLJ10377	3.04
443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	3.04
423570	AW838306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	3.04
443653	AA137043	Hs.9663	NM_013374:Homo sapiens programmed cell d	3.04
451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	3.04
444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	3.04
407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	3.04
423022	AA320525	Hs.201076	Hs.201076:ESTs	3.04
453450	AW797627	Hs.347459	Hs.347459:Homo sapiens cDNA FLJ13900 fis	3.04
412708	R26830	Hs.106137	Hs.106137:Homo sapiens mRNA for OK/SW-CL	3.04
448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	3.04
443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	3.03
439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	3.03
412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	3.03
444309	U83236	Hs.10803	Hs.10803:calcium and integrin binding 1	3.03
412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	3.03
430354	AA954810	Hs.239784	Hs.239784:scribble	3.03
414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	3.03
421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	3.02
451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	3.02
428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	3.02
447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.02
436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.02
417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	3.02
444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	3.02
418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	3.01
414421	AI521130	Hs.355126	(locuslink)NM_144686:Homo sapiens hypoth	3.01
424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	3.01
442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	3.01
437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	3.01
436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	3.00
438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	3.00
415697	AI365603	Hs.279696	Hs.279696:DKFZP566I1024 protein	3.00
437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	3.00
436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	3.00
450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	3.00
445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.00
406868	AA505445	Hs.300697	Hs.300697:immunoglobulin heavy constant	3.00
424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	3.00
408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	3.00
417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rh-related antige	3.00

TABLE 11B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861456 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
459306	223120_-4	AW578452
452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183
451129	1495511_1	BE072881 AI762181 BE072946

TABLE 11C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406399	9256288	Minus	63448-63554
403220	7630969	Plus	64338-64517
403218	7630969	Plus	58039-58149
403221	7630969	Plus	66294-66438,66936-67124
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
400529	9796988	Plus	138232-138423
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
403739	7630882	Plus	44563-44766,48209-48483,52255-52495
403219	7630969	Plus	61858-61995
404826	6572184	Plus	47726-48046
400750	8119067	Plus	198991-199168,199316-199548
400846	9188605	Plus	39310-39474
401179	9438647	Plus	113477-113893
400847	9188605	Plus	44643-44835
404854	7143420	Plus	14260-14537
400448	9887687	Minus	177372-177674
404240	5002624	Minus	116132-116407,116653-116922
402829	8918414	Plus	101532-101852,102006-102263
406363	9256114	Plus	14403-14602,17000-17147,17241-17368
402104	8119072	Plus	122409-122600
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
400836	8954179	Plus	677-1188
400845	9188605	Plus	34428-34612
403217	7630969	Plus	54089-54163,55427-55623
405387	6587915	Minus	3769-3833,5708-5895
405203	7230116	Plus	125295-125463

Table 12A lists about 1006 genes up-regulated in cervical cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" cervical cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" cervical cancer level was set to the 93rd percentile value amongst cervical cancers. The "average" normal adult tissue level was set to the 93rd percentile value amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 12A: 1006 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
402075	U19557	Hs.123035	squamous cell carcinoma antigen 2 (SCCA2)	81.1
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	43.6
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial coll	38.9
435094	AI560129	Hs.329062	EST	30.3
439606	W79123	Hs.58561	G protein-coupled receptor 87	28.8
452240	AI591147	Hs.61232	ESTs	27.0
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin bi	26.0
417034	NM_006183	Hs.80962	neurotensin	25.5
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, cl	24.5
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.7

	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	21.2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	20.5
	418345	AJ001696	Hs.241407	serine proteinase inhibitor 13 (PI13; serpin	20.1
	452461	N78223	Hs.108106	transcription factor	19.8
5	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, cl	19.2
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	17.5
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-type,	16.4
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	16.3
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.2
10	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-C	15.9
	421373	AA808229	Hs.167771	ESTs	15.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	15.4
	441459	AI919142	Hs.214233	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.6
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	13.8
15	412719	AW016610	Hs.129911	ESTs	13.4
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	13.3
	431753	X76029	Hs.2841	neuromedin U	13.2
	438817	AI023799	Hs.163242	ESTs	13.1
	404996			Target Exon	13.1
20	443211	AI128388	Hs.143655	ESTs	12.9
	414764	AW013887	Hs.72047	ESTs	12.9
	428618	AA885360	Hs.160199	Target CAT	12.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.7
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal	12.6
25	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.6
	432656	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein produ	12.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	12.6
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin D 24	12.3
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.2
30	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	11.6
	415989	AI267700	Hs.317584	ESTs	11.5
	452638	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.4
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	11.3
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	11.0
35	449260	AA741180	Hs.29879	ESTs	11.0
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN HOMEOB	10.7
	406467			Target Exon	10.5
	439926	AW014875	Hs.137007	ESTs	10.2
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, pr	10.2
40	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	10.2
	414422	AA147224	Hs.337232	Homeo box A13	10.2
	442660	AW138174	Hs.130651	ESTs	10.1
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu or sig	10.0
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN ALU SU	9.9
45	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	9.8
	400195	NM_007057		NM_007057*:Homo sapiens ZW10 interactor (ZWIN	9.8
	422426	W79117	Hs.58559	ESTs	9.7
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical p	9.7
	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN ALU SU	9.4
50	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP)	9.4
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothetical p	9.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	9.1
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP40	9.1
55	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.0
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.0
	426427	M86699	Hs.169840	TTK protein kinase	9.0
	429538	BE182592	Hs.11261	small proline-rich protein 2A	9.0
	446232	AI281848	Hs.194691	retinoic acid induced 3	8.9
60	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	8.9
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDNA clo	8.9
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	8.9
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.9
	430486	BE062109	Hs.241551	chloride channel, calcium activated, family m	8.7
65	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	8.7
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	8.7
	407642	AW178963		gb:MR0-ST0032-200899-001-b11 ST0032 Homo sapi	8.7
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily, m	8.7
	458027	L49054	Hs.85195	myeloid leukemia factor 1	8.4
70	424086	AI351010	Hs.102267	lysyl oxidase	8.3
	420092	AA814043	Hs.88045	ESTs	8.3
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	8.3
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human, odont	8.2
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	8.2
75	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adren	8.2
	440834	AA907027	Hs.128606	ESTs	8.2
	452724	R84810	Hs.30464	cyclin E2	8.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (from c	8.1
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine h	8.0
80	429228	AI553633	Hs.337139	ESTs	7.9
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome region 14	7.9
	425710	AF030880	Hs.159275	solute carrier family, member 4	7.8
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	7.8

435159	AA668879	Hs.116649	ESTs	7.7
439232	N48590	Hs.46693	ESTs	7.7
437616	AI797163	Hs.207954	ESTs	7.6
406554			Target Exon	7.4
433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	7.4
424098	AF077374	Hs.139322	small proline-rich protein 3	7.3
418134	AA397769	Hs.86617	ESTs	7.2
446364	AB006624	Hs.14912	KIAA0286 protein	7.2
447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (yeast	7.1
414148	BE084049		gb:PM0-BT0651-270400-003-f02 BT0651 Homo sapi	7.0
429548	AW138872	Hs.135288	ESTs	7.0
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	7.0
450192	AA263143	Hs.24596	RAD51-interacting protein	7.0
450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila ho	6.9
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone COL0454	6.9
427821	AA470158	Hs.98202	ESTs	6.9
436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794 prote	6.9
425761	AW664214	Hs.196729	ESTs	6.9
450028	AI912012	Hs.200737	ESTs	6.8
409719	AI769160	Hs.108681	Homo sapiens brain tumor associated protein N	6.8
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	6.8
413573	AI733859	Hs.149089	ESTs	6.8
422330	D30783	Hs.115263	epiregulin	6.8
454988	AW850140		gb:IL3-CT0219-261099-023-D11 CT0219 Homo sapi	6.8
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E2	6.8
403471			Target Exon	6.7
409041	AB033025	Hs.50081	KIAA1199 protein	6.7
407839	AA045144	Hs.161566	ESTs	6.6
415652	T79213	Hs.272073	ESTs	6.6
420900	AL045633	Hs.44269	ESTs	6.6
444271	AW452569	Hs.149804	ESTs	6.6
410153	BE311926	Hs.15830	hypothetical protein FLJ12691	6.5
448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.5
431622	AW979271	Hs.293184	ESTs	6.5
457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202	6.4
424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	6.4
414812	X72755	Hs.77367	monokine induced by gamma interferon	6.4
425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	6.3
446435	AW206737	Hs.253582	ESTs	6.3
421948	L42583	Hs.334309	keratin 6A	6.3
419335	AW960146	Hs.284137	hypothetical protein FLJ12888	6.3
429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-protein	6.2
406747	AI925153	Hs.217493	annexin A2	6.2
453884	AA355925	Hs.36232	KIAA0186 gene product	6.2
423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapiens c	6.2
421773	W69233	Hs.112457	ESTs	6.2
457435	AW972024	Hs.142653	ret finger protein	6.1
450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HEMBB10	6.1
427043	AA397679	Hs.3991	ESTs	6.1
409723	AW885757	Hs.257862	ESTs	6.1
459462	AA481396	Hs.105167	ESTs	6.1
423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	6.0
427217	AA399272	Hs.144341	ESTs	6.0
441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein [H.s	6.0
437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferritin a	6.0
430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	5.9
416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein [H.s	5.9
413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.9
434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced prote	5.9
414299	AA142989	Hs.71730	ESTs	5.8
439292	AA090421	Hs.5555	hypothetical protein MGC5347	5.8
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin (140	5.8
413625	AW451103	Hs.71371	ESTs	5.8
416049	AI970536	Hs.16603	hypothetical protein FLJ13163	5.8
415064	AA159804	Hs.149305	hypothetical protein MGC2603	5.7
425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor ty	5.7
451381	BE241831	Hs.172330	hypothetical protein MGC2705	5.7
415900	Z43758	Hs.26037	ESTs	5.7
444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
449611	AI970394	Hs.197075	ESTs	5.7
420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapi	5.7
438639	AI278360	Hs.31409	ESTs	5.7
414972	BE263782	Hs.77695	KIAA0008 gene product	5.7
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	5.6
428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone COL0042	5.6
407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.6
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	5.5
432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase 3)	5.5
451307	AW293207	Hs.211516	ESTs	5.5
441531	AW291239	Hs.271111	ESTs	5.5
418663	AK001100	Hs.41690	desmocollin 3	5.5
410659	AI080175	Hs.68826	ESTs	5.5
432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo sapi	5.5

	431255	AA497043	Hs.115685	ESTs	5.5
	407366	AF026942		gb:Homo sapiens clg33 mRNA, partial sequence.	5.5
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	5.4
	418502	R99288	Hs.35152	ESTs	5.4
5	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens cDNA	5.4
	439579	AF086400		gb:Homo sapiens full length insert cDNA clone	5.4
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (gale	5.4
	408536	AW381532	Hs.135188	ESTs	5.4
	408758	NM_003686	Hs.47504	exonuclease 1	5.4
10	451411	AA017492	Hs.135655	EST	5.4
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.3
	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	5.3
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin 6)	5.2
	420026	AI831190	Hs.166676	ESTs	5.2
15	427356	AW023482	Hs.97849	ESTs	5.2
	420440	NM_002407	Hs.97644	mammaglobin 2	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
	445259	AI798994	Hs.152923	ESTs	5.2
	457345	AI699933	Hs.192175	ESTs	5.2
20	453161	AA628608	Hs.61656	ESTs	5.2
	445019	AI205540	Hs.281295	ESTs	5.2
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	5.2
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	5.2
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	5.2
25	443179	AI928402	Hs.6933	hypothetical protein FLJ12684	5.2
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, choline, al	5.2
	441020	W79283	Hs.35962	ESTs	5.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	5.1
	419520	AB009303	Hs.90800	matrix metalloproteinase 16 (membrane-inserte	5.1
30	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	5.1
	405547			NM_018833*:Homo sapiens transporter 2, ATP-bi	5.1
	435206	AI432364	Hs.160594	ESTs	5.1
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	5.1
	439223	AW238299	Hs.250618	UL16 binding protein 2	5.1
35	413251	AI932903	Hs.211535	ESTs	5.1
	426320	W47595	Hs.169300	transforming growth factor, beta 2	5.1
	458829	AI557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3',	5.0
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	5.0
	432473	AI202703	Hs.152414	ESTs	5.0
40	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino acid	5.0
	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	5.0
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, protein-gl	5.0
	432867	AW016936	Hs.233364	ESTs	5.0
	449448	D60730	Hs.57471	ESTs	5.0
45	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (from c	4.9
	405657			C7000246:gi|72477|pir||DVHY1C multidrug resis	4.9
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1	4.9
	446704	AI337228	Hs.197083	ESTs	4.9
	434376	AA631492	Hs.23921	hypothetical protein DKFZp547A023	4.9
50	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypothetic	4.9
	421155	H87879	Hs.102267	lysyl oxidase	4.9
	443335	T89697	Hs.16645	ESTs	4.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell growt	4.8
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.8
55	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elast	4.8
	441720	AI346487	Hs.28739	ESTs	4.8
	442980	AA857025	Hs.8878	kinesin-like 1	4.8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.8
	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosome seg	4.8
60	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosyltran	4.8
	418939	AW630803	Hs.89497	lamin B1	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
	411958	AA099020		gb:zn45h01.s1 Stratagene HeLa cell s3 937216	4.7
	433858	N69243	Hs.192974	hypothetical protein FLJ12735	4.7
65	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	4.7
	418379	AA218940	Hs.137516	fidgetin-like 1	4.7
	401747			Homo sapiens keratin 17 (KRT17)	4.7
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	4.7
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	4.7
70	457465	AW301344	Hs.122908	DNA replication factor	4.6
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.6
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapi	4.6
	401137			Target Exon	4.6
	401575			Target Exon	4.6
75	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL0667	4.6
	421978	AJ243662	Hs.110196	NICE-1 protein	4.6
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.6
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PLACE10	4.6
	450510	AA010056	Hs.242998	ESTs	4.6
80	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.6
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, type II	4.6
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino acid	4.5
	449416	AI651016	Hs.246311	ESTs	4.5

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416168	H23687		gb:yn72d12.r1 Soares adult brain N2b5HB55Y Ho	4.5
447033	AI357412	Hs.157601	ESTs	4.5
446353	AI290919	Hs.153661	ESTs	4.5
443715	AI583187	Hs.9700	cyclin E1	4.5
454707	AW814989		gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapi	4.5
435435	T89473	Hs.192328	ESTs	4.5
412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	4.4
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	4.4
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.4
430919	AA489041	Hs.295448	ESTs	4.4
435313	AI769400	Hs.189729	ESTs	4.4
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.4
433322	H50621	Hs.134156	ESTs, Weakly similar to I38022 hypothetical p	4.4
416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (p150)	4.4
408908	BE296227	Hs.250822	serine/threonine kinase 15	4.4
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein ho	4.4
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.4
414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, cl	4.4
418216	AA662240	Hs.283099	AF15q14 protein	4.4
446252	AI283125	Hs.150009	ESTs	4.4
447519	U46258	Hs.339665	ESTs	4.4
425916	NM_006786	Hs.162200	urotensin 2	4.3
409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalinin (10	4.3
416320	H47867	Hs.34024	ESTs	4.3
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth facto	4.3
441582	BE550200	Hs.127197	ESTs	4.3
414132	AI801235	Hs.48480	ESTs	4.3
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homology to	4.3
411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (RHAMM)	4.3
433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.3
428613	AB037749	Hs.186928	KIAA1328 protein	4.3
425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter tra	4.3
447078	AW885727	Hs.301570	ESTs	4.3
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	4.3
428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.3
405708			Target Exon	4.3
433405	AW157566	Hs.156892	ESTs	4.3
456443	AW967500	Hs.133543	ESTs	4.3
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	4.2
448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	4.2
412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequence	4.2
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.2
455365	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi	4.2
452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothetical p	4.2
430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothetical p	4.2
423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	4.2
427666	AI791495	Hs.180142	calmodulin-like skin protein	4.2
444602	AI174456	Hs.271925	ESTs, Moderately similar to I38022 hypothetic	4.2
417791	AW965339	Hs.111471	ESTs	4.2
444266	AI424984	Hs.125465	ESTs	4.2
439394	AA149250	Hs.56105	ESTs	4.2
457336	AW969657	Hs.291029	ESTs	4.2
429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothetical p	4.2
404440			NM_021048:Homo sapiens melanoma antigen, fami	4.2
449228	AJ403107	Hs.148590	protein related with psoriasis	4.2
437144	AL049466	Hs.7859	ESTs	4.2
448599	AW860912		gb:QV0-CT0387-170200-121-c05 CT0387 Homo sapi	4.2
431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like protein	4.2
419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.2
444361	W76027	Hs.23920	hypothetical protein FLJ11105	4.2
458116	AW977549	Hs.47367	KIAA1785 protein	4.1
444105	AW189097	Hs.166597	ESTs	4.1
426010	AA136563	Hs.1975	hypothetical protein FLJ21007	4.1
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor, cl	4.1
408096	BE250162	Hs.83765	dihydrofolate reductase	4.1
457620	AA602711	Hs.336753	EST	4.1
402048			Target Exon	4.1
427025	AA397589	Hs.97523	ESTs	4.1
423515	AA327017	Hs.162204	ESTs	4.1
423891	AK002042	Hs.134795	Homo sapiens cDNA FLJ11180 fis, clone PLACE10	4.1
455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo sapi	4.1
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	4.1
426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	4.1
423738	AB002134	Hs.132195	airway trypsin-like protease	4.1
448243	AW369771	Hs.52620	integrin, beta 8	4.1
411559	BE144081		gb:MR0-HT0165-030200-007-d06 HT0165 Homo sapi	4.1
423553	AA405635	Hs.96854	ESTs, Weakly similar to DYLX_HUMAN CYTOPLASMI	4.1
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	4.1
424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypothetical p	4.1
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE10	4.1
424745	AA214618	Hs.152759	activator of S phase kinase	4.0
433384	AI021992	Hs.124244	ESTs	4.0
448995	AI613276	Hs.5662	guanine nucleotide binding protein (G protein	4.0

	448504	AI858128	Hs.171136	ESTs	4.0
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (from c	4.0
	432441	AW292425	Hs.163484	ESTs	4.0
	424794	M85646	Hs.210696	ESTs	4.0
5	432184	AW971125		gb:EST383212 MAGE resequences, MAGL Homo sapi	4.0
	408321	AW405882	Hs.44205	cortistatin	4.0
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	4.0
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.0
	447724	AW298375	Hs.24477	ESTs	4.0
10	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y79AA10	4.0
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.0
	420252	AW270404	Hs.193161	ESTs	4.0
	412811	H06382	Hs.21400	ESTs	4.0
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	4.0
15	438390	AI422017		gb:tf45f12.x1 NCI_CGAP_Brn23 Homo sapiens cDN	4.0
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	4.0
	429900	AA460421	Hs.30875	ESTs	4.0
	421270	H56037	Hs.108146	ESTs	3.9
	430733	AW975920	Hs.283361	ESTs	3.9
20	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo sapi	3.9
	424131	AA335714	Hs.199665	ESTs	3.9
	457059	BE561665	Hs.177677	exosome component Rrp40	3.9
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	3.9
	404959			NM_025001*:Homo sapiens hypothetical protein	3.9
25	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.9
	428536	AI143139	Hs.2288	visinin-like 1	3.9
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H.sapi	3.9
	432757	AF113013	Hs.278919	PRO0806 protein	3.9
	418686	Z36830	Hs.87268	annexin A8	3.9
30	437845	AA769578	Hs.90488	ESTs	3.9
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein produ	3.9
	419312	AA831850	Hs.58149	hypothetical protein MGC14136	3.9
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	3.9
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	3.9
35	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.9
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HEMBB10	3.9
	442163	AI791749	Hs.128896	ESTs	3.9
	438656	H85310	Hs.209456	ESTs, Weakly similar to NG22 [H.sapiens]	3.9
	406560			ENSP00000016943*:CDNA	3.8
40	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33)	3.8
	404132			Target Exon	3.8
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46668	ESTs	3.8
	433289	AF005258		gb:Homo sapiens laminin alpha 3b chain mRNA,	3.8
45	436149	AI754308	Hs.159452	ESTs	3.8
	446292	AF081497	Hs.279682	Rh type C glycoprotein	3.8
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bindi	3.8
	405545			(MDR/TAP) (TAP2)	3.8
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	3.8
50	409687	T51125	Hs.8493	ESTs	3.8
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo sapie	3.8
	415532	R14780	Hs.12826	ESTs	3.8
	402047	AK001921	Hs.169575	hypothetical protein MGC2550	3.8
	415317	Z43388		gb:HSC1AF121 normalized infant brain cDNA Hom	3.8
55	438777	AA825487	Hs.142179	ESTs	3.8
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolysis bu	3.7
	405943			Target Exon	3.7
	430686	NM_001942	Hs.2633	desmoglein 1	3.7
60	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.7
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	3.7
	418582	BE244318	Hs.213194	hypothetical protein MGC10895	3.7
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.7
	433849	BE465884	Hs.280728	ESTs	3.7
65	449592	AI655494	Hs.195718	ESTs	3.7
	453028	AB006532	Hs.31442	RecQ protein-like 4	3.7
	435612	AA693537	Hs.321411	ESTs	3.7
	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clone 22d	3.7
	418735	N48769	Hs.44609	ESTs	3.7
70	444707	AI188613	Hs.41690	desmocollin 3	3.7
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.7
	450613	AI702055		gb:tq20g10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	3.7
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.7
	432837	AA310693	Hs.87329	HSPC072 protein	3.7
75	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SU	3.7
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.7
	449978	AI806335	Hs.200829	ESTs, Weakly similar to T30171 ninein - mouse	3.7
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapi	3.7
	409582	R27430	Hs.271565	ESTs	3.6
80	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANTIGEN	3.6
	458446	AW394104	Hs.43744	ESTs, Moderately similar to I54374 gene NF2 p	3.6
	433040	H70423	Hs.300511	ESTs	3.6
	452193	AA987351	Hs.184993	ESTs	3.6

	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rect	3.6
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.6
	459575	BE080825		gb:QV1-BT0631-180200-078-c08 BT0631 Homo sapi	3.6
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.6
5	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.6
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.6
	427131	AA448460	Hs.112017	GE36 gene	3.6
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	3.6
	420373	AW968228		gb:EST380198 MAGE resequences, MAGJ Homo sapi	3.6
10	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromosomes 2	3.6
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.6
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA10	3.6
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.6
	434321	AA629368		gb:zu78a11.s1 Soares_testis_NHT Homo sapiens	3.6
15	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	3.6
	427335	AA448542	Hs.251677	G antigen 7B	3.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	3.6
	426749	AI623718	Hs.105618	ESTs	3.6
20	443899	AW842283	Hs.79933	cyclin I	3.6
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H.sapi	3.6
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	mammaglobin 1	3.5
	408867	AA437199	Hs.656	cell division cycle 25C	3.5
25	428508	BE252383	Hs.184668	SBBI31 protein	3.5
	431120	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens cDNA	3.5
	401780			NM_005557*:Homo sapiens keratin 16 (focal non	3.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sapiens	3.5
	456671	AB011142	Hs.114293	KIAA0570 gene product	3.5
30	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP10 (HT	3.5
	435244	N77221	Hs.187824	ESTs	3.5
	436246	AW450963	Hs.119991	ESTs	3.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	3.5
	443113	AI040686	Hs.132908	ESTs	3.5
35	443341	AW631480	Hs.8688	ESTs	3.5
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.5
	418347	AA216419		gb:nc16e03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA	3.5
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo sapi	3.5
	408633	AW963372	Hs.46677	PRO2000 protein	3.5
40	427878	C05766	Hs.181022	CGI-07 protein	3.5
	419945	AW290975	Hs.118923	ESTs	3.5
	448372	AW445166	Hs.170802	ESTs	3.5
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen 1NFLS	3.5
	411274	NM_002776	Hs.69423	kallikrein 10	3.5
45	400666			NM_002425:Homo sapiens matrix metalloproteina	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
	402639			Target Exon	3.4
	454891	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapi	3.4
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet-de	3.4
50	456296	AA829976	Hs.239114	mannosidase, alpha, class 1A, member 2	3.4
	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.4
	429274	AI379772	Hs.99206	ESTs	3.4
	430704	AW813091	Hs.335799	ESTs	3.4
	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo sapi	3.4
55	451778	AI826131	Hs.71243	ESTs, Weakly similar to zinc finger protein [	3.4
	430397	AI924533	Hs.105607	bicarbonate transporter related protein 1	3.4
	432113	AA935065	Hs.152385	ESTs	3.4
	449722	BE280074	Hs.23960	cyclin B1	3.4
	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapi	3.4
60	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.4
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.4
	417009	AA191719	Hs.314714	ESTs	3.4
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moiety X	3.4
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen induci	3.4
65	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PLACE20	3.4
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	3.4
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens cDNA	3.4
	403274			Target Exon	3.4
	435360	AF105366	Hs.4876	solute carrier family 12 (potassium/chloride	3.4
70	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2 prote	3.4
	443462	AI064690	Hs.171176	ESTs	3.3
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens cDNA	3.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from c	3.3
75	449101	AA205847	Hs.23016	G protein-coupled receptor	3.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	3.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	3.3
	419751	AW195581	Hs.93121	KIAA0761 protein	3.3
	404782			C7001692*:gi|6724096|gb|AAF26844.1| (AF195021	3.3
80	415613	R20233		gb:yg18h11.r1 Soares infant brain 1NIB Homo s	3.3
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical p	3.3
	406599			Target Exon	3.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.3

	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo sapi	3.3
	421107	AA283822	Hs.55606	ESTs, Weakly similar to S47072 finger protein	3.3
	436985	AA740946	Hs.150895	ESTs	3.3
	443903	AI220547	Hs.135223	ESTs	3.3
5	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (from c	3.3
	447153	AA805202	Hs.315562	ESTs	3.3
	450769	AA057418	Hs.33654	ESTs	3.3
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	3.3
	402481			NM_001821*:Homo sapiens choroideremia-like (R	3.3
10	459394	BE409894	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, complete	3.3
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-1 [H.	3.3
	417708	N74392	Hs.50495	ESTs	3.3
	414869	AA157291	Hs.21479	ubinuclein 1	3.3
	441690	R81733	Hs.33106	ESTs	3.3
15	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.3
	412246	AI160873	Hs.69233	zinc finger protein	3.3
	412903	BE007967	Hs.155795	ESTs	3.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placental)	3.3
	451177	AI969716	Hs.13034	ESTs	3.3
20	409990	AA079337		gb:zm95b09.r1 Stratagene colon HT29 (937221)	3.3
	418462	BE001596	Hs.85266	integrin, beta 4	3.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	3.3
	405196			C2000662*:gi|7512792|pir||T12482 hypothetical	3.3
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA libra	3.3
25	432917	NM_014125	Hs.279812	PRO0327 protein	3.3
	448251	BE280486	Hs.84045	hypothetical protein FLJ20288	3.3
	415025	AW207091	Hs.72307	ESTs	3.3
	420218	AW958037	Hs.286	ribosomal protein L4	3.2
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB10	3.2
30	447762	AI939461	Hs.161370	ESTs	3.2
	414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731 Homo sapi	3.2
	445038	AI635444	Hs.143917	dJ467N11.1 protein	3.2
	448666	NM_014953	Hs.323346	KIAA1008 protein	3.2
	402800			Target Exon	3.2
35	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.2
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cere	3.2
	455203	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapi	3.2
	459666	W27362		gb:30g7 Human retina cDNA randomly primed sub	3.2
	401458			Target Exon	3.2
40	432361	AI378562	Hs.159585	ESTs	3.2
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLICING F	3.2
	405336			Target Exon	3.2
	446563	BE326588	Hs.141454	ESTs	3.2
	449276	AW241510	Hs.252713	ESTs	3.2
45	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo sapi	3.2
	420591	X53655	Hs.99171	neurotrophin 3	3.2
	401486			C4000647*:gi|4758508|ref|NP_004253.1| airway	3.2
	432979	AA573263	Hs.120860	ESTs	3.2
	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.2
50	438325	AA804258	Hs.123229	ESTs	3.2
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha-1C-a	3.2
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cysteine-r	3.2
	421777	BE562088	Hs.108196	HSPC037 protein	3.2
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone ADKA02	3.2
55	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone LNG004	3.2
	402337			Target Exon	3.2
	420930	AW888650		gb:CM4-NT0007-130500-551-f06 NT0007 Homo sapi	3.2
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HEMBA10	3.2
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.1
60	437641	AA811452	Hs.291911	ESTs	3.1
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
	434208	T92641	Hs.127648	hypothetical protein PRO2176	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.1
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.1
65	458923	Y12812	Hs.24422	regulatory factor X-associated protein	3.1
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A receptor, ep	3.1
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDNA clo	3.1
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevisiae,	3.1
	445885	AI734009	Hs.127699	KIAA1603 protein	3.1
70	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.1
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine protein k	3.1
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo sapi	3.1
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription factor	3.1
	455987	BE178323		gb:RC3-HT0600-240400-023-g05 HT0600 Homo sapi	3.1
75	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA, part	3.1
	423887	AL080207	Hs.134585	DKFZP434G232 protein	3.1
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.1
	447815	AI432199	Hs.247084	ESTs	3.1
	441974	AI683782	Hs.128245	ESTs	3.1
80	446474	AI301227	Hs.150186	hypothetical protein DKFZp566K1946	3.1
	452166	AI948607	Hs.264680	ESTs	3.1
	451659	BE379761	Hs.14248	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1

	447701	BE619526	Hs.255527	hypothetical protein MGC14128	3.1
	443648	AI085377	Hs.143610	ESTs	3.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.1
	449441	AI656040	Hs.196532	ESTs	3.1
5	458145	AI239457	Hs.130794	ESTs	3.1
	444588	AI221321	Hs.167559	ESTs	3.1
	450832	AW970602	Hs.105421	ESTs	3.1
	449425	AW103433	Hs.195684	ESTs	3.1
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT2RP30	3.1
10	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	3.1
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB55Y Ho	3.1
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S. cere	3.1
	404107			Target Exon	3.1
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.1
15	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	3.1
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM040	3.1
	442824	BE178065	Hs.144081	ESTs	3.1
	435061	AI651474	Hs.163944	ESTs	3.1
	420589	AA419360	Hs.192708	ESTs	3.0
20	434569	AI311295	Hs.8294	KIAA0196 gene product	3.0
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B, membe	3.0
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional act	3.0
	402892			Target Exon	3.0
	406087			Target Exon	3.0
25	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Ho	3.0
	435990	AI015862	Hs.131793	ESTs	3.0
	442577	AA292998	Hs.163900	ESTs	3.0
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter tra	3.0
30	458154	AW816379	Hs.335018	ESTs	3.0
	416809	N67253	Hs.271691	ESTs	3.0
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.0
	437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens cDN	3.0
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.0
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810027O1	3.0
	445505	AI971156	Hs.148891	ESTs	3.0
	425005	AI565851		gb:tn07g03.x1 NCI_CGAP_Bm25 Homo sapiens cDN	3.0
	435673	AF202961	Hs.284200	Homo sapiens uncharacterized gastric protein	3.0
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA	3.0
40	453509	AL040021	Hs.252674	ESTs, Weakly similar to alternatively spliced	3.0
	455750	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapi	3.0
	407777	AA161071	Hs.71465	squalene epoxidase	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	3.0
	417734	Z42667	Hs.6724	ESTs	3.0
45	449676	AW380579	Hs.209657	ESTs	3.0
	445425	AI223511	Hs.300722	ESTs	3.0
	427061	AB032971	Hs.173392	KIAA1145 protein	3.0
	433584	AW295399		gb:UI-H-BI2-ahv-h-03-0-UI.s1 NCI_CGAP_Sub4 Ho	3.0
	444477	AI150548	Hs.23155	ESTs	3.0
50	446255	AI283257	Hs.257090	ESTs	3.0
	400612			C10001034:gi|7513113|pir||T13078 KIAA0992 pro	3.0
	450841	AI741466	Hs.270515	ESTs	3.0
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	3.0
	433871	W02410	Hs.205555	ESTs	3.0
55	401994			Target Exon	3.0
	449272	AW137656	Hs.197645	ESTs	3.0
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	3.0
	400250			Eos Control	3.0
	408015	AW136771	Hs.244349	epidermal differentiation complex protein lik	3.0
60	436414	BE264633	Hs.143638	WD repeat domain 4	3.0
	432220	AI571306	Hs.232224	ESTs	3.0
	420831	AA280824	Hs.190035	ESTs	3.0
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_Ut2 Homo sapiens cDNA	3.0
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG repeat r	3.0
65	428262	AI651324	Hs.7298	biphenyl hydrolase-like (serine hydrolase; br	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone COL070	3.0
	417308	H60720	Hs.81892	KIAA0101 gene product	3.0
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.0
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2 (dihy	3.0
70	423556	R72694	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1	3.0
	426890	AA393167	Hs.41294	ESTs	2.9
	436333	AA709270	Hs.136672	EST	2.9
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.9
	402556			C1001383*:gi|538695|pir||A61183 hypothetical	2.9
75	411098	AW817238		gb:QV0-ST0247-090200-105-b07 ST0247 Homo sapi	2.9
	435399	AA679463		gb:ac50c03.s1 Stratagene hNT neuron (937233)	2.9
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.9
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone HEP016	2.9
	410658	AW105231	Hs.192035	ESTs	2.9
80	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	2.9
	412279	BE245511		gb:TCBAP1D3235 Pediatric pre-B cell acute lym	2.9
	405277			ENSP00000211621*:Keratin, type II cytoskeleta	2.9
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapiens c	2.9

	455319	AW895387		gb:QV4-NN0038-300300-157-c10 NN0038 Homo sapi	2.9
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	2.9
	413306	AW303544	Hs.118654	ESTs	2.9
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.9
5	434423	NM_006769	Hs.3844	LIM domain only 4	2.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.9
	412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapi	2.9
	436148	BE005252	Hs.321583	Homo sapiens cDNA FLJ20779 fis, clone COL0507	2.9
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.9
10	404981			ENSP00000252242*:Keratin, type II cytoskeleta	2.9
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced by tu	2.9
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA, part	2.9
	401760			Target Exon	2.9
	443859	NM_013409	Hs.9914	follistatin	2.9
15	404253			NM_021058*:Homo sapiens H2B histone family, m	2.9
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	2.9
	435867	AA954229	Hs.114052	ESTs	2.9
	429035	BE549781	Hs.270475	ESTs	2.9
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega-hydr	2.9
20	446417	AI299050		gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA	2.9
	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.9
	452452	BE393822	Hs.29645	Homo sapiens mRNA; cDNA DKFZp761C029 (from cl	2.9
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	2.9
	450698	W31489	Hs.95044	ESTs, Weakly similar to I38022 hypothetical p	2.9
25	439430	AF124250	Hs.6564	cervical cancer anti-estrogen resistance 3	2.9
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.9
	438268	AA782163	Hs.293502	ESTs	2.9
	401781			Target Exon	2.9
	439625	AF086453	Hs.58611	ESTs	2.9
30	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetical p	2.9
	410743	AA089474	Hs.272153	ESTs	2.9
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog o	2.9
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME	2.9
	443479	AF027219	Hs.9443	zinc finger protein 202	2.9
35	442601	AI684969	Hs.46772	ESTs	2.9
	405932			C15000305:gi|3806122|gb|AAC69198.1| (AF097887	2.9
	405454			C12000541:gi|5729884|ref|NP_006539.1| IGF-II	2.9
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	2.9
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	2.9
40	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	2.9
	414581	AA256213	Hs.72010	ESTs	2.9
	411268	AK000512	Hs.69388	hypothetical protein FLJ20505	2.9
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_1NFLS	2.9
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	2.9
45	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	2.9
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.9
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein produ	2.9
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical p	2.9
	435711	AF226667	Hs.58553	CTP synthase II	2.9
50	419088	AI538323	Hs.52620	integrin, beta 8	2.8
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clone IF	2.8
	429299	AI620463	Hs.293984	hypothetical protein MGC13102	2.8
	451702	AW665452	Hs.246503	ESTs	2.8
	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.8
55	405281			NM_002864:Homo sapiens pregnancy-zone protein	2.8
	438161	BE089028	Hs.20158	ESTs, Weakly similar to S34159 transcription	2.8
	409103	AF251237	Hs.112208	XAGE-1 protein	2.8
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.8
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mis5, S	2.8
60	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.8
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-like	2.8
	452730	AA027952	Hs.165216	ESTs	2.8
	413083	BE064528		gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapi	2.8
	437030	AA742577	Hs.303781	EST	2.8
65	438113	AI467908	Hs.8882	ESTs	2.8
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone LNG096	2.8
	440994	AI160011	Hs.193341	ESTs	2.8
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HEMBA10	2.8
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	2.8
70	410310	J02931	Hs.62192	coagulation factor III (thromboplastin, tissu	2.8
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.8
	433788	AI810534	Hs.161275	ESTs	2.8
	403806			Target Exon	2.8
	437182	AL080098		gb:Homo sapiens mRNA; cDNA DKFZp564C1072 (fro	2.8
75	453955	AW579207	Hs.304666	ESTs, Weakly similar to I78885 serine/threoni	2.8
	420795	AA323037	Hs.128645	sorting nexin 16	2.8
	452696	AI826645	Hs.211534	ESTs	2.8
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.8
	438052	AA776564	Hs.41891	zinc finger 1111	2.8
80	441755	AW450826	Hs.127786	ESTs	2.8
	427961	AW293165	Hs.143134	ESTs	2.8
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	2.8
	450451	AW591528	Hs.202072	ESTs	2.8

	406831	N73448	Hs.50272	ESTs, Weakly similar to RS1A_HUMAN 40S RIBOSO	2.8
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.8
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.8
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.8
5	448979	AI611378	Hs.192610	ESTs	2.8
	409143	AW025980	Hs.138965	ESTs, Weakly similar to I38022 hypothetical p	2.8
	410664	NM_006033	Hs.65370	lipase, endothelial	2.8
	444550	BE250716	Hs.87614	ESTs	2.8
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.8
10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.8
	445941	AI267371	Hs.172636	ESTs	2.8
	459719	AW749511	Hs.301554	ESTs, Weakly similar to AF133298 1 cytochrome	2.8
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP20	2.8
	456456	AA477609	Hs.89563	nuclear cap binding protein subunit 1, 80kD	2.8
15	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothetical p	2.8
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	2.8
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.8
	439846	T63959	Hs.228320	hypothetical protein FLJ23537	2.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	2.8
20	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.8
	455091	BE079752		gb:RC6-BT0627-140200-011-A04 BT0627 Homo sapi	2.8
	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo sapi	2.8
	452571	W31518	Hs.34665	ESTs	2.8
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	2.8
25	426343	NM_014642	Hs.169387	KIAA0036 gene product	2.8
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated	2.8
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromosomes 4	2.7
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.7
	429128	AA446869	Hs.119316	ESTs	2.7
30	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	2.7
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.7
	403763			NM_001059*:Homo sapiens tachykinin receptor 3	2.7
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetic	2.7
	406753	AA505665	Hs.217493	annexin A2	2.7
35	415747	AA381209		gb:EST94257 Activated T-cells I Homo sapiens	2.7
	419875	AA853410	Hs.93557	proenkephalin	2.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical p	2.7
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.7
	456181	L36463	Hs.1030	ras inhibitor	2.7
40	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen 1NFLS	2.7
	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBUL	2.7
	435347	AW014873	Hs.116963	ESTs	2.7
	457339	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC FINGE	2.7
	417398	N78541	Hs.177366	ESTs	2.7
45	408380	AF123050	Hs.44532	diubiquitin	2.7
	437724	AW444828	Hs.184323	ESTs	2.7
	408680	AK000093	Hs.46821	hypothetical protein FLJ20086	2.7
	454202	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo sapi	2.7
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RecA ho	2.7
50	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.7
	406092			Target Exon	2.7
	447748	AI422023	Hs.161338	ESTs	2.7
	443236	AI079496	Hs.134169	ESTs	2.7
	433743	AF075312	Hs.236760	Homo sapiens clone HQ0262	2.7
55	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related protein	2.7
	405675			Target Exon	2.7
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila inaD-like)	2.7
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	2.7
	448592	N69546	Hs.44563	hypothetical protein	2.7
60	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA10	2.7
	407287	AI678812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	2.7
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
	412977	AA125910	Hs.191461	ESTs	2.7
	431721	AB032996	Hs.268044	KIAA1170 protein	2.7
65	417357	AF260257	Hs.131917	retinitis pigmentosa GTPase regulator interac	2.7
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the p	2.7
	416294	D86980	Hs.79170	KIAA0227 protein	2.7
	458201	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Cyclop	2.7
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog 2	2.7
70	401230			NM_014191*:Homo sapiens sodium channel, volta	2.7
	422058	AA862231	Hs.334443	ESTs	2.7
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.7
	430152	AB001325	Hs.234642	aquaporin 3	2.7
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.7
75	443500	AV646388	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (from cl	2.7
	418030	BE207573	Hs.83321	neuromedin B	2.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	2.7
	418869	AW516565		gb:xq01d05.x1 Soares_NHCeC_cervical_tumor Hom	2.7
	431688	AA513906		gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	2.7
80	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	2.7
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.7
	414737	AI160386	Hs.125087	ESTs	2.7
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.7

	446659	AI335361	Hs.226376	ESTs	2.7
	419833	AA251131	Hs.220697	ESTs	2.7
	411819	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo sapi	2.6
	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothetical p	2.6
5	446102	AW168067	Hs.252956	ESTs	2.6
	441408	AI733249	Hs.126897	ESTs	2.6
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse transc	2.6
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	2.6
	421470	R27496	Hs.1378	annexin A3	2.6
10	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	2.6
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.6
	431832	AW276866	Hs.192715	ESTs	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
	433288	AI368873	Hs.271257	ESTs, Weakly similar to I38022 hypothetical p	2.6
15	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothetical p	2.6
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo sapi	2.6
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein [H.s	2.6
	401260			C1001031*:gi|7305041|ref|NP_038876.1| erythro	2.6
20	435136	R27299	Hs.10172	ESTs	2.6
	412108	AA100293	Hs.185043	ESTs	2.6
	434442	AA737415	Hs.152826	ESTs	2.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	2.6
	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase domain 15	2.6
25	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	2.6
	409594	AA076118		gb:zm18e06.s1 Stratagene pancreas (937208) Ho	2.6
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (937208) Ho	2.6
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.6
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor	2.6
30	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.6
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	2.6
	411465	AW847663		gb:IL3-CT0213-280100-056-F02 CT0213 Homo sapi	2.6
	408625	AW243323	Hs.266785	ESTs	2.6
35	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.6
	439245	NM_013381	Hs.6510	thyrotropin-releasing hormone degrading ectoe	2.6
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit of	2.6
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)	2.6
	401050			NM_014155*:Homo sapiens HSPC063 protein (HSPC	2.6
40	405897			Target Exon	2.6
	451153	BE092900		gb:CM2-BT0742-100400-147-h04 BT0742 Homo sapi	2.6
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC FINGE	2.6
	440159	AI637599	Hs.126127	ESTs	2.6
	404184			NM_030903*:Homo sapiens olfactory receptor, f	2.6
45	428552	AW274560	Hs.129520	ESTs	2.6
	401367			Target Exon	2.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated fac	2.6
50	449432	AW451361	Hs.196529	ESTs	2.6
	425062	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger protein)	2.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE10	2.6
	450705	U90304	Hs.25351	iroquois homeobox protein 5	2.6
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.6
55	408391	AW859276		gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapi	2.6
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mouse)	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to ARL-	2.6
	453331	AI240665	Hs.8895	ESTs	2.6
60	447175	AI365208	Hs.293606	ESTs	2.6
	451878	AI821027	Hs.8429	ESTs	2.6
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	2.6
	418282	AA215535	Hs.98133	ESTs	2.6
	434557	AW855466	Hs.271866	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.6
65	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.6
	420894	AA744597	Hs.88854	ESTs	2.6
	435663	AI023707	Hs.134273	ESTs	2.6
	448037	AW195634	Hs.170401	ESTs	2.6
	418067	AI127958	Hs.83393	cystatin E/M	2.6
70	439524	BE542950	Hs.155548	ESTs	2.6
	402298			Target Exon	2.6
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.6
	407471	D55644		gb:Human spleen PABL (pseudoautosomal boundar	2.6
	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, complete	2.6
75	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	2.6
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothetical p	2.6
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from c	2.6
	425415	M13903	Hs.157091	involucrin	2.6
	444826	AI674482	Hs.148441	ESTs	2.6
80	413331	BE083950		gb:PM0-BT0651-260200-001-b11 BT0651 Homo sapi	2.6
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.6
	405041			C3001706*:gi|1345652|sp|P15989|CA36_CHICK COL	2.6
	413864	BE175582		gb:RC5-HT0580-100500-022-C01 HT0580 Homo sapi	2.6

	438746	AI885815	Hs.184727	ESTs	2.5
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapi	2.5
	433365	AF026944	Hs.293797	ESTs	2.5
	412723	AA648459	Hs.335951	hypothetical protein AF301222	2.5
5	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.5
	411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo sapi	2.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapi	2.5
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telencepha	2.5
	414883	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
10	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.5
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (from cl	2.5
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associated fac	2.5
	455549	AW994222		gb:RC3-BN0036-250200-012-e02 BN0036 Homo sapi	2.5
	409676	AA077118	Hs.197298	NS1-binding protein	2.5
15	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	2.5
	429413	NM_014058	Hs.201877	DESC1 protein	2.5
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	2.5
	452834	AI638627	Hs.105685	KIAA1688 protein	2.5
20	424354	NM_014314	Hs.145612	RNA helicase	2.5
	455095	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo sapi	2.5
	431241	AA496799	Hs.36958	ESTs	2.5
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (connexin	2.5
	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.5
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.5
	458175	AW296024	Hs.150434	ESTs	2.5
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein type	2.5
	453379	AA035261	Hs.61753	ESTs	2.5
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothetical p	2.5
30	412313	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo sapi	2.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	2.5
	443757	H05479	Hs.62314	ESTs	2.5
	449300	AI656959	Hs.222165	ESTs	2.5
	434913	AW872860	Hs.11056	RALBP1 protein	2.5
35	448946	AI652855	Hs.23363	hypothetical protein FLJ10983	2.5
	437327	AL353942	Hs.306504	Homo sapiens mRNA; cDNA DKFZp761L23121 (from	2.5
	450262	AW409872	Hs.184846	Homo sapiens, Similar to zinc finger protein	2.5
	453204	R10799	Hs.191990	ESTs	2.5
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	2.5
40	449344	AI640355	Hs.312691	ESTs	2.5
	439436	BE140845	Hs.57868	ESTs	2.5
	449867	AI672379	Hs.122970	hypothetical protein FLJ21579	2.5
	452220	BE158006	Hs.212296	ESTs	2.5
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
45	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapien	2.5
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	2.5
	415030	D31118	Hs.191735	hypothetical protein MGC10520	2.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	2.5
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	2.5
50	400301	X03635	Hs.1657	estrogen receptor 1	2.5
	429386	AK001795	Hs.201179	hypothetical protein FLJ10933	2.5
	423949	AI014546	Hs.130912	ESTs	2.5
	411768	NM_013371	Hs.71979	interleukin 19	2.5
	436961	AW375974	Hs.156704	ESTs	2.5
55	431124	AF284221	Hs.59506	doublesex and mab-3 related transcription fac	2.5
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	2.5
	418717	AI334430	Hs.86984	ESTs	2.5
	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	2.5
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.5
60	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogene hom	2.5
	442966	AI394036	Hs.132237	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECI	2.5
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN ALU SU	2.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor	2.5
	440381	AA917808	Hs.190495	ESTs	2.5
65	403983			Target Exon	2.5
	451340	AW936273		gb:QV0-DT0020-090200-107-g07 DT0020 Homo sapi	2.5
	447888	BE620911	Hs.126889	ESTs	2.5
	441794	AW197794	Hs.253338	ESTs	2.5
	424153	AA451737	Hs.141496	MAGE-like 2	2.5
70	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.5
	435647	AI653240	Hs.49823	ESTs	2.5
	428780	AI478578	Hs.50636	ESTs	2.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.5
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fascin h	2.5
75	428054	AI948688	Hs.266619	ESTs	2.5
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	2.5
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S. cere	2.5
	443362	AI053464	Hs.166505	ESTs	2.5
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.5
80	438214	H06076	Hs.26320	TRABID protein	2.5
	446745	AW118189	Hs.156400	ESTs	2.5
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.5
	426333	AW269088	Hs.118183	hypothetical protein FLJ22833	2.5

TABLE 12B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407642	1007175_1	AW178963 AW845721 BE141041 AW806977 AW845690 AW845691 AW845724 AW176564 AW845705 AW845603 AW845729 AW845722 AW178966 AW845693 AW845585 AW845707 BE141053 BE141046 AW845570 AW845575 BE141043 BE141039 BE141070 AW062443 AW806980 AW845643 AW806969 AW845686 BE141054 BE141040 BE141044 BE141042 AW845571 AW845604 BE141047 BE141071 AW062442 AW845633 AW178968
408391	1055687_1	AW859276 AW859274 AW190959 T91463
408690	107490_1	AW864542 AA056567 AW882724
409594	114249_1	AA076118 AA975618 AA076220
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
409990	116644_1	AA079337 AA079338 AW272100
410008	116812_1	AA079552 BE142525 BE142527
410049	1172307_1	AW579475 AW939654 AW939655
410784	1221005_1	AW803201 BE079700 BE062940
411098	1232093_1	AW817238 AW993985 AW993998
411171	1234393_1	AW820260 AW820332 R94406
411465	1246768_1	AW847663 AW847861 AW861080
411559	1249417_1	BE144081 BE144190 AW851155
411819	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
411958	126717_1	AA099020 AW751275 AW751276 AW751289
412279	1287332_1	BE245511 BE246133 AW935247
412313	1288355_1	AW936832 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW936760 AW936819
412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
412367	1291505_1	AW945964 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039 AW946045 AW946028 AW946036
412879	1334272_1	BE092219 BE092361 BE006789
413083	1348639_1	BE064528 BE064589 BE064561
413331	1361726_1	BE083950 BE084017 BE084016
413864	1395788_1	BE175582 BE175514 BE175505 BE175591 BE175530
414147	142127_-1	BE091634
414148	142133_1	BE084049 AW292907 AA135984
415317	1533847_1	Z43388 F05453 R19673 R20275 H06917
415613	1540602_1	R20233 F12901 T74740
415747	155189_1	AA381209 AA381245 AA167683
416120	1571266_1	H46739 H51513 H19779
416168	1574545_1	H23687 H46460 H40239
416548	1600181_1	H62953 N76608 N72413
417742	1696282_1	R64719 Z44680 R12451
418347	174149_1	AA216419 F03238 AA229517
418869	179863_1	AW516565 AA229762 AA230035
419807	188252_1	R77402 AA262462 AA250988 R06794
420373	193194_1	AW968228 AA259146 W01465
420637	195241_1	AW976153 AA278945 AA747691
420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
422689	219896_1	AW856665 AA315006 AW954733
423733	231476_1	AA330281 AA330232 AW962521
423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
423841	232507_1	AW753967 AA370795 AA331630 AW962550
425005	245908_1	AI565851 AA349656 R24798
429163	300543_1	AA884766 AW974271 AA592975 AA447312
431120	328264_1	AA492588 AA492498 AA492571
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
431688	336609_1	AA513906 AA847734 AI357044
432184	342677_1	AW971125 AA527731 N52655 AI821508 AA532420
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432869	355475_1	AW974094 AA569074 AA602574
433289	36202_-1	AF005258
433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
433644	371919_1	AW342028 AA641080 AA603282
434321	383473_1	AA629368 AW849574 AW849573
435399	405576_1	AA679463 AW813779 AW813709
437182	43421_1	AL080098 AL037472 AA432051
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003
438966	467436_1	AW979074 AA834841 AA828650
438993	467651_1	AA828995 AA834879 AI926361

	439579	47404_1	AF086400 W79232 W73990
	440320	491930_1	AA879294 N67538 AI474541
	444910	624951_1	AI201849 BE069007 AW946544
	446417	676384_1	AI299050 BE256910
5	447197	711623_1	R36075 AI366546 R36167
	448599	770766_1	AW860912 AI540866
	449034	794817_1	AI624049 AW117770 AI858360
	450024	82296_1	AA005129 AA679084 AA694399
	450613	840016_1	AI702055 R89204 R86260
10	451105	859083_1	AI761324 AW880941 AW880937
	451153	86054_1	BE092900 AA015877 AA018521
	451340	86640_1	AW936273 AW340350 AA017208
	454202	1050507_1	AW178363 AW846011 AW845964 AW845988 AW845977 AW846002
	454241	1067807_1	BE144666 BE184942 AW238414 BE184946
15	454707	1230250_1	AW814989 AW814852 AW814808
	454891	1239217_1	AW837349 AW837355 AW882717
	454988	1248607_1	AW850140 AW850195 AW850192
	455091	1252939_1	BE079752 BE079868 BE148989 AW855532 BE148818 BE148815 BE148796
	455092	1252971_1	BE152428 AW855572 AW855607
20	455095	1252987_1	AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605
	455203	1259973_1	AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455319	1279172_1	AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538
	455365	1284681_1	AW948343 AW948341 AW902855 AW984737
25	455549	1324696_1	AW994222 AW994377
	455666	1349545_1	BE065813 BE065788 BE065889 BE065832
	455750	1355998_1	BE075114 BE075283 BE075118
	455838	1374605_1	BE145808 BE145807 BE181883
	455987	1397735_1	BE178323 BE177978
30	457405	333127_1	AA504860 AA504911
	458829	773443_1	AI557388 BE158936
	459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 12C

35

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
40 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400612	9929646	Minus	151513-151662
400666	8118496	Plus	17982-18115,20297-20456
401050	8117628	Minus	78449-79425
401137	2547238	Minus	598-1009
401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
401260	8076883	Minus	86008-86355
401367	9796198	Minus	145356-145807
401458	9187886	Plus	76485-77597
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401575	7229804	Minus	76253-76364
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402048	8072512	Plus	43936-44078
402298	6598824	Plus	36758-37953
402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
402481	9797406	Plus	87891-88991
402556	9863723	Plus	13579-14026
402639	9958129	Minus	20167-22383
402800	6010175	Plus	43921-44049,46181-46273
402892	8086844	Minus	194384-194645
403274	8072441	Minus	104069-104179,105683-105859
403471	9930659	Minus	85867-85963
403763	7229888	Minus	43575-43887
403806	8140491	Plus	146390-146678
403983	8576059	Minus	82441-82701
404107	8099028	Minus	201699-202363
404132	6981900	Plus	11307-12434
404184	4581418	Minus	12652-13548
404253	9367202	Minus	55675-56055
404440	7528051	Plus	80430-81581
404782	9910094	Minus	15455-15589
404959	7407964	Plus	45243-45368
404981	4432779	Minus	20626-20770,22513-22721
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405041	7547195	Plus	121230-121714
405196	7230083	Minus	135716-135851

405277	3980473	Plus	23471-23572
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405336	6094635	Plus	33267-33563
405454	7656575	Plus	133807-134053
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405547	1054740	Plus	124361-124520,124914-125050
405657	4827303	Minus	104132-104293
405675	4557087	Plus	70304-70630
405708	4156182	Plus	55030-55604
405897	6758795	Plus	59828-60535
405932	7767812	Minus	123525-123713
405943	6758796	Plus	20605-20812
406087	9123919	Minus	7234-7626
406092	9123919	Plus	251370-251797,252168-252882
406467	9795551	Plus	182212-182958
406554	7711566	Plus	106956-107121
406560	7711569	Minus	35162-35292
406599	8248616	Plus	10933-11086

TABLE 13A: 465 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES, LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 13A lists about 465 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 12A, except that the ratio was greater than or equal to 1.7, and the 96th percentile value amongst cervical cancers was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
PPDomains: Predicted Protein Domains
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigeneID	PPDomains	Unigene Title	R1
425650	NM_001944	Hs.1925	TM,cadherin,Cadherin_C_term	desmoglein 3 (pemphigus vulgaris antigen)	43.6
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interstitial	38.9
439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
452240	AI591147	Hs.61232	TM	ESTs	27.0
424046	AF027866	Hs.138202	SS,TM,serpin	serine (or cysteine) proteinase inhibitor	24.5
400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stromelysin	20.5
418345	AJ001696	Hs.241407	SS,TM,serpin	serine proteinase inhibitor 13(PI13; se	20.1
423017	AW178761	Hs.227948	SS,serpin	serine (or cysteine) proteinase inhibitor	19.2
428227	AA321649	Hs.2248	SS,TM,IL8	small inducible cytokine subfamily B (Cys	15.9
447164	AF026941	Hs.17518	TM,IBR	Homo sapiens cig5 mRNA, partial sequence	13.8
414764	AW013887	Hs.72047	TM	ESTs	12.9
416661	AA634543	Hs.79440	TM	IGF-II mRNA-binding protein 3	12.7
427585	D31152	Hs.179729	SS,C1q,Collagen	collagen, type X, alpha 1 (Schmid metaphy	12.6
406467			TM,efhand	Target Exon	10.5
428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromelysin 1	10.2
418882	NM_004996	Hs.89433	TM,ABC_membrane,ABC_tran	ATP-binding cassette, sub-family C (CFTR/	9.4
419247	S65791	Hs.89764	TM,KH-domain	fragile X mental retardation 1	9.1
446232	AI281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
424905	NM_002497	Hs.153704	TM,pkinase	NIMA (never in mitosis gene a)-related ki	8.9
422420	U03398	Hs.1524	TM,tubulin,TNF	tumor necrosis factor (ligand) superfamil	8.7
427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA1794 p	6.9
444342	NM_014398	Hs.10887	Lamp	similar to lysosome-associated membrane g	6.8
422330	D30783	Hs.115263	SS,TM,EGF	epiregulin	6.8
447342	AI199268	Hs.19322	SS,lipocalin	Homo sapiens, Similar to RIKEN cDNA 20103	6.8
407839	AA045144	Hs.161566	TM,cadherin,Cadherin_C_term	ESTs	6.6
410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
414812	X72755	Hs.77367	SS,TM,IL8	monokine induced by gamma interferon	6.4
421773	W69233	Hs.112457	SS	ESTs	6.2
413385	M34455	Hs.840	TM,IDO	indoleamine-pyrrole 2,3 dioxygenase	5.9
413753	U17760	Hs.75517	SS,laminin_EGF,laminin_Nterm,adh_short	laminin, beta 3 (nicein (125kD), kalinin	5.8
432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collagenase	5.5
418663	AK001100	Hs.41690	TM,cadherin	desmocollin 3	5.5
407366	AF026942		TM,IBR	gb:Homo sapiens cig33 mRNA, partial seque	5.5
433091	Y12642	Hs.3185	SS,TM,UPAR_LY6	lymphocyte antigen 6 complex, locus D	5.4
408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPase_C, N	ESTs	5.4
420440	NM_002407	Hs.97644	SRCRUteroglobin	mammaglobin 2	5.2
437044	AL035864	Hs.69517	TM	cDNA for differentially expressed CO16 ge	5.1
405547			SS,TM,ABC_membrane,ABC_tran,ig	NM_018833*:Homo sapiens transporter 2, AT	5.1
439223	AW238299	Hs.250618	SS	UL16 binding protein 2	5.1
426320	W47595	Hs.169300	SS,TM,TGF-beta,TGFb_propeptide	transforming growth factor, beta 2	5.1
423634	AW959908	Hs.1690	TM	heparin-binding growth factor binding pro	5.0
426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 3 (E polypeptide, protei	5.0
409744	AW675258	Hs.56265	TM,metalthio,Kelch	Homo sapiens mRNA; cDNA DKFZp586P2321 (fr	4.9

444461	R53734	Hs.25978	TM	ESTs, Weakly similar to 2109260A B cell g	4.8
410361	BE391804	Hs.62661	SS,TM,GBP	guanylate binding protein 1, interferon-i	4.8
423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrophage e	4.8
450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domai	4.8
401575	NA		TM	Target Exon	4.6
428484	AF104032	Hs.184601	TM	solute carrier family 7 (cationic amino a	4.5
425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
431808	M30703	Hs.270833	SS,TM,EGF	amphiregulin (schwannoma-derived growth f	4.3
434699	AA643687	Hs.149425	TM,Nucleoside_tra2	Homo sapiens cDNA FLJ11980 fis, clone HEM	4.3
406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprotein 9	4.2
404440			TM,MAGE	NM_021048:Homo sapiens melanoma antigen,	4.2
449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
444105	AW189097	Hs.166597	TM,cadherin	ESTs	4.1
409632	W74001	Hs.55279	SS,serpin	serine (or cysteine) proteinase inhibitor	4.1
423515	AA327017	Hs.162204	SS,TM,UPAR_LY6	ESTs	4.1
423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
423553	AA405635	Hs.96854	TM	ESTs, Weakly similar to DYLX_HUMAN CYTOPL	4.1
445537	AJ245671	Hs.12844	TM,ras	EGF-like-domain, multiple 6	4.0
446989	AK001898	Hs.16740	TM	hypothetical protein FLJ11036	4.0
428536	AI143139	Hs.2288	TM,efhand,Syndecan	visinin-like 1	3.9
413801	M62246	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	3.9
429441	AJ224172	Hs.204096	Uteroglobin	lipophilin B (uteroglobin family member),	3.9
409601	AF237621	Hs.80828	TM,filamentfilament,C2	keratin 1 (epidermolytic hyperkeratosis)	3.8
439238	N47305	Hs.46668	TM	ESTs	3.8
446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
405545			SS,TM,proteasome,ig,ABC_memb,tranABC_tran,	(MDR/TAP) (TAP2)	3.8
422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
423217	NM_000094	Hs.1640	SS,TM,fn3,vwa,Collagen,Kunitz_BPTI	collagen, type VII, alpha 1 (epidermolysi	3.7
430686	NM_001942	Hs.2633	SS,TM,cadherin,Cadherin_C_term	desmoglein 1	3.7
444707	AI188613	Hs.41690	TM,cadherin	desmocollin 3	3.7
409582	R27430	Hs.271565	TM	ESTs	3.6
408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, delayed-	3.6
400441	M15530	Hs.99879	TM,G-alpha	B-cell growth factor 1 (12kD)	3.6
413278	BE563085	Hs.833	TM,ubiquitinlaminin_G,laminin_EGF,kazal	interferon-stimulated protein, 15 kDa	3.6
426514	BE616633	Hs.170195	SS,TGFb_propeptide,TGF-beta	bone morphogenetic protein 7 (osteogenic	3.6
424927	AW973666	Hs.153850	SS	hypothetical protein C321D2.4	3.6
408591	AF015224	Hs.46452	SS,TM,Uteroglobin	mammaglobin 1	3.5
407756	AA116021	Hs.38260	SS,UCH-1,UCH-2	ubiquitin specific protease 18	3.5
407137	T97307		TM,GDA1_CD39	gb:ye53h05.s1 Soares fetal liver spleen 1	3.5
411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metalloprot	3.5
412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acyltransf	endothelial cell growth factor 1 (platele	3.4
450650	T65617	Hs.101257	TM	hypothetical protein MGC3295	3.4
451778	AI826131	Hs.71243	ig	ESTs, Weakly similar to zinc finger prote	3.4
430397	AI924533	Hs.105607	SS,TM	bicarbonate transporter related protein 1	3.4
449722	BE280074	Hs.23960	TM,cyclin	cyclin B1	3.4
422487	AJ010901	Hs.198267	TM,vwd	mucin 4, tracheobronchial	3.4
449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
418994	AA296520	Hs.89546	SS,TM,lectin_c,sushi,EGF	selectin E (endothelial adhesion molecule	3.3
421379	Y15221	Hs.103982	SS,TM,IL8	small inducible cytokine subfamily B (Cys	3.3
414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cadherin	cadherin 3, type 1, P-cadherin (placental	3.3
418462	BE001596	Hs.85266	SS,TM,integrin_B,fn3	integrin, beta 4	3.3
424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatinase B,	3.3
401486	NA		SS,TM,trypsin	C4000647*:gi|4758508|ref|NP_004253.1| air	3.2
408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, clone AD	3.2
427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	3.2
452934	AA581322	Hs.4213	SS,TM,ig	hypothetical protein MGC16207	3.1
448988	Y09763	Hs.22785	SS,TM	gamma-aminobutyric acid (GABA) A receptor	3.1
439750	AL359053	Hs.57664	TM,integrin_B,Ricin_B_lectinrrm	Homo sapiens mRNA full length insert cDNA	3.1
414696	AF002020	Hs.76918	SS,TM,Patched	Niemann-Pick disease, type C1	3.1
435604	AA625279	Hs.26892	TM	uncharacterized bone marrow protein BM040	3.1
453883	AI638516	Hs.22630	TM,Ets,SAM_PNT	cofactor required for Sp1 transcriptional	3.0
448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,isodh,pkinase,DSPc,Ribosomal_	solute carrier family 6 (neurotransmitter	3.0
444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
437938	AI950087		TM,histone,ig,MHC_I	gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens	3.0
424441	X14850	Hs.147097	TM,histone	H2A histone family, member X	3.0
427061	AB032971	Hs.173392	TM	KIAA1145 protein	3.0
409703	NM_006187	Hs.56009	SS	2'-5'-oligoadenylate synthetase 3 (100 kD	3.0
447313	U92981	Hs.18081	TGF-beta	Homo sapiens clone DT1P1B6 mRNA, CAG repe	3.0
431070	AW408164	Hs.249184	ABC_tran	transcription factor 19 (SC1)	2.9
446269	AW263155	Hs.14559	TM	hypothetical protein FLJ10540	2.9
421190	U95031	Hs.102482	TM,vwd	mucin 5, subtype B, tracheobronchial	2.9
452732	BE300078	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.9
443859	NM_013409	Hs.9914	SS,kazal	follistatin	2.9
446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid omega-	2.9
449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOCH	2.9
418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kinase,SCO1-SenC	ESTs	2.9
431629	AU077025	Hs.265827	SS,tRNA_antiSH2,SH3,pkinase	interferon, alpha-inducible protein (clon	2.8
445873	AA250970	Hs.251946	SS,rrm,PABPpkinase,14-3-3,rrm	poly(A)-binding protein, cytoplasmic 1-li	2.8
438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
410310	J02931	Hs.62192	SS,TM,Tissue_fac	coagulation factor III (thromboplastin, t	2.8

411558	AA102670	Hs.70725	SS,TM	gamma-aminobutyric acid (GABA) A receptor 2.8
413273	U75679	Hs.75257	TM,ig,pkinase	stem-loop (histone) binding protein 2.8
426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product 2.8
433345	AI681545	Hs.152982	SS	hypothetical protein FLJ13117 2.7
452234	AW084176	Hs.223296	TM	ESTs, Weakly similar to I38022 hypothetic 2.7
456181	L36463	Hs.1030	TM,RA,VPS9	ras inhibitor 2.7
408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor,sushi	diubiquitin 2.7
422278	AF072873	Hs.114218	TM,Frizzled,Fz	frizzled (Drosophila) homolog 6 2.7
446839	BE091926	Hs.16244	TM	mitotic spindle coiled-coil related prote 2.7
416250	AA581386	Hs.73452	TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Claudin	hypothetical protein MGC10791 2.7
407287	AI678812		TM,rascadherin	gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens 2.7
412977	AA125910	Hs.191461	TGF-beta	ESTs 2.7
400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of t 2.7
425483	AF231022	Hs.158159	EGF,cadherin,laminin_G	FAT tumor suppressor (Drosophila) homolog 2.7
430152	AB001325	Hs.234642	SS,TM,MIP	aquaporin 3 2.7
444006	BE395085	Hs.10086	SS,TM	type I transmembrane protein Fn14 2.7
418869	AW516565		TM,RasGAP,IQ,WW	gb:xq01d05.x1 Soares_NHCeC_cervical_tumor 2.7
416658	U03272	Hs.79432	SS,TM,EGF,TB	fibrillin 2 (congenital contractural arac 2.6
410290	AA402307	Hs.322844	SS,TM,Sema,TIG,Plexin_repeat	hypothetical protein DKFZp564A176 2.6
419667	AU077005	Hs.92208	SS,TM,disintegrin,Reprolysin,Pep_M12B_propep	a disintegrin and metalloproteinase domai 2.6
406671	AA129547	Hs.285754	TM,pkinase,Plexin_repeat,Sema,TIG,LIM	met proto-oncogene (hepatocyte growth fac 2.6
434444	AI765276	Hs.101257	TM	hypothetical protein MGC3295 2.6
421817	AF146074	Hs.108660	TM,ABC_tran,ABC_membrane,Rhomboid	ATP-binding cassette, sub-family C (CFTR/ 2.6
431890	X17033	Hs.271986	vwa,FG-GAP,integrin_A	integrin, alpha 2 (CD49B, alpha 2 subunit 2.6
452281	T93500	Hs.28792	TGF-beta,TGFb_propeptide	Homo sapiens cDNA FLJ11041 fis, clone PLA 2.6
421506	BE302796	Hs.105097	TM,TK	thymidine kinase 1, soluble 2.6
453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep,Reprolysin	ESTs 2.6
447197	R36075		TM,SDF	gb:yh88b01.s1 Soares placenta Nb2HP Homo 2.5
459688	U72671	Hs.151250	SS,TM,ig	intercellular adhesion molecule 5, telenc 2.5
437412	BE069288	Hs.34744	TM,ABC_tran,ABC_membrane,Rhomboid	Homo sapiens mRNA; cDNA DKFZp547C136 (fro 2.5
429413	NM_014058	Hs.201877	trypsin	DESC1 protein 2.5
424420	BE614743	Hs.146688	TM,MAPEG	prostaglandin E synthase 2.5
427239	BE270447	Hs.174070	TM,UQ_con	ubiquitin carrier protein 2.5
407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170 2.5
431130	NM_006103	Hs.2719	SS,TM,wap	epididymis-specific, whey-acidic protein 2.5
453379	AA035261	Hs.61753	FAN,kringle,trypsin	ESTs 2.5
421733	AL119671	Hs.1420	SS,TM,ig,pkinase	fibroblast growth factor receptor 3 (acho 2.5
452220	BE158006	Hs.212296	TM,integrin_A,FG-GAP	ESTs 2.5
417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186 2.5
440381	AA917808	Hs.190495	TM	ESTs 2.5
441794	AW197794	Hs.253338	TM	ESTs 2.5
439108	AW163034	Hs.6467	SS,TM	synaptogyrin 3 2.5
401103	NA		TM,vwd	C12001233:gi|7305361|ref|NP_038652.1| oto 2.4
430630	AW269920	Hs.2621	TM,cystatin	cystatin A (stefin A) 2.4
430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401 2.4
415621	AI648602	Hs.55468	TM,histone,Sec1sugar_tr	ESTs 2.4
402745			SS,TM,EGF,ldl_recept_b,thyroglobulin_1	NM_002508:Homo sapiens nidogen (enactin) 2.4
407758	D50915	Hs.38365	SS,TM	KIAA0125 gene product 2.4
457570	AA579426		TM	gb:nf37c09.s1 NCI_CGAP_Pr2 Homo sapiens c 2.4
429574	BE268321	Hs.208912	SS,TM	hypothetical protein MGC861 2.4
431211	M86849	Hs.323733	SS,TM,connexin	gap junction protein, beta 2, 26kD (conne 2.4
452865	AI924046	Hs.119567	SS,TM,PMP22_Claudin	ESTs, Weakly similar to A47582 B-cell gro 2.4
420511	AF052692	Hs.98485	SS,TM,connexin	gap junction protein, beta 3, 31kD (conne 2.4
437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969 2.4
437846	AA773866	Hs.244569	TM	esophagus cancer-related gene-2 2.4
418432	M14156	Hs.85112	Insulin	insulin-like growth factor 1 (somatomedin 2.3
438108	AI471795	Hs.287776	TM	vanilloid receptor-related osmotically ac 2.3
453406	AI192987	Hs.61784	pkinase,Furin-like,Recep_L_domain	hypothetical protein FLJ14451 2.3
435542	AA687376	Hs.269533	pkinase,RhoGEF,ig,PH,SH3	ESTs 2.3
434517	AA635690	Hs.337251	TM	hypothetical protein MGC2487 2.3
431630	NM_002204	Hs.265829	SS,TM,FG-GAP,integrin_A	integrin, alpha 3 (antigen CD49C, alpha 3 2.3
422310	AA316622	Hs.98370	SS,TM,fn3,ig,pkinase,Ribosomal_L36e,p450	cytochrome P450, subfamily IIS, polypepti 2.3
441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	Fanconi anemia, complementation group G 2.3
416091	AF295370	Hs.283082	SS,TM,Defensin_beta	defensin, beta 3 2.3
429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membrane-ins 2.3
409402	AF208234	Hs.695	TM,cystatin	cystatin B (stefin B) 2.3
432284	AA532807	Hs.105822	TM,pkinase	ESTs 2.3
408243	Y00787	Hs.624	SS,TM,IL8	interleukin 8 2.3
423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26 2.3
408713	NM_001248	Hs.47042	GDA1_CD39	ectonucleoside triphosphate diphosphohydr 2.3
440502	AI824113	Hs.78281	RGS,GoLoco,RBD	regulator of G-protein signalling 12 2.3
429929	AB014583	Hs.226275	TM	KIAA0683 gene product 2.3
439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylhydrolas 2.3
428953	AA306610	Hs.194676	SS,TM,TNFR_c6,arf,Stathmin,DEAD	tumor necrosis factor receptor superfamil 2.3
439398	AA284267	Hs.221504	SS	ESTs 2.2
440371	BE268550	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA, 2.2
452203	X57522	Hs.158164	SS,TM,ABC_tran,ABC_membrane	transporter 1, ATP-binding cassette, sub- 2.2
407811	AW190902	Hs.40098	SS	cysteine knot superfamily 1, BMP antagoni 2.2
432078	BE314877	Hs.24553	TM	hypothetical protein FLJ12541 similar to 2.2
429113	D28235	Hs.196384	SS,TM,EGF	prostaglandin-endoperoxide synthase 2 (pr 2.2
452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypothetic 2.2
428434	AW363590	Hs.65551	SS	Homo sapiens, Similar to DNA segment, Chr 2.2
429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0 2.2

417903	NM_002342	Hs.1116	SS,TM,ASC,TNFR_c6	lymphotoxin beta receptor (TNFR superfami	2.2
422012	AW403423	Hs.110746	SS,homeobox,pou	HCR (a-helix coiled-coil rod homologue)	2.2
433090	AI720050	Hs.145362	SS,TM	immortalization-upregulated protein	2.2
417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltransfera	2.2
409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
417433	BE270266	Hs.82128	SS,TM,LRRCT,LRRNT,LRR	5T4 oncofetal trophoblast glycoprotein	2.2
416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators of di	2.2
425999	AW513051	Hs.332981	TM,FAD_binding_2,P53PA,Ribosomal_S2,FAD_bindi	ESTs, Weakly similar to I38022 hypothetic	2.2
452799	AI948829	Hs.213786	TM	ESTs	2.2
414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficient (S.	2.2
448153	Y10805	Hs.20521	SS,TM,Na_Ca_Ex	HMT1 (hnRNP methyltransferase, S. cerevis	2.2
428969	AF120274	Hs.194689	SS	artemin	2.2
443171	BE281128	Hs.9030	SS,TM,7tm_1,rrm	TONDU	2.2
408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
409533	AW969543	Hs.21291	TM	mitogen-activated protein kinase kinase k	2.2
408201	AK000568	Hs.43654	TM	hypothetical protein FLJ20561	2.1
408996	AI979168	Hs.82226	TM	glycoprotein (transmembrane) nmb	2.1
417900	BE250127	Hs.82906	TM,WD40,pro_Isomerase	CDC20 (cell division cycle 20, S. cerevis	2.1
437191	NM_006846	Hs.331555	SS,TM,kazal	serine protease inhibitor, Kazal type, 5	2.1
412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	2.1
431117	AF003522	Hs.250500	SS,TM,DSL,EGF	delta (Drosophila)-like 1	2.1
447674	BE270640	Hs.19192	TM,pkinaseras,arf	cyclin-dependent kinase 2	2.1
409651	H96643	Hs.283565	bZIPcofilin_ADF,EGF	FOS-like antigen-1	2.1
440495	AA887212	Hs.14161	TM,NSFNa_Ca_Ex	hypothetical protein DKFZp434I1930	2.1
429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TILa,vwd,EPO_TPO	procollagen C-endopeptidase enhancer	2.1
421013	M62397	Hs.1345	TM	mutated in colorectal cancers	2.1
447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,ig,MAM	protein tyrosine phosphatase, receptor ty	2.1
449224	AW995911	Hs.299883	fn3	hypothetical protein FLJ23399	2.1
452679	Z42387	Hs.83883	TM	transmembrane, prostate androgen induced	2.1
409956	AW103364	Hs.727	SS,TGF-beta,TGFb_propeptide	inhibin, beta A (activin A, activin AB al	2.1
438580	AA811262	Hs.299202	TM,pkinasesugar_tr	ESTs	2.1
406400			SS,TM,trypsin	NM_007196:Homo sapiens kallikrein 8 (neur	2.1
424965	AW956282	Hs.144609	TM	Homo sapiens, Similar to RIKEN cDNA 57305	2.1
412270	AC005262	Hs.73797	TM,G-alpha	guanine nucleotide binding protein (G pro	2.1
428471	X57348	Hs.184510	TM,14-3-3	stratifin	2.1
427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprolysin	metallocarboxypeptidase CPX-1	2.1
416498	U33632	Hs.79351	TM	potassium channel, subfamily K, member 1	2.1
423453	AW450737	Hs.128791	SS,Granin,CDP-OH_P_transf	CGI-09 protein	2.1
417944	AU077196	Hs.82985	SS,COLFI,Collagen,vwc	collagen, type V, alpha 2	2.1
424197	AF096834	Hs.142989	SS,TM,CSD	germ cell specific Y-box binding protein	2.1
446163	AA026880	Hs.25252	TM,fn3	prolactin receptor	2.1
417331	AW411297	Hs.81972	TM,SH2,PID	SHC (Src homology 2 domain-containing) tr	2.1
430413	AW842182	Hs.241392	IL8,PX	small inducible cytokine A5 (RANTES)	2.1
421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2_ATPase	ATPase, Ca transporting, type 2C, member	2.1
407305	AA715284		TM,pkinase,Sema,Plexin_repeat,TIG,LIM	gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens c	2.1
407792	AI077715	Hs.39384	SS	putative secreted ligand homologous to fj	2.0
418695	AA447014	Hs.193261	SS	hypothetical protein MGC2991	2.0
439738	BE246502	Hs.9598	TM,RasGAP,IQ,WW	sema domain, immunoglobulin domain (Ig),	2.0
433398	AW843150	Hs.112412	TM,PMP22_Claudin	ESTs	2.0
456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
446872	X97058	Hs.16362	TM	pyrimidinergic receptor P2Y, G-protein co	2.0
419726	U50330	Hs.1274	SS,TM,Astacin,CUB,EGF	bone morphogenetic protein 1	2.0
410116	AW630671	Hs.58636	SS,TM	squamous cell carcinoma antigen recognize	2.0
426500	NM_014638	Hs.170156	TM	KIAA0450 gene product	2.0
452194	AI694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	2.0
418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
425855	AF135025	Hs.159679	SS,trypsin	kallikrein 12	2.0
434346	AA630445	Hs.116773	TM,Ferric_reduct	ESTs	2.0
426274	D38122	Hs.2007	TM,TNF	tumor necrosis factor (ligand) superfamil	2.0
440008	AW051683	Hs.277686	TM,RhoGEF,FYVE,PH	ESTs	2.0
424634	NM_003613	Hs.151407	ig,tsp_1	cartilage intermediate layer protein, nuc	2.0
446641	AL049229	Hs.15787	TM,pkinase,rrm	Homo sapiens mRNA; cDNA DKFZp564O1016 (fr	2.0
418851	AI417828	Hs.192435	TM	ESTs	2.0
440351	AF030933	Hs.7179	TM,Rad1,Cadherin_C_term	RAD1 (S. pombe) homolog	2.0
439496	BE616501	Hs.32343	SS	Homo sapiens, Similar to RIKEN cDNA 11100	2.0
454197	BE140966		TM,Ammonium_transpkinesin,Ammonium_transp	gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
433573	AF234887	Hs.57652	TM,7tm_2,GPStRNA-synt_2b,Seryl_tRNA_N	cadherin, EGF LAG seven-pass G-type recep	2.0
429211	AF052693	Hs.198249	TM,connexin	gap junction protein, beta 5 (connexin 31	2.0
420737	L08096	Hs.99899	SS,TM,TNF	tumor necrosis factor (ligand) superfamil	2.0
455333	AW897851		TM,Glyco_hydro_2	gb:RC1-NN0063-100500-022-c08 NN0063 Homo	2.0
414784	NM_000344	Hs.288986	SS,TM,BIR	survival of motor neuron 1, telomeric	2.0
435836	AW292532	Hs.250175	TM,GNS1_SUR4	homolog of yeast long chain polyunsaturat	2.0
411789	AF245505	Hs.72157	TM,ig,LRRCT	DKFZP564I1922 protein	2.0
441455	AJ271671	Hs.7854	TM,ras,DENN	zinc/iron regulated transporter-like	2.0
426068	AF029778	Hs.166154	SS,TM,DSL,EGF,NUDIX	jagged 2	2.0
439733	AL365412	Hs.107203	TM,Sm	hypothetical protein from EUROIMAGE 17593	2.0
435014	BE560898	Hs.10026	TM,Ribosomal_L17	mitochondrial ribosomal protein L17	1.9
457819	AA057484	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	1.9
422737	M26939	Hs.119571	SS,Collagen,COLFI	collagen, type III, alpha 1 (Ehlers-Danlo	1.9
431104	AW970859	Hs.313503	Sema,ig	ESTs	1.9
432210	AI567421	Hs.273330	TM,laminin_G,laminin_EGF,kazalubiquitin	Homo sapiens, clone IMAGE:3544662, mRNA,	1.9
436511	AA721252	Hs.291502	TM,disintegrin,Reprolysin,Pep_M12B_propep,pkinase,	ESTs	1.9
419216	AU076718	Hs.164021	SS,IL8	small inducible cytokine subfamily B (Cys	1.9

432169	Y00971	Hs.2910	TM,Pribosyltran	phosphoribosyl pyrophosphate synthetase 2	1.9
441128	AA570256	Hs.54628	TM,ras	ESTs, Weakly similar to T23273 hypothetic	1.9
447160	AA330310	Hs.24181	TM	ESTs	1.9
419138	U48508	Hs.89631	TM,RYDR_ITPR,RyR,SPRY	ryanodine receptor 1 (skeletal)	1.9
457817	AA247751	Hs.79572	TM,hemopexin,Peptidase_M10	cathepsin D (lysosomal aspartyl protease)	1.9
431009	BE149762	Hs.48956	SS,TM,connexin	gap junction protein, beta 6 (connexin 30	1.9
428957	NM_003881	Hs.194679	SS,TM,vwc,IGFBP,tsp_1	WNT1 inducible signaling pathway protein	1.9
418546	AA224827		TM,vwa,FG-GAP,integrin_A	gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens c	1.9
400749			SS,TM,ldl_recept_a,fn3,ldl_recept_b	NM_003105*:Homo sapiens sortilin-related	1.9
408369	R38438	Hs.182575	F-protein	solute carrier family 15 (H??? transporte	1.9
422765	AW409701	Hs.1578	TM,BIR	baculoviral IAP repeat-containing 5 (surv	1.9
417409	BE272506	Hs.82109	TM,Syndecan	syndecan 1	1.9
407720	AB037776	Hs.38002	TM,calponin,CH	KIAA1355 protein	1.9
418830	BE513731	Hs.88959	TM,CDP-OH_P_transf,MCM	hypothetical protein MGC4816	1.9
434769	AA648884	Hs.134278	TM,CDP-OH_P_transfMCM	Homo sapiens cDNA FLJ12676 fis, clone NT2	1.9
421593	NM_017436	Hs.105956	SS,TM	globotriaosylceramide/CD77 synthase; Gb3/	1.9
426064	BE387014	Hs.166146	TM,WH1	Homer, neuronal immediate early gene, 3	1.9
404604	NA		TM	Target Exon	1.9
422753	AI928995	Hs.1575	SS,TM,Sm	small nuclear ribonucleoprotein D3 polype	1.9
422739	H20106	Hs.119591	SS,Clat_adaptor_s	adaptor-related protein complex 2, sigma	1.9
433068	NM_006456	Hs.288215	SS,Pribosyltran	sialyltransferase	1.9
419594	AA013051	Hs.91417	TM	topoisomerase (DNA) II binding protein	1.9
428188	M98447	Hs.22	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 1 (K polypeptide epiderm	1.9
428343	AL043021	Hs.12705	TM,Rhomboid,HMG_boxTPR	ESTs	1.9
429592	AB029041	Hs.209646	Troponin	KIAA1118 protein	1.9
431620	AA126109	Hs.264981	C2,PH,RasGAP,NTP_transf_2	2'-5'-oligoadenylate synthetase 2 (69-71	1.9
424670	W61215	Hs.116651	ig	epithelial V-like antigen 1	1.9
428373	AI751656	Hs.183986	SS,TM,ig	poliovirus receptor-related 2 (herpesviru	1.9
453449	W16752	Hs.32981	SS,ig,Sema	sema domain, immunoglobulin domain (Ig),	1.9
432304	AA932186	Hs.69297	TM,7tm_1	ESTs	1.9
432673	AB028859	Hs.278605	TM,DnaJ,DnaJ_CDnaJ	DnaJ (Hsp40) homolog, subfamily B, member	1.9
416207	NM_014745	Hs.336433	SS,TM,zf-DHHC	Homo sapiens, clone MGC:2908, mRNA, compl	1.9
408988	AL119844	Hs.49476	TM,Plexin_repeat,Sema,tsp_1	Homo sapiens clone TUA8 Cri-du-chat regio	1.9
417426	NM_002291	Hs.82124	SS,laminin_EGF,laminin_Nterm	laminin, beta 1	1.9
443883	AA114212	Hs.9930	SS,TM,serpin,Marek_A	serine (or cysteine) proteinase inhibitor	1.9
433328	AW298159	Hs.23644	SS,TM	ESTs, Weakly similar to S65824 reverse tr	1.9
419981	AA897581	Hs.128773	TM,Ski_Sno	ESTs	1.8
420931	AF044197	Hs.100431	SS,TM,IL8	small inducible cytokine B subfamily (Cys	1.8
415023	AA932146	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCIA00164 mRNA seque	1.8
413644	BE154910	Hs.278793	TM,Glyco_hydro_2	ESTs, Weakly similar to Z195_HUMAN ZINC F	1.8
449987	AW079749	Hs.184719	TM,ABC_tran,ABC_membraneIon_trans	ESTs, Weakly similar to ALU1_HUMAN ALU SU	1.8
421340	F07783	Hs.1369	SS,sushi	decay accelerating factor for complement	1.8
417866	AW067903	Hs.82772	SS,TM,Collagen,COLFI,TSPN	collagen, type XI, alpha 1	1.8
430259	BE550182	Hs.127826	TM,transmembrane4RasGEF,RA	RalGEF-like protein 3, mouse homolog	1.8
432998	AA835948	Hs.153307	TM,SDF	ESTs	1.8
431671	NM_016937	Hs.267289	TM,NA	polymerase (DNA directed), alpha	1.8
411773	NM_006799	Hs.72026	trypsin	protease, serine, 21 (testisin)	1.8
425247	NM_005940	Hs.155324	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 11 (stromelysin	1.8
422976	AU076657	Hs.1600	TM,cpn60_TCP1,Sema	chaperonin containing TCP1, subunit 5 (ep	1.8
425159	NM_004341	Hs.154868	SS,TM,GATase,OTCace,CPSase_L_chain,Dihydrooro	carbamoyl-phosphate synthetase 2, asparta	1.8
447776	AI525625	Hs.130181	Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.8
426908	AW815163	Hs.172851	SS,TM,fusion_gly,Myosin_tailadh_short	arginase, type II	1.8
408116	AA251393	Hs.289052	TM,Na_Ca_ExCam_acyltransf	Homo sapiens, Similar to RIKEN cDNA 54304	1.8
417847	AI521558	Hs.7331	Uteroglobin	hypothetical protein FLJ22316	1.8
415791	H09366	Hs.78853	SS,TM,UNG	uracil-DNA glycosylase	1.8
407903	AI287341	Hs.154029	TM,ubiquitin,laminin_G,laminin_EGF,kazal	bHLH factor Hes4	1.8
422511	AU076442	Hs.117938	TM,p450	collagen, type XVII, alpha 1	1.8
414117	W88559	Hs.1787	TM,ion_trans,K_tetra	proteolipid protein 1 (Pelizaeus-Merzbach	1.8
426841	AI052358	Hs.193726	TM,asp	ESTs	1.8
415272	AA164215	Hs.203186	TM,TPR,pkinase,ig,B56	ESTs	1.8
426440	BE382756	Hs.169902	TM,sugar_tr,Fork_head	solute carrier family 2 (facilitated gluc	1.8
419488	AA316241	Hs.90691	FGF	nucleophosmin/nucleoplasmin 3	1.8
418452	BE379749	Hs.85201	SS,TM,lectin_c	C-type (calcium dependent, carbohydrate-r	1.8
431363	M86528	Hs.266902	SS,NGF	neurotrophin 5 (neurotrophin 4/5)	1.8
440975	AW499914	Hs.7579	SS,TM	hypothetical protein FLJ10402	1.8
438962	BE046594		TGF-beta,bZIP	gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	1.8
414602	AW630088	Hs.76550	SS	Homo sapiens mRNA; cDNA DKFZp564B1264 (fr	1.8
418054	NM_002318	Hs.83354	TM,mito_carr,Lysyl_oxidase	lysyl oxidase-like 2	1.8
440501	AA887391	Hs.202229	TM,Galactosyl_T	ESTs	1.8
449309	AW589823	Hs.224189	TM	ESTs	1.8
421461	AW291023	Hs.97255	TM,Lysyl_oxidase,SCP2,Band_7	ESTs, Weakly similar to A46010 X-linked r	1.8
412584	X54870	Hs.74085	TM,lectin_c	DNA segment on chromosome 12 (unique) 248	1.8
441565	AW953575	Hs.303125	TM	p53-induced protein PIGPC1	1.8
431837	T79326	Hs.326553	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	1.8
436251	BE515065	Hs.296585	SS,Y_phosphataseTIG	nucleolar protein (KKE/D repeat)	1.8
448633	AA311426	Hs.21635	TM,EGF,laminin_G,fibrinogen_C,F5_F8_type_C,tubulin	tubulin, gamma 1	1.8
424291	AL120051	Hs.144700	TM,Ephrin,Hist_deacetyl	ephrin-B1	1.8
415388	AF018081	Hs.78409	SS,TM,TSPN,Collagen	collagen, type XVIII, alpha 1	1.8
435550	AI224456	Hs.4934	TM,LRR,LRRCT	H.sapiens polyA site DNA	1.8
448568	AA149121	Hs.71947	TM,LRRCT	ESTs	1.8
439246	AI498072	Hs.77783	SS,TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Cla	membrane-associated tyrosine- and threoni	1.8
410001	AB041036	Hs.57771	SS,TM,trypsin	kallikrein 11	1.8
417312	AW888411	Hs.81915	SS,Stathmin	leukemia-associated phosphoprotein p18 (s	1.8

444152	AI125694	Hs.149305	TM	hypothetical protein MGC2603	1.8
453454	AW052006	Hs.8551	TM	PRP4/STK/WD splicing factor	1.8
449320	AB030835	Hs.23476	SS,adenylatekinase	Cip1-interacting zinc finger protein	1.8
428329	AA426091	Hs.98453	TM,Gal-bind_lectin	ESTs, Moderately similar to R27328 2 [H.s	1.8
452875	BE275760	Hs.30928	TM,Apolipoproteinig	DNA segment on chromosome 19 (unique) 117	1.8
444031	BE271513	Hs.25303	TM,Peptidase_M10,hemopexin	hypothetical protein FLJ13154	1.8
443534	AI076123		TM	gb:oy92e04.x1 Soares_fetal_liver_spleen_1	1.8
413313	NM_002047	Hs.75280	TM,WHEP-TRS,7tm_2	glycyl-tRNA synthetase	1.8
452874	AK001061	Hs.30925	SS	hypothetical protein FLJ10199	1.8
453140	AA032238	Hs.170531	TM	ESTs	1.8
418641	BE243136	Hs.86947	SS,TM,disintegrin,Pep_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domai	1.8
432925	AA878324	Hs.192734	SS	ESTs	1.8
453857	AL080235	Hs.35861	TM	DKFZP586E1621 protein	1.8
457663	AW371946	Hs.337459	TM	ESTs	1.8
452873	AK001247	Hs.30922	TM	hypothetical protein FLJ10385	1.8
436396	AI683487	Hs.152213	SS,wnt	wingless-type MMTV integration site famil	1.8
452835	AK001269	Hs.30738	TM	hypothetical protein FLJ10407	1.7
459647	R34107	Hs.198287	ig	pregnancy specific beta-1-glycoprotein 11	1.7
418245	AA088767	Hs.83883	TM,PEPCK	transmembrane, prostate androgen induced	1.7
448484	BE613340	Hs.334725	TM	Homo sapiens, Similar to RIKEN cDNA 94300	1.7
431369	BE184455	Hs.251754	SS,wap	secretory leukocyte protease inhibitor (a	1.7
434877	AW974792	Hs.292171	TM	ESTs	1.7
428923	BE047698	Hs.188785	TM	ESTs	1.7
402915	NA		TM,HCO3_cotransp	ENSP00000202587*:Bicarbonate transporter-	1.7
420185	AL044056	Hs.158047	TM	ESTs	1.7
445739	AW136354	Hs.145303	TM	ESTs	1.7
409435	AI810721	Hs.95424	TM,p450	ESTs	1.7
408688	AI634522	Hs.152925	TM	KIAA1268 protein	1.7
420085	AI741909	Hs.44680	TM	hypothetical protein FLJ20979	1.7
433933	AI754389	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCIA00164 mRNA seque	1.7
430965	AA489732	Hs.154918	hormone_rec,Prog_receptor,zf-C4	ESTs	1.7
414703	BE243877	Hs.76941	SS,TM,Na_K-ATPaseE2F_TDP	ATPase, Na? transporting, beta 3 polypept	1.7
423464	NM_016240	Hs.128856	TM,Collagen	CSR1 protein	1.7
416737	AF154335	Hs.79691	SS,TM,LIM,PDZsugar_tr,PDZ,LIM	LIM domain protein	1.7
409012	AL117435	Hs.49725	TM,RhoGEFzf-DHHC,adh_short	DKFZP434I216 protein	1.7
423804	AW403448	Hs.1706	TM,IRF	interferon-stimulated transcription facto	1.7
410418	D31382	Hs.63325	SS,TM,trypsin,tdl_recept_a	transmembrane protease, serine 4	1.7
440028	AW473675	Hs.125843	TM	ESTs, Weakly similar to T17227 hypothetic	1.7
457646	AA725650	Hs.112948	TM,SPRY	ESTs	1.7
445439	BE243084	Hs.12719	SS,TGF-beta	regulator of nonsense transcripts 1	1.7
420426	AA262045	Hs.36567	TM,Galactosyl_T_2ATP-synt_C	Homo sapiens cDNA FLJ14227 fis, clone NT2	1.7
431341	AA307211	Hs.251531	TM,proteasome	proteasome (prosome, macropain) subunit,	1.7
412338	AA151527	Hs.69485	TM,Sema,Plexin_repeatTIG,Plexin_repeat	hypothetical protein FLJ12436	1.7
414799	AI752416	Hs.77326	SS,thyroglobulin_1,IGFBP	insulin-like growth factor binding protei	1.7
452700	AI859390	Hs.288940	TM,DIX,RGS,thiored	five-span transmembrane protein M83	1.7
430877	NM_005269	Hs.2693	GST_C,tRNA-synt_1,WHEP-TRS,TGF-beta	glioma-associated oncogene homolog (zinc	1.7
428624	AI125222	Hs.98712	TM,thiored,Y_phosphatase,MAM,ig,fn3MSP_domain	hypothetical protein DKFZp434H0311	1.7
444065	AW449415	Hs.10260	TM,ion_trans	Homo sapiens cDNA FLJ11341 fis, clone PLA	1.7
416319	AI815601	Hs.79197	SS,TM,ig	CD83 antigen (activated B lymphocytes, im	1.7
429367	AB007867	Hs.278311	Sema,Plexin_repeat,TIG	plexin B1	1.7
430425	AA531428	Hs.241412	TM	apolipoprotein L, 2	1.7
441668	AI611973	Hs.127525	TM,Ammonium_transp	ESTs	1.7
418469	U34879	Hs.85279	SS,TM,adh_short	hydroxysteroid (17-beta) dehydrogenase 1	1.7
450835	BE262773	Hs.25584	TM,ArfGap	hypothetical protein FLJ10767	1.7
418859	AA229558		TM	gb:nc15d10.s1 NCI_CGAP_Pr1 Homo sapiens c	1.7
425304	AA463844	Hs.31339	TM,ig,ITAM	fibroblast growth factor 11	1.7
423635	X85019	Hs.130181	TM,Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.7
414820	AA371931	Hs.77422	TM,ion_trans,LIM,Synaptophysin	proteolipid protein 2 (colonic epithelium	1.7
440654	AW014242	Hs.159998	TM,connexin	ESTs	1.7
412276	BE262621	Hs.73798	SS,MIF	macrophage migration inhibitory factor (g	1.7
422087	X58968	Hs.111301	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 2 (gelatinase A,	1.7
407151	H25836	Hs.301527	SS,TNF	ESTs, Moderately similar to unknown [H.sa	1.7
410726	AI623859	Hs.15936	TM,PX	ESTs	1.7
452012	AA307703	Hs.279766	TM,kinesin	kinesin family member 4A	1.7
433627	AF078866	Hs.284296	TM,SURF4,SURF1,DEADlipocalin	Homo sapiens cDNA: FLJ22993 fis, clone KA	1.7
409220	BE243323	Hs.51233	TM,death,TNFR_c6	tumor necrosis factor receptor superfamil	1.7
427082	AB037858	Hs.173484	TM,mito_carr	hypothetical protein FLJ10337	1.7
426410	BE298446	Hs.305890	TM,Bcl-2,BH4	BCL2-like 1	1.7
433598	AI762836	Hs.271433	TM,Cytidylyltransf,SIR27tm_2	ESTs, Moderately similar to ALU2_HUMAN AL	1.7
436495	BE258943	Hs.290874	TM,Armadillo_seg	ESTs, Weakly similar to ALU8_HUMAN ALU SU	1.7
422032	AA476966	Hs.110857	TM,TFIIS,RNA_POL_M_15KDserpin,hormone_rec,zf-C4	polymerase (RNA) III (DNA directed) polyp	1.7
429736	AF125304	Hs.212680	SS,TNFR_c6	tumor necrosis factor receptor superfamil	1.7
427600	AW630918	Hs.179774	TM,Transglutamin_C,Transglutamin_N,Transglut_core	proteasome (prosome, macropain) activator	1.7
431981	AA664069	Hs.115779	laminin_B,laminin_EGF	ESTs	1.7
407736	N41744	Hs.19978	TM,Sulfatase	CGI-30 protein	1.7
420187	AK001714	Hs.95744	TM	hypothetical protein similar to ankyrin r	1.7
424620	AA101043	Hs.151254	SS,TM,trypsin	kallikrein 7 (chymotryptic, stratum corne	1.7
430488	D19589	Hs.13453	TM	hypothetical protein FLJ14753	1.7
423393	R37772	Hs.21420	TM,thioredpkinase	p21-activated protein kinase 6	1.7
444051	N48373	Hs.10247	SS,ig		

TABLE 13B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
408344	105240_1	AA053843 BE162213
418546	176677_1	AA224827 T59708 T59843 BE156903
418859	179717_1	AA229558 AA345492 AA229582
418869	179863_1	AW516565 AA229762 AA230035
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438962	467390_1	BE046594 BE046667 AA828585 AI207343
443534	572957_1	AI076123 AI244834 AI695239
447197	711623_1	R36075 AI366546 R36167
454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969 BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975 BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013 BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646 BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671 AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
455333	1281044_1	AW897851 AW897852
457570	357443_1	AA579426 AA579436 AA573736

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
401103	8568122	Minus	98330-98449
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401575	7229804	Minus	76253-76364
402745	9212200	Minus	76516-76690
402915	7406502	Minus	140-276
404440	7528051	Plus	80430-81581
404604	9212537	Minus	72019-72509
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405547	1054740	Plus	124361-124520,124914-125050
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406467	9795551	Plus	182212-182958

TABLE 14A: 209 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

Table 14A lists about 209 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 12A, except that the ratio was greater than or equal to 2.0, and the 96th percentile value amongst cervical cancers was greater than or equal 40 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulatable by small molecules (e.g. pkinase, peptidase, phosphatase, ATPase, or ion_transporter domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
PPDomains: Predicted Protein Domains
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigeneID	PPDomains	Unigene Title	R1
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interst	38.9
439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (strome	20.5
415817	U88967	Hs.78867	SS,TM,Y_phosphatase,carb_anhyd	protein tyrosine phosphatase, recep	16.4
416209	AA236776	Hs.79078	TM,HORMA	MAD2 (mitotic arrest deficient, yea	15.4
404996	NM_001333	Hs.87417	Peptidase_C1	CTSL2 Cathepsin L2	13.1

428618	AA885360	Hs.160199	pkinase	Target CAT	12.7
429486	AF155827	Hs.203953	helicase_C,SNF2_Nhelicase_C	hypothetical protein FLJ10339	12.6
419183	U60669	Hs.89663	p450	cytochrome P450, subfamily XXIV (vi	12.3
428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromel	10.2
420759	T11832	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	10.2
458194	AW383618	Hs.265459	p450	ESTs, Moderately similar to ALU2_HU	9.4
446232	AI281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
424905	NM_002497	Hs.153704	TM,pkinase	NIMA (never in mitosis gene a)-rela	8.9
452291	AF015592	Hs.28853	TM,pkinase	CDC7 (cell division cycle 7, S. cer	8.7
424086	AI351010	Hs.102267	Lysyl_oxidase	lysyl oxidase	8.3
425710	AF030880	Hs.159275	TM,Sulfate_transp,STAS	solute carrier family, member 4	7.8
433133	AB027249	Hs.104741	TM,Collagen,pkinase	PDZ-binding kinase; T-cell originat	7.4
447254	NM_004153	Hs.17908	SS,AAA,BAH	origin recognition complex, subunit	7.1
431941	AK000106	Hs.272227	pkinase,Furin-like,Recep_L_dom	Homo sapiens cDNA FLJ20099 fis, clo	6.9
427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA	6.9
403471	NA		SS,TM,trypsin	Target Exon	6.7
410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
457405	AA504860		TM,7tm_2	gb:ab03a10.s1 Stratagene fetal reti	6.4
421948	L42583	Hs.334309	filament,HCO3_cotranspfilament	keratin 6A	6.3
439292	AA090421	Hs.5555	TM,AAA,Ferric_reduct	hypothetical protein MGC5347	5.8
413625	AW451103	Hs.71371	TM,E1-E2_ATPase,Hydrolase	ESTs	5.8
425695	NM_005401	Hs.159238	TM,Band_41,Y_phosphatase	protein tyrosine phosphatase, non-r	5.7
438394	BE379623	Hs.27693	SS,pro_Isomerase	peptidylprolyl Isomerase (cyclophil	5.6
432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collag	5.5
408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPa	ESTs	5.4
432226	AW182766	Hs.273558	Cytidylyltransf	phosphate cytidylyltransferase 1, c	5.2
419520	AB009303	Hs.90800	TM,hemopexin,Peptidase_M10	matrix metalloproteinase 16 (membra	5.1
426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutam	transglutaminase 3 (E polypeptide,	5.0
421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldose_epim,E	lysyl oxidase	4.9
423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrop	4.8
450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep	a disintegrin and metalloproteinase	4.8
418379	AA218940	Hs.137516	AAA	fidgetin-like 1	4.7
457465	AW301344	Hs.122908	Pribosyltran,Sulfatase	DNA replication factor	4.6
412333	AW937485		TM,7tm_1	gb:QV3-DT0044-221299-045-b09 DT0044	4.6
450510	AA010056	Hs.242998	DNA_topoisoII,DNA_topoisoIVIGF	ESTs	4.6
436291	BE568452	Hs.5101	abhydrolase	protein regulator of cytokinesis 1	4.6
446353	AI290919	Hs.153661	HECTpkinase	ESTs	4.5
435435	T89473	Hs.192328	lipase,PLAT	ESTs	4.5
425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
433322	H50621	Hs.134156	TM,ion_transNB-ARC,CARD,mito_c	ESTs, Weakly similar to I38022 hypo	4.4
408908	BE296227	Hs.250822	TM,pkinase	serine/threonine kinase 15	4.4
444781	NM_014400	Hs.11950	PH,lactamase_B	GPI-anchored metastasis-associated	4.4
428479	Y00272	Hs.184572	pkinase	cell division cycle 2, G1 to S and	4.2
406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprot	4.2
423035	AW449679	Hs.156739	TM,Glyco_transf_8	H.sapiens XG mRNA (clone PEP11)	4.2
449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
457030	AI301740	Hs.173381	TM,Dihydroorotase	dihydropyrimidinase-like 2	4.1
448995	AI613276	Hs.5662	adenylatekinase	guanine nucleotide binding protein	4.0
415857	AA866115	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	4.0
438390	AI422017		TM,DSL,7tm_1 7tm_1	gb:tf45f12.x1 NCI_CGAP_Brn23 Homo s	4.0
429900	AA460421	Hs.30875	pkinase	ESTs	4.0
446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, de	3.6
424296	AI631874	Hs.155140	pkinase	casein kinase 2, alpha 1 polypeptid	3.6
436246	AW450963	Hs.119991	connexinhormone_rec,zf-C4	ESTs	3.5
411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metal	3.5
426920	AA393351	Hs.132121	PDEase	ESTs	3.5
412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acy	endothelial cell growth factor 1 (p	3.4
430704	AW813091	Hs.335799	Epimerase	ESTs	3.4
455092	BE152428		Sulfatase	gb:CM0-HT0323-151299-126-b04 HT0323	3.4
453775	NM_002916	Hs.35120	AAA,PI3_PI4_kinase,PI3Ka,PI3K_	replication factor C (activator 1)	3.4
438993	AA828995		integrin_B	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap	3.4
426572	AB037783	Hs.170623	hormone_rec,zf-C4	hypothetical protein FLJ11183	3.4
449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
427660	AI741320	Hs.114121	hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23228 fis, cl	3.3
402481			TM,GDI,7tm_1	NM_001821*:Homo sapiens choroiderem	3.3
414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
412246	AI160873	Hs.69233	SulfotransferACOX	zinc finger protein	3.3
418462	BE001596	Hs.85266	SS,TM,integrin_B,fn3	integrin, beta 4	3.3
424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatin	3.3
401486	NA		SS,TM,trypsin	C4000647*:gi|4758508|ref|NP_004253.	3.2
408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, cl	3.2
427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	3.2
402337			SS,p450	Target Exon	3.2
420930	AW888650		ribonuclease_T2	gb:CM4-NT0007-130500-551-f06 NT0007	3.2
443426	AF098158	Hs.9329	pkinase	chromosome 20 open reading frame 1	3.1
439750	AL359053	Hs.57664	TM,integrin_B,Ricin_B_lectinm	Homo sapiens mRNA full length inser	3.1
420039	NM_004605	Hs.94581	CARD,SulfotransferDAGKc	sulfotransferase family, cytosolic,	3.0
448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,isodh,pkina	solute carrier family 6 (neurotrans	3.0

444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
450841	AI741466	Hs.270515	pro_isomerase	ESTs	3.0
428262	AI651324	Hs.7298	death,pkinase	biphenyl hydrolase-like (serine hyd	3.0
435399	AA679463		pkinase	gb:ac50c03.s1 Stratagene hNT neuron	2.9
446733	AA853360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid	2.9
449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN	2.9
418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kin	ESTs	2.9
431629	AU077025	Hs.265827	SS,tRNA_antiSH2,SH3,pkinase	interferon, alpha-inducible protein	2.8
445873	AA250970	Hs.251946	SS,rrm,PABPpkinase,14-3-3,rrm	poly(A)-binding protein, cytoplasmi	2.8
438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
422589	AW856665		helicase_C,SNF2_Nhelicase_C	gb:RC3-CT0297-290100-013-d03 CT0297	2.8
439453	BE264974	Hs.6566	SS,AAA	thyroid hormone receptor interactor	2.8
413582	AW295647	Hs.71331	carb_anhydrase	hypothetical protein MGC5350	2.8
410664	NM_006033	Hs.65370	TM,lipase,PLAT	lipase, endothelial	2.8
456456	AA477609	Hs.89563	FBPase	nuclear cap binding protein subunit	2.8
413273	U75679	Hs.75257	TM,ig,pkinase	stem-loop (histone) binding protein	2.8
426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
403763			TM,7tm_1	NM_001059*:Homo sapiens tachykinin	2.7
408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor	diubiquitin	2.7
401230			SS,TM,ion_trans,IQ	NM_014191*:Homo sapiens sodium chan	2.7
418030	BE207573	Hs.83321	SS,TM,Peptidase_S26,Bombesin	neuromedin B	2.7
445640	AW969626	Hs.31704	TM,alpha-amylase	ESTs, Weakly similar to KIAA0227 [H	2.7
432865	AI753709	Hs.152484	TM,ion_transNB-ARC,CARD,WD40,m	ESTs, Weakly similar to I38022 hypo	2.6
419667	AU077005	Hs.92208	SS,TM,disintegrin,Reprolysin,P	a disintegrin and metalloproteinase	2.6
406671	AA129547	Hs.285754	TM,pkinase,Plexin_repeat,Sema,	met proto-oncogene (hepatocyte grow	2.6
412530	AA766268	Hs.256273	abhydrolase	hypothetical protein FLJ13346	2.6
431890	X17033	Hs.271986	vwa,FG-GAP,integrin_A	integrin, alpha 2 (CD49B, alpha 2 s	2.6
404184	NA		SS,TM,7tm_1	NM_030903*:Homo sapiens olfactory r	2.6
428450	NM_014791	Hs.184339	pkinase,KA1	KIAA0175 gene product	2.6
425698	NM_016112	Hs.159241	TM,pkinase,ion_trans	polycystic kidney disease 2-like 1	2.6
453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep	ESTs	2.6
444826	AI674482	Hs.148441	pkinase,SAM	ESTs	2.6
414987	AA524394	Hs.294022	connexinhormone_rec,zf-C4,conn	hypothetical protein FLJ14950	2.6
438746	AI885815	Hs.184727	Ribosomal_S2,transferrin	ESTs	2.5
429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
421733	AL119571	Hs.1420	SS,TM,ig,pkinase	fibroblast growth factor receptor 3	2.5
452220	BE158006	Hs.212296	TM,integrin_A,FG-GAP	ESTs	2.5
417975	AA641836	Hs.30065	SS,trypsin	hypothetical protein FLJ23186	2.5
400301	X03635	Hs.1657	TM,Oest_recep,zf-C4,hormone_re	estrogen receptor 1	2.5
408938	AA059013	Hs.22607	Y_phosphatase	ESTs	2.4
411643	AI924519	Hs.192570	DEAD,helicase_C	hypothetical protein FLJ22028	2.4
446638	AL133063	Hs.15783	TM,pkinase	Homo sapiens mRNA; cDNA DKFZp434P11	2.4
430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
417655	AA780791	Hs.14014	Peptidase_M41,AAApkinase	hypothetical protein FLJ14813	2.4
448005	AW207437	Hs.170378	pkinase	ESTs	2.4
423973	AF038461	Hs.136574	TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase, 12R t	2.4
437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
425397	J04088	Hs.156346	DNA_topoisoII,DNA_topoisoIVIGF	topoisomerase (DNA) II alpha (170kD	2.4
432777	AA564991	Hs.269477	alpha-amylase	ESTs	2.4
421247	BE391727	Hs.102910	TM,tRNA-synt_1,SPRYF5_F8_type_	general transcription factor IIH, p	2.4
425465	L18964	Hs.1904	TM,pkinase,DAG_PE-bind,OPR,pki	protein kinase C, iota	2.4
419281	H96452	Hs.42189	TM,E1-E2_ATPase,HMA,Hydrolase	ESTs	2.4
434205	AF119861	Hs.283032	SH3,efhand,C2,PH,RhoGEF,AAA,PG	hypothetical protein PRO2015	2.4
453406	AI192987	Hs.61784	pkinase,Furin-like,Recep_L_dom	hypothetical protein FLJ14451	2.3
435542	AA687376	Hs.269533	pkinase,RhoGEF,ig,PH,SH3	ESTs	2.3
443151	AI827193	Hs.132714	DNA_mis_repair,HATPase_cAcylph	ESTs	2.3
431630	NM_002204	Hs.265829	SS,TM,FG-GAP,integrin_A	integrin, alpha 3 (antigen CD49C, a	2.3
422310	AA316622	Hs.98370	SS,TM,fn3,ig,pkinase,Ribosomal	cytochrome P450, subfamily IIS, pol	2.3
441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	Fanconi anemia, complementation gro	2.3
414907	X90725	Hs.77597	SS,TM,pkinase,POLO_box	polo (Drosophia)-like kinase	2.3
439810	AL109710	Hs.85568	aconitase,Aconitase_C	EST	2.3
429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membra	2.3
432284	AA532807	Hs.105822	TM,pkinase	ESTs	2.3
452947	AW130413		alpha-amylase	gb:xf50f04.x1 NCI_CGAP_Gas4 Homo sa	2.3
423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
453941	U39817	Hs.36820	DEAD,HRDC,helicase_C	Bloom syndrome	2.3
439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylhy	2.3
424439	AA579635	Hs.1770	DNA_ligase	ligase I, DNA, ATP-dependent	2.2
452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypo	2.2
429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2
434149	Z43829	Hs.19574	TM,EPH_lbd,fn3,pkinase,SAM	hypothetical protein MGC5469	2.2
417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltra	2.2
409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators	2.2
414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficien	2.2
443171	BE281128	Hs.9030	SS,TM,7tm_1,rrm	TONDU	2.2
430637	BE160081	Hs.256290	S_100Peptidase_M16	S100 calcium-binding protein A11 (c	2.2
452367	U71207	Hs.29279	SS,Hydrolase	eyes absent (Drosophila) homolog 2	2.2
408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. c	2.1

424490	AJ278016	Hs.55565	TM,pkinase,ank	ankyrin repeat domain 3	2.1
412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	2.1
410855	X97795	Hs.66718	SNF2_N,helicase_C	RAD54 (S.cerevisiae)-like	2.1
418804	AA809632		HATPase_c,HSP90,PHD,zf-C2H2	gb:nz17h04.s1 NCI_CGAP_GCB1 Homo sa	2.1
447674	BE270640	Hs.19192	TM,pkinaseras,arf	cyclin-dependent kinase 2	2.1
450663	H43540	Hs.25292	SS,TM,RNase_HII	ribonuclease HI, large subunit	2.1
408805	H69912	Hs.48269	TM,pkinase	vaccinia related kinase 1	2.1
429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TILa,vwd,EP	procollagen C-endopeptidase enhance	2.1
447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,ig,MAM	protein tyrosine phosphatase, recep	2.1
428273	AI867228	Hs.303211	Glycos_transf_2	ESTs	2.1
404274			SS,TM,pkinase,fn3	NM_002944*:Homo sapiens v-ros avian	2.1
403133			pkinase,K_tetra,Band_41,RhoGEF	Target Exon	2.1
440249	AI246590	Hs.337275	VHL,TatD_DNase	ESTs	2.1
438580	AA811262	Hs.299202	TM,pkinasesugar_tr	ESTs	2.1
406400			SS,TM,trypsin	NM_007196:Homo sapiens kallikrein 8	2.1
427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprot	metallocarboxypeptidase CPX-1	2.1
423453	AW450737	Hs.128791	SS,Granin,CDP-OH_P_transf	CGI-09 protein	2.1
433716	AA608808	Hs.225118	Acylphosphatase	ESTs	2.1
420757	X78592	Hs.99915	TM,hormone_rec,Androgen_recep,	androgen receptor (dihydrotestoster	2.1
425018	BE245277	Hs.154196	DNase_I,K_tetra	E4F transcription factor 1	2.1
421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2	ATPase, Ca transporting, type 2C, m	2.1
457288	AA521458	Hs.192738	pro_isomerase	ESTs	2.1
407305	AA715284		TM,pkinase,Sema,Plexin_repeat,	gb:nv35f03.r1 NCI_CGAP_Br5 Homo sap	2.1
456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
422429	AA310527		pkinase,RGS,PHpkinase,PH,RGS	gb:EST181333 Jurkat T-cells V Homo	2.0
402974	NM_001501	Hs.129715	GnRHhormone5,hormone4	gonadotropin-releasing hormone 2	2.0
458016	AW188099	Hs.131813	pkinase	ESTs	2.0
452194	AI694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfa	2.0
428028	U52112	Hs.182018	TM,pkinase,MBD	interleukin-1 receptor-associated k	2.0
427747	AW411425	Hs.180655	pkinase,lipoxygenase,PLATIIpox	serine/threonine kinase 12	2.0
452841	T17431	Hs.65412	TM,DEAD,helicase_C	DEAD/H (Asp-Glu-Ala-Asp/His) box po	2.0
449539	W80363	Hs.58446	pkinase,Furin-like,Recep_L_dom	ESTs	2.0
418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
430076	AA465115	Hs.318773	AAA,BAH	KIAA1836 protein	2.0
425749	AW328587	Hs.159448	Ribosomal_L7Ae,LRR,LRRCT,pkina	surfeit 2	2.0
425855	AF135025	Hs.159679	SS,trypsin	kallikrein 12	2.0
400135	L40027	Hs.118890	pkinase	glycogen synthase kinase 3 alpha	2.0

TABLE 14B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
418804	179138_1	AA809632 AI917245 AI701732 AA228406
420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
422429	216469_1	AA310527 AW962295 Z44865 H06641
422689	219896_1	AW856665 AA315006 AW954733
435399	405576_1	AA679463 AW813779 AW813709
438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003
438993	467651_1	AA828995 AA834879 AI926361
452947	939810_1	AW130413 AI932362
455092	1252971_1	BE152428 AW855572 AW855607
457405	333127_1	AA504860 AA504911

TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
402481	9797406	Plus	87891-88991
403133	7331427	Plus	38314-38634
403471	9930659	Minus	85867-85983
403763	7229888	Minus	43575-43887
404184	4581418	Minus	12652-13548
404274	9885189	Plus	104127-104318
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

TABLE 15A: 752 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 15A lists about 752 genes up-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 12A, except that the ratio was greater than or equal to 7.0, the denominator was the median value for three non-malignant cervical specimens, and the 96th percentile value amongst cervical cancers was greater than or equal 80 units.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigeneID	Unigene Title	R1
414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	58.3
411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HEMBA1004341	36.2
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-Cys), mem	35.6
421508	NM_004833	Hs.105115	absent in melanoma 2	33.6
443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit, beta type, 1	32.0
454390	AB020713	Hs.56966	KIAA0906 protein	30.5
416065	BE267931	Hs.78996	proliferating cell nuclear antigen	30.4
433226	AW503733	Hs.9414	KIAA1488 protein	30.0
413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein,	29.4
411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	28.9
414132	AI801235	Hs.48480	ESTs	28.3
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	28.1
448569	BE382657	Hs.21486	signal transducer and activator of transcription 1, 9	27.4
432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	27.2
418963	BE304571	Hs.89529	aldo-keto reductase family 1, member A1 (aldehyde red	26.9
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform I	26.5
449722	BE280074	Hs.23960	cyclin B1	26.2
414812	X72755	Hs.77367	monokine induced by gamma interferon	25.3
408405	AK001332	Hs.44672	hypothetical protein FLJ10470	25.1
432917	NM_014125	Hs.279812	PRO0327 protein	24.6
412530	AA766268	Hs.266273	hypothetical protein FLJ13346	23.6
457465	AW301344	Hs.122908	DNA replication factor	23.1
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049	22.9
429083	Y09397	Hs.227817	BCL2-related protein A1	22.9
401405			Target Exon	22.8
426272	AW450671	Hs.189284	ESTs	22.7
424878	H57111	Hs.221132	ESTs	22.6
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin 6)	22.5
444371	BE540274	Hs.239	forkhead box M1	22.2
418030	BE207573	Hs.83321	neuromedin B	22.0
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-	21.6
400196			Eos Control	21.3
416795	AI497778	Hs.20509	HBV pX associated protein-8	21.2
424355	AF011333	Hs.153563	lymphocyte antigen 75	21.0
438011	BE466173	Hs.145696	splicing factor (CC1.3)	20.7
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, progelatin	20.3
436923	AW293704	Hs.122658	ESTs	20.2
415791	H09366	Hs.78853	uracil-DNA glycosylase	20.0
448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moiety X)-type m	19.6
435647	AI653240	Hs.49823	ESTs	19.6
431049	AA846575	Hs.103267	hypothetical protein FLJ22548 similar to gene trap PA	19.5
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.5
428433	AA521410	Hs.41371	ESTs	19.4
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated	19.3
417308	H60720	Hs.81892	KIAA0101 gene product	19.2
429574	BE268321	Hs.208912	hypothetical protein MGC861	19.2
407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	19.0
408901	AK001330	Hs.48855	hypothetical protein FLJ10468	19.0
438899	AF085833	Hs.135624	ESTs	19.0
456362	AW973003	Hs.179909	hypothetical protein FLJ22995	18.9
438598	AI805943	Hs.326067	hypothetical protein MGC5178	18.8
408908	BE296227	Hs.250822	serine/threonine kinase 15	18.8
427488	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B	18.6
400195			NM_007057*:Homo sapiens ZW10 interactor (ZWINT), tran	18.5
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)	18.4
410324	AW292539	Hs.30177	ESTs	18.3
453028	AB006532	Hs.31442	RecQ protein-like 4	18.1
410508	AI538438	Hs.159087	ESTs	18.1
432503	AA551196	Hs.188952	ESTs	17.9
430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	17.7
430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo sapiens cDNA	17.6
449962	AA004879	Hs.187820	ESTs	17.3
425408	AB002375	Hs.156814	KIAA0377 gene product	17.1
440774	AI420611	Hs.127832	ESTs	16.8
408201	AK000568	Hs.43654	hypothetical protein FLJ20561	16.7
436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothetical protein [	16.7
426897	AW976570	Hs.97387	ESTs	16.5
447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical protein F	16.5

	433159	AB035898	Hs.150587	kinesin-like protein 2	16.3
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	16.3
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional activation,	16.3
	453941	U39817	Hs.36820	Bloom syndrome	16.1
5	438461	AW075485	Hs.286049	phosphoserine aminotransferase	16.0
	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTE	16.0
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP2006454	15.7
	407720	AB037776	Hs.38002	KIAA1355 protein	15.6
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1 protein - mou	15.6
10	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elastase)	15.5
	419777	D60134	Hs.270975	ESTs	15.3
	453886	R66282	Hs.20247	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	15.2
	443715	AI583187	Hs.9700	cyclin E1	15.2
	407786	AA687538	Hs.38972	tetraspan 1	15.2
15	431910	AK000142	Hs.101774	hypothetical protein FLJ23045	15.2
	417634	W27202	Hs.82327	glutathione synthetase	15.1
	432692	AW974944	Hs.200577	ESTs	15.1
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), membe	15.1
	427999	AI435128	Hs.181369	ubiquitin fusion degradation 1-like	15.0
20	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	15.0
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clone IFI-6-16)	14.9
	435354	AA678267	Hs.117115	ESTs	14.8
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	14.8
	416109	AI420311	Hs.126550	suppressor of K transport defect 1	14.8
25	417933	X02308	Hs.82962	thymidylate synthetase	14.7
	438970	AA837782	Hs.321058	ESTs	14.7
	409680	W31092	Hs.55847	mitochondrial ribosomal protein 64	14.7
	432401	NM_013330	Hs.274479	NME7	14.6
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.5
30	420734	AW972872	Hs.293736	ESTs	14.5
	434256	AI378817	Hs.191847	ESTs	14.5
	418269	AA806113	Hs.189025	ESTs	14.3
	427372	AW960673	Hs.177530	ATP synthase, H transporting, mitochondrial F1 comple	14.3
	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU CLASS	14.2
35	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	14.2
	429966	BE081342	Hs.283037	HSPC039 protein	14.2
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-inducible, 67	14.1
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	14.0
	418803	U50079	Hs.88556	histone deacetylase 1	14.0
40	434094	AA305599	Hs.238205	hypothetical protein PRO2013	14.0
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	13.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding pr	13.9
	433255	AI274270	Hs.96840	KIAA1527 protein	13.9
	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	13.8
45	449801	AA477355	Hs.288300	hypothetical protein FLJ23231	13.8
	447078	AW885727	Hs.301570	ESTs	13.8
	441240	AA923749	Hs.132442	ESTs	13.8
	439398	AA284267	Hs.221504	ESTs	13.6
	404630			Target Exon	13.6
50	408321	AW405882	Hs.44205	cortistatin	13.6
	426427	M86699	Hs.169840	TTK protein kinase	13.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	13.5
	403055			C2002219*:gi|12737280|ref|XP_006682.2| keratin 18 [Ho	13.5
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	13.5
55	425261	BE385099	Hs.334727	hypothetical protein MGC3017	13.3
	439926	AW014875	Hs.137007	ESTs	13.3
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesin	13.2
	451141	AW772713	Hs.247186	ESTs	13.2
	447390	X95384	Hs.18426	translational inhibitor protein p14.5	13.2
60	419828	T81422	Hs.14922	ESTs	13.2
	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell growth factor	13.2
	410058	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	13.1
	407595	BE350012	Hs.248365	ESTs	13.1
	432721	AL121478	Hs.180532	glucose phosphate isomerase	13.1
65	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associ	13.0
	413314	BE081585		gb:QV2-BT0635-210400-156-b07 BT0635 Homo sapiens cDNA	13.0
	430929	AA489166	Hs.156933	ESTs	12.9
	449571	AW016812	Hs.200266	ESTs	12.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the prostate	12.8
70	417105	X60992	Hs.81226	CD6 antigen	12.6
	434263	N34895	Hs.44648	ESTs	12.6
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferritin associate	12.6
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	12.5
	437056	AI147061		gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	12.5
75	438768	AI307416	Hs.184675	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	12.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	12.5
	450738	AA010907	Hs.184456	hypothetical protein	12.4
	418205	L21715	Hs.83760	troponin I, skeletal, fast	12.4
	442994	AI026718	Hs.16954	ESTs	12.4
80	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone HEP20977	12.4
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	12.4
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylg	12.3
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	12.3

	410245	C17908	Hs.194125	ESTs	12.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	12.3
	418941	AA452970	Hs.155218	E1B-55kDa-associated protein 5	12.3
	432325	AW973209	Hs.261782	ESTs	12.3
5	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	12.3
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dystonia)	12.2
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone LNG00818	12.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	12.2
	427295	AW291212	Hs.293943	hypothetical protein MGC11266	12.2
10	415443	T07353	Hs.7948	ESTs	12.1
	429770	AI766047	Hs.99736	ESTs	12.1
	428955	AA579297	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	12.1
	435244	N77221	Hs.187824	ESTs	12.1
	432810	AA863400	Hs.23054	ESTs	12.1
15	434423	NM_005769	Hs.3844	LIM domain only 4	12.0
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit, beta type, 9	12.0
	459273	AW608906	Hs.334767	hypothetical protein MGC5629	12.0
	419945	AW290975	Hs.118923	ESTs	11.9
	442159	AW163390	Hs.278554	heterochromatin-like protein 1	11.9
20	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566	11.9
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	11.8
	401557			Target Exon	11.8
	434408	AI031771	Hs.132586	ESTs	11.8
	406747	AI925153	Hs.217493	annexin A2	11.8
25	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein (EGP) (KSA)	11.8
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor 1	11.8
	445655	AA873830	Hs.167746	B cell linker protein	11.7
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	11.7
	427527	AI809057	Hs.302063	immunoglobulin heavy constant mu	11.7
30	432287	AK001057	Hs.274268	Homo sapiens cDNA FLJ10195 fis, clone HEMBA1004771	11.6
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C W	11.6
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	11.6
	447082	T85314	Hs.42644	thioredoxin-like	11.5
	409931	BE293233	Hs.129771	ESTs	11.4
35	426172	AA371307	Hs.125056	ESTs	11.4
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(hnRNP methyltr	11.4
	456880	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcriptional enha	11.4
	433849	BE465884	Hs.280728	ESTs	11.4
	430519	AF129534	Hs.49210	F-box only protein 4	11.4
40	434442	AA737415	Hs.152826	ESTs	11.3
	457205	AI905780	Hs.198272	Target CAT	11.3
	422713	AA902780	Hs.119325	Huntingtin-interacting protein A	11.3
	443491	AW499665	Hs.9456	SWI/SNF related, matrix associated, actin dependent r	11.3
	424339	BE257148	Hs.145416	endoglycan	11.3
45	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	11.3
	450208	AI686945	Hs.272062	ESTs	11.2
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific factor 3, 73kD	11.2
	424965	AW956282	Hs.144609	Homo sapiens, Similar to RIKEN cDNA 5730578N08 gene,	11.2
	442737	AB002319	Hs.8663	KIAA0321 protein	11.2
50	409113	AA074897		gb:zm85a05.r1 Stratagene ovarian cancer (937219) Homo	11.2
	415782	AA169345	Hs.123177	ESTs	11.1
	417958	AA767382	Hs.193417	ESTs	11.1
	402539	AW502761	Hs.30909	KIAA0430 gene product	11.0
	413677	AW503116	Hs.301819	zinc finger protein 146	11.0
55	414706	AW340125	Hs.75989	KIAA0097 gene product	11.0
	421632	AA825426	Hs.238832	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	11.0
	438995	AI277986	Hs.164875	ESTs	11.0
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	10.9
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 3'	10.9
60	451655	H85689	Hs.225560	ESTs	10.9
	429237	AA448417	Hs.104990	ESTs	10.9
	427719	AI393122	Hs.134726	ESTs	10.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	10.8
	410093	AW589558	Hs.296120	ESTs, Weakly similar to KIAA0970 protein [H.sapiens]	10.8
65	400080			Eos Control	10.8
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643	10.8
	401539			NM_002675:Homo sapiens promyelocytic leukemia (PML),	10.8
	446099	T93096	Hs.17126	hypothetical protein MGC15912	10.7
	451066	AI758660	Hs.206132	ESTs	10.7
70	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypothetical protein [	10.7
	451730	AF095687	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	10.7
	428054	AI948688	Hs.266619	ESTs	10.6
	441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (from clone DKFZ	10.6
	438654	AI005270	Hs.123543	ESTs	10.6
75	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kinase	10.6
	449035	AI815728	Hs.19980	DNA polymerase epsilon p12 subunit	10.6
	436137	AI056769	Hs.133512	ESTs	10.6
	417863	AB000450	Hs.82771	vaccinia related kinase 2	10.6
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside triphosphate pyrop	10.6
80	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen inducible gene	10.6
	454355	AW812535		gb:CM4-ST0182-051099-021-c09 ST0182 Homo sapiens cDNA	10.6
	435542	AA687376	Hs.269533	ESTs	10.6
	431386	AA504359	Hs.110067	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	10.5

	416564	AW795793	Hs.179827	Homo sapiens cDNA FLJ12257 fis, clone MAMMA1001501, h	10.5
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT2RM4002390	10.5
	408329	AF155510	Hs.44227	heparanase	10.5
	410146	AW592655		gb:hf45f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA c	10.5
5	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (	10.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	10.4
	407241	M34516		gb:Human omega light chain protein 14.1 (Ig lambda ch	10.4
	435061	AI651474	Hs.163944	ESTs	10.4
	409653	AW451693	Hs.220826	ESTs	10.4
10	428294	AA425488		gb:zw46d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	10.4
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sensitivity prote	10.4
	408809	AW274673	Hs.279706	ESTs, Weakly similar to A47582 B-cell growth factor p	10.4
	410174	AA306007	Hs.59461	DKFZP434C245 protein	10.4
	424792	U92538	Hs.153138	origin recognition complex, subunit 5 (yeast homolog)	10.3
15	422406	AF025441	Hs.116206	Opa-interacting protein 5	10.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelati	10.3
	413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human mucosal lymph	10.3
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypothetical protein [	10.3
	448119	H38587	Hs.82295	dedicator of cyto-kinesis 1	10.2
20	457288	AA521458	Hs.192738	ESTs	10.2
	402025			NM_021624:Homo sapiens histamine H4 receptor (HRH4),	10.2
	440572	AW183778	Hs.249584	ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN	10.2
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside transporters), m	10.2
	443780	NM_012068	Hs.9754	activating transcription factor 5	10.1
25	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapiens cDNA 5' en	10.1
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	10.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	10.1
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo sapiens cDNA	10.1
	422470	AB017919	Hs.117232	peptidyl arginine deiminase, type V	10.1
30	449501	AI652924	Hs.231942	ESTs	10.1
	420731	AL042052	Hs.104432	ESTs	10.1
	404345	AA730407	Hs.159156	protocadherin 11	10.1
	400438	AF185611		Target	10.1
	438170	AI916685	Hs.194601	ESTs	10.1
35	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	10.1
	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	10.1
	427766	AA412258	Hs.188817	ESTs	10.1
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.0
	403038			Target Exon	10.0
40	434674	AA831879	Hs.136985	ESTs	10.0
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTE	10.0
	439428	AA835825	Hs.190490	ESTs	10.0
	403310			Target Exon	9.9
	408392	U28831	Hs.44566	KIAA1641 protein	9.9
45	421849	AW410872	Hs.108894	hypothetical protein FLJ20411	9.9
	433384	AI021992	Hs.124244	ESTs	9.9
	443343	BE409809	Hs.301005	purine-rich element binding protein B	9.9
	437267	AW511443	Hs.258110	ESTs	9.9
	455978	AI310151	Hs.173524	ESTs	9.9
50	435851	AA700946	Hs.191933	ESTs	9.9
	452243	AL355715	Hs.28555	programmed cell death 9	9.9
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	9.9
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	9.9
	436669	AA535975	Hs.174308	Homo sapiens, clone IMAGE:3453347, mRNA, partial cds	9.8
55	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), member 2	9.8
	417087	AA193193	Hs.188325	Homo sapiens cDNA FLJ11484 fis, clone HEMBA1001835	9.8
	455855	BE147440		gb:RC1-HT0229-080100-015-f09 HT0229 Homo sapiens cDNA	9.8
	410390	AA876905	Hs.125286	ESTs	9.8
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid transpo	9.8
60	442660	AW138174	Hs.130651	ESTs	9.8
	436186	BE390717	Hs.5074	similar to S. pombe dim1	9.8
	425773	NM_015556	Hs.172180	KIAA0440 protein	9.8
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	9.7
	418347	AA216419		gb:nc16e03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone si	9.7
65	448752	AA593867	Hs.300842	KIAA1608 protein	9.7
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone THYRO1001322	9.7
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	9.7
	430752	AA485330	Hs.303278	ESTs	9.7
	436523	BE612990	Hs.5212	single-strand selective monofunctional uracil DNA gly	9.7
70	415740	N80486	Hs.39911	Homo sapiens mRNA for FLJ00089 protein, partial cds	9.7
	411930	F06485	Hs.7740	oxysterol binding protein-like 1	9.7
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H	9.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical protein [	9.6
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA1011 protein	9.6
75	434957	AF283775	Hs.35380	x 001 protein	9.6
	407292	AA876638		gb:nz45e06.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone s	9.6
	459109	AW292447	Hs.140821	ESTs	9.6
	457892	AA744389		gb:ny51e10.s1 NCI_CGAP_Pr18 Homo sapiens cDNA clone s	9.6
	432074	AA525248	Hs.149723	ESTs	9.6
80	440463	AI733087	Hs.129994	ESTs	9.6
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	9.6
	445326	AI220072	Hs.165893	ESTs	9.6
	434953	BE049102	Hs.121573	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALI [H.sap	9.6

	420361	N92054	Hs.194718	zinc finger protein 265	9.6
	415853	H06016	Hs.100855	ESTs	9.6
	429599	AA806106	Hs.123664	ESTs	9.6
	417037	BE083936	Hs.80976	antigen identified by monoclonal antibody KI-67	9.6
5	449317	AW293413	Hs.132906	19A24 protein	9.6
	436588	AA759233	Hs.126506	ESTs	9.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	9.5
	401069			C11000374*:gi|10764778|gb|AAG22817.1|AF302150_1 (AF30	9.5
	414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PLACE1008851	9.5
10	409902	AI337658	Hs.156351	ESTs	9.5
	432258	AW973078	Hs.293039	ESTs	9.5
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serine/threonine-s	9.5
	405536			NM_005805:Homo sapiens 26S proteasome-associated pad1	9.5
	418216	AA662240	Hs.283099	AF15q14 protein	9.5
15	434573	AW372340	Hs.159717	ESTs	9.5
	439354	AF086174		gb:Homo sapiens full length insert cDNA clone ZB94A08	9.5
	455410	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo sapiens cDNA	9.5
	400736			Target Exon	9.5
	419474	AW968619	Hs.155849	ESTs	9.4
20	406464			C17000168:gi|7294725|gb|AAF50062.1| (AE003544) CG7547	9.4
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	9.4
	427258	AA400091	Hs.39421	ESTs	9.4
	404680			Target Exon	9.4
	433840	AA129782	Hs.3576	Homo sapiens mRNA full length insert cDNA clone EUROI	9.4
25	423642	AW452650	Hs.157148	hypothetical protein MGC13204	9.4
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapiens]	9.4
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	9.4
	451846	T65840	Hs.11762	ESTs	9.4
	419988	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, complete cds	9.4
30	402967			Target Exon	9.3
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.3
	441075	AA915991	Hs.179214	ets variant gene 3	9.3
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, p	9.3
	404649			Target Exon	9.3
35	420897	AW139261	Hs.232280	ESTs	9.3
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	9.3
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	9.3
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothetical protein [	9.3
	420101	AW500529	Hs.95180	KIAA0767 protein	9.3
40	428166	AA423849	Hs.79530	M5-14 protein	9.3
	420022	AA256253	Hs.120817	ESTs	9.3
	444020	R92962	Hs.35052	ESTs	9.3
	454765	AW819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo sapiens cDNA	9.3
	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA, partial cds	9.3
45	418506	AA084248	Hs.85339	G protein-coupled receptor 39	9.3
	415009	C75253	Hs.220950	ESTs	9.3
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.3
	433348	AA877996	Hs.125376	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase	9.2
	417881	AI879117		gb:au54g09.y1 Schneider fetal brain 00004 Homo sapien	9.2
50	446354	AW449650	Hs.202249	ESTs	9.2
	427018	AA397538	Hs.136280	Homo sapiens cDNA: FLJ22288 fis, clone HRC04157	9.2
	434410	AA632644		gb:np87b07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone s	9.2
	448072	AI459306	Hs.24908	ESTs	9.2
	457322	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257	9.2
55	424317	AI865032	Hs.26017	ESTs	9.2
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	9.2
	404112	BE302729	Hs.173162	neighbor of COX4	9.2
	433334	AI927208	Hs.231958	matrix metalloproteinase 28	9.1
	434960	AW374941	Hs.72545	ESTs	9.1
60	431658	BE409917	Hs.266935	tRNA selenocysteine associated protein	9.1
	439158	R60323	Hs.193888	ESTs	9.1
	443081	H86858	Hs.132909	ESTs	9.1
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	9.1
	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN SURFEIT LOCUS	9.1
65	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	9.1
	430780	N95102	Hs.334858	hypothetical protein MGC12250	9.1
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defective, S. cere	9.1
	418379	AA218940	Hs.137516	fidgetin-like 1	9.1
	431405	AI470895	Hs.252574	ribosomal protein L10a	9.0
70	405454			C12000541:gi|5729884|ref|NP_006539.1| IGF-II mRNA-bin	9.0
	438362	AA805678	Hs.12326	ESTs	9.0
	401940			Target Exon	9.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.0
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	9.0
75	459086	AA021163	Hs.22287	ESTs	9.0
	418653	AI734064	Hs.136212	ESTs	9.0
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	9.0
	437534	AA814471	Hs.291800	ESTs	9.0
	435074	AI760944	Hs.116937	ESTs	9.0
80	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA, complete cds	9.0
	442829	AW263123	Hs.127554	ESTs	9.0
	431675	AA699965	Hs.202375	ESTs	9.0
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	8.9

	420183	W92885	Hs.143408	ESTs	8.9
	421133	AA814971	Hs.257634	ESTs	8.9
	407605	W03512	Hs.6479	hypothetical protein MGC13272	8.9
	441370	AI242433	Hs.270085	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	8.9
5	437966	AW891130	Hs.38173	ESTs	8.9
	426360	AW290981	Hs.211296	ESTs, Weakly similar to 2109260A B cell growth factor	8.8
	448111	AA053486	Hs.20315	interferon-induced protein with tetratricopeptide rep	8.8
	408021	AW137133	Hs.245867	ESTs	8.8
	429228	AI553633	Hs.337139	ESTs	8.8
10	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1) mRNA, partia	8.8
	431184	AW970116	Hs.310616	ESTs	8.8
	425219	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	8.8
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDNA clone EUROI	8.8
	432573	AA553612	Hs.324696	KIAA1594 protein	8.8
15	450881	W80462	Hs.270521	ESTs, Highly similar to ALU2_HUMAN ALU SUBFAMILY SB S	8.8
	437835	AI146771	Hs.158008	ESTs	8.8
	453204	R10799	Hs.191990	ESTs	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
	408805	H69912	Hs.48269	vaccinia related kinase 1	8.7
20	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuolar proton pu	8.7
	422583	AA410506	Hs.27973	KIAA0874 protein	8.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	8.7
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	8.7
	454132	AW131759	Hs.248286	ESTs	8.7
25	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	8.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-like	8.7
	441525	AW241867	Hs.127728	ESTs	8.7
	459539	AI279186		gb:qm24a04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone 3'	8.7
	443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	8.7
30	424255	AI192657	Hs.143897	dysferlin, limb girdle muscular dystrophy 2B (autosom	8.7
	459435	AA320038		gb:EST22383 Adipose tissue, white II Homo sapiens cDN	8.7
	443117	AI248826	Hs.42029	ESTs	8.6
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	8.6
	442505	AW003775	Hs.198248	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, p	8.6
35	430901	AA488833	Hs.126711	ESTs, Weakly similar to I38588 reverse transcriptase	8.6
	439223	AW238299	Hs.250618	UL16 binding protein 2	8.6
	417739	Z43995		gb:HSC1QB121 normalized infant brain cDNA Homo sapien	8.6
	415961	H10983	Hs.155919	ESTs	8.6
	424042	Y10601	Hs.137674	ankyrin-like with transmembrane domains 1	8.6
40	451035	AU076785	Hs.430	plastin 1 (I isoform)	8.6
	447155	AA100605	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPOSIS LOCUS PRO	8.6
	412668	AA456195	Hs.10056	hypothetical protein FLJ14621	8.6
	458042	AW058464	Hs.6430	protein with polyglutamine repeat; calcium (ca2) home	8.6
	456530	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKF	8.6
45	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	8.6
	445006	W91903	Hs.124814	ESTs	8.6
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolo	8.5
	455161	BE145900		gb:MR0-HT0208-221299-204-b12 HT0208 Homo sapiens cDNA	8.5
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cerevisiae)	8.5
50	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	8.5
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interacting protein	8.5
	415018	U49395	Hs.77807	purinergic receptor P2X, ligand-gated ion channel, 5	8.5
	404534			C11001758*:gi|12621132|ref|NP_075243.1| MEGF1 [Rattus	8.5
	438451	AI081972	Hs.220261	ESTs	8.5
55	435176	AA744875	Hs.189413	ESTs	8.5
	443245	AI040955	Hs.151973	hypothetical protein FLJ23511	8.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	8.5
	457478	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), catalytic subuni	8.5
	403839			Target Exon	8.5
60	434932	BE613162	Hs.284135	hypothetical protein MGC3036	8.5
	420991	AW504814	Hs.121004	Homo sapiens mRNA for FLJ00111 protein, partial cds	8.4
	457854	BE547674	Hs.204169	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	8.4
	455994	BE179190		gb:RC0-HT0613-210300-032-f07 HT0613 Homo sapiens cDNA	8.4
	402796			Target Exon	8.4
65	423426	AW389579	Hs.128434	Homo sapiens ELISC-1 mRNA, partial cds	8.4
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (from clone DKF	8.4
	404110			NM_020245*:Homo sapiens tubby super-family protein (T	8.4
	424441	X14850	Hs.147097	H2A histone family, member X	8.4
	433155	AL037035	Hs.100426	Homo sapiens cervical cancer metastasis-suppressor 1 (B	8.4
70	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	8.4
	406867	AA157857	Hs.182265	keratin 19	8.4
	418278	AI088489	Hs.83937	hypothetical protein	8.4
	458696	AW375333	Hs.199890	ESTs	8.4
	456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	8.4
75	403152	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene homolog-like	8.4
	407649	BE066724	Hs.37427	erythrocyte membrane protein band 4.1 (elliptocytosis	8.4
	448387	AI874402	Hs.170810	ESTs	8.4
	433671	AW138797	Hs.132906	19A24 protein	8.4
	425891	AI041717	Hs.132141	ESTs	8.4
80	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 protein [H.sapie	8.4
	439079	AF085937	Hs.38348	ESTs	8.4
	458115	BE091587		gb:IL2-BT0731-240400-069-H04 BT0731 Homo sapiens cDNA	8.4
	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associated	8.4

	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	8.3
	443056	AI457996	Hs.132578	ESTs	8.3
	410391	H17881	Hs.15043	Homo sapiens clone FLB5227 PRO1367 mRNA, complete cds	8.3
	407989	AW135208	Hs.256092	ESTs	8.3
5	410536	N39533		gb:yv27d04.s1 Soares fetal liver spleen 1NFLS Homo sa	8.3
	452273	AI870685	Hs.231022	ESTs	8.3
	454297	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	8.3
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	8.3
	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) b	8.3
10	432891	AF161483	Hs.279761	HSPC134 protein	8.3
	419923	AW081455	Hs.120219	ESTs	8.2
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone KAT11914	8.2
	435452	AA831004	Hs.124874	ESTs	8.2
	418683	U90908	Hs.87241	hypothetical protein from clones 23549 and 23762	8.2
15	440065	W03476	Hs.266331	hypothetical protein MGC4595	8.2
	439752	T78968	Hs.14411	ESTs	8.2
	447983	AW612726	Hs.282113	ESTs, Weakly similar to I38022 hypothetical protein [	8.2
	441966	AA568689	Hs.16131	hypothetical protein FLJ12876	8.2
	408182	AA047854		gb:zf49g04.r1 Soares retina N2b4HR Homo sapiens cDNA	8.2
20	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	8.2
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OVARC1002143	8.2
	414962	AF273304	Hs.235376	XPMC2 protein	8.2
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), soluble	8.2
	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	8.2
25	413940	AI633205	Hs.159914	ESTs, Weakly similar to I78885 serine/threonine-speci	8.2
	437277	AA748016	Hs.123370	ESTs	8.2
	431445	AA505135	Hs.44037	ESTs	8.1
	418927	BE349635	Hs.190284	ESTs	8.1
	452446	AA086123	Hs.297856	ESTs	8.1
30	445380	AI222019	Hs.144838	ESTs	8.1
	421174	AW969058	Hs.291974	ESTs, Moderately similar to A46010 X-linked retinopat	8.1
	444374	AA009841	Hs.11039	hypothetical protein MGC2722	8.1
	417247	N58024		gb:yv63c01.s1 Soares fetal liver spleen 1NFLS Homo sa	8.1
	438335	AI498421	Hs.243168	ESTs	8.1
35	445235	AI564022	Hs.138207	ESTs	8.1
	422585	NM_016186	Hs.118620	protein Z-dependent protease inhibitor precursor	8.1
	442522	AI087038	Hs.146592	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	8.1
	430684	AI808979	Hs.293193	ESTs	8.1
	446442	BE221533	Hs.257858	ESTs	8.1
40	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypothetical protein [	8.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein product [H.sa	8.0
	449539	W80363	Hs.58446	ESTs	8.0
	406663	U24683	Hs.302063	immunoglobulin heavy constant mu	8.0
	423767	H18283	Hs.132753	F-box only protein 2	8.0
45	450937	R49131	Hs.26267	ATP-dependant interferon response protein 1	8.0
	430977	AA490069	Hs.306676	Homo sapiens cDNA FLJ14302 fis, clone PLACE2000003	8.0
	455677	BE066061	Hs.8867	cysteine-rich, angiogenic inducer, 61	8.0
	436706	AA725808	Hs.194609	ESTs	8.0
	459407	N92114		gb:za22h11.r1 Soares fetal liver spleen 1NFLS Homo sa	8.0
50	444132	AK000452	Hs.10340	hypothetical protein FLJ20445	8.0
	437149	AI686651	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2	8.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	8.0
	411298	AW835858		gb:PM0-LT0017-031299-001-h07 LT0017 Homo sapiens cDNA	8.0
	432571	AF151054	Hs.278429	hepatocellular carcinoma-associated antigen 59	8.0
55	416295	AI064824	Hs.193385	ESTs	8.0
	427485	AF039652	Hs.178655	ribonuclease H1	8.0
	409857	AW501908		gb:UI-HF-BR0p-ajp-c-12-0-UI.r1 NIH_MGC_52 Homo sapien	7.9
	433854	AA610649	Hs.333239	ESTs	7.9
	458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo sapiens cDNA	7.9
60	423573	AA328504		gb:EST31993 Embryo, 12 week I Homo sapiens cDNA 5' en	7.9
	404495			C8001441*:gi|8923061|ref|NP_060114.1| hypothetical pr	7.9
	443135	AI376331	Hs.156103	ESTs	7.9
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	7.9
	413283	R78669	Hs.23756	hypothetical protein similar to swine acylneuraminate	7.9
65	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	7.9
	434197	AA627223		gb:nq63b04.s1 NCI_CGAP_Ov6 Homo sapiens cDNA clone si	7.9
	436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor protein 1	7.9
	434502	AW974915	Hs.116550	ESTs	7.9
	435507	AI143579	Hs.26510	vacuolar protein sorting 33B (yeast homolog)	7.9
70	444896	AI201480	Hs.144856	ESTs	7.9
	419320	H96666	Hs.6137	ESTs	7.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	7.9
	425569	AA359597	Hs.301701	Homo sapiens cDNA FLJ12073 fis, clone HEMBB1002387	7.9
	445209	AW294230	Hs.80988	collagen, type VI, alpha 3	7.9
75	449193	AI637997	Hs.195653	ESTs	7.9
	447397	BE247676	Hs.18442	E-1 enzyme	7.9
	455037	BE144549		gb:MR0-HT0167-081199-001-a02 HT0167 Homo sapiens cDNA	7.9
	453367	AW732847	Hs.70573	PKCI-1-related HIT protein	7.8
	439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothetical protein D	7.8
80	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	7.8
	406562			NM_004520*:Homo sapiens kinesin heavy chain member 2	7.8
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor 3, subunit 8	7.8
	413500	BE144914		gb:CM3-HT0183-181099-023-b05 HT0183 Homo sapiens cDNA	7.8

	436216	AA380887	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1,	7.8
	418623	AW194757	Hs.266804	ESTs	7.8
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapiens cDNA	7.8
	430146	AW815330		gb:QV0-ST0215-060100-083-a09 ST0215 Homo sapiens cDNA	7.8
5	441841	AA971819	Hs.176083	ESTs	7.8
	457677	AA628890	Hs.158701	ESTs	7.8
	421090	BE301870	Hs.101813	solute carrier family 9 (sodium/hydrogen exchanger),	7.8
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	7.8
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo sapiens cDNA	7.8
10	406410			C5000010*:gi|10440464|dbj|BAB15765.1| (AK024475) FLJ0	7.8
	453579	AI204463	Hs.61857	ESTs	7.8
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogene homolog-lik	7.7
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone COL05135	7.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa protein.	7.7
15	440777	AA994020	Hs.128553	ESTs	7.7
	446424	AW134529	Hs.244647	ESTs	7.7
	448004	AW451477	Hs.257456	ESTs	7.7
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S	7.7
	427080	AW068287	Hs.173466	ras-related C3 botulinum toxin substrate 2 (rho famil	7.7
20	451693	BE220445	Hs.279635	ESTs	7.7
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	7.7
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	7.7
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (polypyrimidin	7.7
	425423	NM_005897	Hs.157180	intracisternal A particle-promoted polypeptide	7.7
25	450663	H43540	Hs.25292	ribonuclease HI, large subunit	7.7
	432585	AA705591	Hs.190209	ESTs	7.7
	402682			Target Exon	7.7
	400247			Eos Control	7.7
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	7.7
30	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (from clone DKF	7.7
	405514			ENSP00000241075:TRRAP PROTEIN.	7.7
	412406	AW948172		gb:RC0-MT0013-280300-021-b06 MT0013 Homo sapiens cDNA	7.7
	440226	AA873387	Hs.207330	ESTs	7.7
	435625	H50654	Hs.113999	ESTs	7.7
35	418529	AW005695	Hs.250897	TRK-fused gene	7.6
	407758	D50915	Hs.38365	KIAA0125 gene product	7.6
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	7.6
	449938	AW970612	Hs.172635	Homo sapiens cDNA: FLJ21367 fis, clone COL03051	7.6
	422893	X98411	Hs.121555	myosin IF	7.6
40	451593	AF151879	Hs.26706	CGI-121 protein	7.6
	424148	BE242274	Hs.1741	integrin, beta 7	7.6
	447519	U46258	Hs.339665	ESTs	7.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	7.6
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	7.6
45	426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger),	7.6
	456926	AB018284	Hs.158688	KIAA0741 gene product	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo sapiens cDNA	7.6
	417086	AA194446	Hs.73451	ESTs, Weakly similar to S55024 nebulin, skeletal musc	7.6
50	418181	U37012	Hs.83727	cleavage and polyadenylation specific factor 1, 160kD	7.5
	436910	AA926944		gb:om68g01.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone 3'	7.5
	401008			Target Exon	7.5
	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacting protein	7.5
	446820	AW295037	Hs.254986	ESTs	7.5
55	439279	AI039473	Hs.130636	ESTs	7.5
	426116	AA868729	Hs.144694	ESTs	7.5
	410098	BE326839	Hs.17433	hypothetical protein FLJ20967	7.5
	422326	AI114875	Hs.78592	eukaryotic translation initiation factor 2B, subunit	7.5
	435513	AW404075	Hs.42785	DC11 protein	7.5
60	421629	N80121	Hs.4983	ESTs	7.4
	434663	AA641972	Hs.130058	ESTs	7.4
	452461	N78223	Hs.108106	transcription factor	7.4
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	7.4
	405417			CX001144*:gi|7242973|dbj|BAA92547.1| (AB037730) KIAA1	7.4
65	414076	AA467736		gb:nc74e05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone, m	7.4
	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	7.4
	449610	AI242042	Hs.14044	ESTs	7.4
	403397			Target Exon	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
70	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant; spastin)	7.4
	404914			NM_004046*:Homo sapiens ATP synthase, H+ transporting	7.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activating fact	7.4
	432820	AI554057	Hs.152477	ESTs	7.4
	418978	T85295	Hs.268606	ESTs	7.4
75	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonine kinase 21)	7.4
	454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo sapiens cDNA	7.4
	434522	AF189259	Hs.283081	gamma-aminobutyric acid (GABA) receptor, theta	7.4
	458236	AW297043	Hs.255604	ESTs, Weakly similar to A47234 homeobox protein H6 [H	7.4
	441043	AA913422	Hs.192104	ESTs	7.4
80	422838	AA524065	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone HSI08202	7.3
	455096	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens cDNA	7.3
	442307	AW027690	Hs.90037	ESTs	7.3
	425453	AW374284	Hs.297215	Homo sapiens chromosome 19, cosmid R26894	7.3

	455327	AW896238	Hs.334805	Homo sapiens cDNA FLJ14604 fis, clone NT2RP1000363, m	7.3
	420982	AW576160	Hs.100729	KIAA0692 protein	7.3
	424563	AA446932	Hs.151428	ret finger protein 2	7.3
	417125	AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein 1	7.3
5	453902	BE502341	Hs.3402	ESTs	7.3
	446842	AI343510	Hs.176992	ESTs	7.3
	454128	AL031259	Hs.41639	programmed cell death 2	7.3
	427011	BE302729	Hs.173162	neighbor of COX4	7.3
	450872	AI742594		gb:wg55h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	7.3
10	451512	AI800236	Hs.207080	ESTs	7.3
	406708	AI282759		gb:qt84a01.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone I	7.3
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypothetical protein [	7.3
	459304	AW005809	Hs.281076	ESTs, Weakly similar to CHD4_HUMAN CHROMODOMAIN HELIC	7.3
	401375			NM_020999*:Homo sapiens neurogenin 3 (NEUROG3), mRNA.	7.3
15	413258	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapiens cDNA	7.3
	406016			Target Exon	7.3
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	7.3
	422742	AA316117	Hs.337128	ESTs	7.3
	440031	BE045970	Hs.244746	ESTs	7.3
20	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ11079 fis, clone PLACE1005111	7.3
	449656	AA002008	Hs.188633	ESTs	7.3
	444310	AI140432	Hs.175936	ESTs	7.3
	459274	AA382590	Hs.170980	KIAA0948 protein	7.3
	425404	BE048060	Hs.133494	Homo sapiens clone TCCCIA00164 mRNA sequence	7.3
25	431150	T63857		gb:yc16e01.s1 Stratagene lung (937210) Homo sapiens c	7.3
	443217	NM_001545	Hs.9078	immature colon carcinoma transcript 1	7.2
	413405	AW022253	Hs.215976	ESTs	7.2
	447653	BE327277	Hs.161145	ESTs	7.2
	414704	NM_014757	Hs.76986	mastermind (Drosophila), homolog of	7.2
30	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, clade B (o	7.2
	409188	AW363284	Hs.32553	ESTs	7.2
	453493	AL039478	Hs.304447	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	456111	AK000150	Hs.78185	MAX-like bHLHZIP protein	7.2
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	7.2
35	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	7.2
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine protease	7.2
	445336	AW815036	Hs.151251	ESTs	7.2
	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	7.2
40	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	7.2
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP3002304	7.2
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polypeptide 1	7.2
	416450	AA180467		gb:zp14g08.s1 Stratagene fetal retina 937202 Homo sap	7.2
	449714	AB033015	Hs.23941	KIAA1189 protein	7.2
45	455447	AW947507		gb:RC0-MT0002-140300-011-a12 MT0002 Homo sapiens cDNA	7.2
	437154	AI023133	Hs.10739	ESTs	7.2
	423059	AW378445	Hs.123080	Homo sapiens unknown protein mRNA, partial cds	7.2
	419092	J05581	Hs.89603	mucin 1, transmembrane	7.2
	426736	AA431615	Hs.130722	ESTs	7.2
50	417748	Z43011	Hs.21169	ESTs	7.2
	434748	AI862604	Hs.211884	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	438929	AW195515	Hs.253177	ESTs	7.2
	452061	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	7.1
	446416	AV658299	Hs.163959	ESTs	7.1
55	415023	AA932146	Hs.133494	Homo sapiens clone TCCCIA00164 mRNA sequence	7.1
	434766	AA742222	Hs.120634	ESTs	7.1
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell growth factor	7.1
	420252	AW270404	Hs.193161	ESTs	7.1
	435403	AA779987	Hs.269658	ESTs	7.1
60	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo sapiens cDNA	7.1
	427908	AA417272	Hs.24122	ESTs	7.1
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitter transporter	7.1
	400098			Eos Control	7.1
	412647	AW975090		gb:EST387196 MAGE resequences, MAGN Homo sapiens cDNA	7.1
65	437234	AI472213	Hs.247711	hypothetical protein FLJ20557	7.1
	453366	AW958751	Hs.28921	zinc finger protein	7.1
	425803	AI825204	Hs.211408	ESTs	7.1
	447383	N24231		gb:yx22a11.r1 Soares melanocyte 2NbHM Homo sapiens cD	7.1
	423864	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	7.1
70	450799	AW407504		gb:UI-HF-BM0-adk-g-12-0-UI.r1 NIH_MGC_38 Homo sapiens	7.1
	409592	BE280951	Hs.55058	EH-domain containing 4	7.1
	453945	NM_005171	Hs.36908	activating transcription factor 1	7.1
	425196	AL037915	Hs.155097	carbonic anhydrase II	7.0
	439778	AL109729	Hs.99364	putative transmembrane protein	7.0
75	417662	R07478	Hs.268845	ESTs	7.0
	438087	AI863770	Hs.190422	ESTs	7.0
	452724	R84810	Hs.30464	cyclin E2	7.0
	448633	AA311426	Hs.21635	tubulin, gamma 1	7.0
	433154	AA578526	Hs.160994	ESTs	7.0
80	440094	AI651558	Hs.270372	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.0
	409253	H91200	Hs.52002	CD5 antigen-like (scavenger receptor cysteine rich fa	7.0
	431270	BE046609		gb:hn41e11.x1 NCI_CGAP_RDF2 Homo sapiens cDNA clone 3	7.0
	407629	AA649242	Hs.62632	ESTs	7.0

	408296	AL117452	Hs.44155	DKFZP586G1517 protein	7.0
	445439	BE243084	Hs.12719	regulator of nonsense transcripts 1	7.0
	427106	AA398193	Hs.97584	ESTs	7.0
	408623	AW811978	Hs.254037	ESTs	7.0
5	426561	AA381437		gb:EST94514 Activated T-cells I Homo sapiens cDNA 5'	7.0
	408492	AA555217	Hs.183684	eukaryotic translation initiation factor 4 gamma, 2	7.0
	428894	AA437066	Hs.271736	ESTs	7.0
	419102	AA234098	Hs.42424	ESTs, Weakly similar to 2004399A chromosomal protein	7.0
	429067	AA446019	Hs.104967	ESTs	7.0
10	422684	BE561617	Hs.119192	H2A histone family, member Z	7.0
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase kinase 5	7.0
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H.	7.0
	443599	AI079559	Hs.134125	ESTs	7.0
	400715			ENSP00000237081*:KIAA1217 PROTEIN (FRAGMENT).	7.0
15	446514	AW449233	Hs.150847	ESTs	7.0
	413992	W26276	Hs.136075	RNA, U2 small nuclear	7.0
	402442			Target Exon	7.0
	419497	NM_006410	Hs.90753	Tat-interacting protein (30kD)	7.0
	439575	W79259		gb:zd75c06.r1 Soares_fetal_heart_NbHH19W Homo sapiens	7.0
20	407027	U63312		gb:Human cosmid LL12NC01-242E1, ETV6 gene, exons 1B a	7.0

Table 15B

25 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
408182	104479_1	AA047854 AA057506 AA053841
409113	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
409857	1156298_1	AW501908 AW502959 AW502540
410146	1178974_1	AW592655 R05927 R06916
410536	1207322_1	N39533 AW753094 AW753093
411298	1237955_1	AW835858 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835 AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838
412406	1293055_1	AW948172 AW948178 AW948169 AW948176 AW948191 AW948192 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181 AW948177 AW948171 AW948183 AW948173
412647	1317604_1	AW975090 N44182
413258	1355998_1	BE075114 BE075283 BE075118
413314	1360034_1	BE081585 BE081717 BE081863 BE081794 BE081659
413500	1373933_1	BE144914 BE394989
414076	141490_1	AA467736 AA135210 AW968166 AA467804
416450	159551_1	AA180467 AA449184 AA464831 AA505048
417247	1660859_1	N58024 T58194 T11693 N64222 T05848
417739	1696198_1	Z43995 R12357 R34740
417881	170544_1	AI879117 AW161351 Z45755 BE003661 AA206949 AA476541
418347	174149_1	AA216419 F03238 AA229517
422429	216469_1	AA310527 AW962295 Z44865 H06641
423573	229714_1	AA328504 AA327783 AW962370
426561	269158_1	AA381437 AA628833 AW407275
428294	289365_1	AA425488 AA496895 F23221
430146	313562_1	AW815330 AW968170 AI732687 AI732725 AA468343 AA467817 AW063961
430151	313668_1	AW968203 AI732757 AA470353 AA468025 AA468479 AI734151
430709	322338_1	R34356 AW969880 AA484613
430848	324621_1	AW021726 AA487752 AA488085
431150	328626_1	T63857 AW971220 AA493469 T63699
431270	330675_1	BE046609 BE046118 AA501504
432363	345469_1	AA534489 AW970240 AW970323
434197	381655_1	AA627223 AA643443 AA650619 AA643463 AA643453 AA643439 AA643438 AW802964 AW821595 AW821594 AA643431 AA643432 AW827513
434407	385744_1	AW815333 AW815409 AA632563
434410	385798_1	AA632644 AA635376 AA664188
436910	429182_1	AA926944 AA767974 AA737237
437056	432262_1	AI147061 AA743380 AA765223 AW976398 AI803927
439354	47146_1	AF086174 W31796 W04694
439575	47400_1	W79259 AF086396 W73927
444314	600667_1	AI140497 AW749625 AW749626 AW749644
447197	711623_1	R36075 AI366546 R36167
447383	71990_1	N24231 BE617964 N36313
450799	847242_1	AW407504 W31274 AI738877
450872	849959_1	AI742594 AI761397 R31198 AI819332 R31257
454355	1130264_1	AW812535 AW812536 AW390307
454639	1227728_1	AW811633 AW811652 AW811898
454765	1233905_1	AW819629 AW854320

455037	1249783_1	BE144549 AW851677 AW851643 AW851711 AW851719
455096	1253078_1	AW855718 AW855740 AW855748
455161	1256167_1	BE145900 AW859906 BE145895 BE145831 BE145914 BE145820 BE145817 BE145890 BE145908
455410	1288380_1	AW936678 AW936637 AW936682 AW936685 AW936817 AW936811 AW936762 AW936653 AW936815 AW936812 AW936683 AW936822 AW936823 AW936821 AW936732 AW936730 AW936781
455447	1292444_1	AW947507 AW947509 AW947791 BE008335
455855	1375834_1	BE147440 BE147708 BE147563 BE147456
455994	1398737_1	BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
457892	432926_1	AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698
458080	471050_1	BE142728 AA834047 AW937124
458115	47705_29	BE091587 BE091730 BE091577 BE091655 BE091729 BE091640 BE091578 BE091727 BE091803 BE091660 BE091721 BE088255 BE076582 AW992312 BE008791 BE082385 BE083504 BE083456 AW997967 AW997991 BE166595 AW843686 AW844334 BE079091 AW603391 BE081427 BE079514 BE184580 BE009962 BE008722 AW579912 AW860561 AW890184 AW795276 AW860410 AW860411 AW610330 AW860564 AW860578 AW862519 BE073924 BE008687 BE073857 BE073921 AW274106 BE011060 AW268120 AI335067 AW793748 AW997736 BE080117 AW867987 AI547161 AW844767 AW393596 AW579444 BE083334 AI547158 AW799863 AA585179 AW992792 AW882215 BE011913 AW997894 AI547159 AW992772 AW581178 AA092247 AW843916 BE079190 AW878478 BE083648 BE066454 AI469937 AW393594 AW579899 AW939276 BE173265 AW878631 AW878638 AW992802 BE079913 AA633638 AW369008 BE076590 AW843456 AW992791 BE173247 AW843921 AW843333 AW878334 BE090235 BE078240 BE066325 AW603276 BE169310 AW817299 BE091641 BE000160 AW898164 AW994624 AW999391 AW862797 AW899438 AW750667 AW939685 AW940017 AI200402 BE167391 AW939318 AW799837 AW939953 AW939681 BE078188 AA449059 BE076595 AW297451 BE076544 AW803372 BE081223 AW939237 BE084239 AI174202 BE077804 BE078028 AA512912 AI124808 AI147524 AI884882 AW939962 AW939254 BE171687 AW998400 AW998348 AW998353 AW998288 AW998303 AW998302 AW998299 AA502748 BE077882 AW998295 BE090238 AW604665 AI423051 BE093093 AW579913 AW606384 BE006143 BE170415 AW998054 BE084608 AW992779 BE088111 AW610555 AW844153 AW939423 BE085404 AW579905 BE080994 AW468482 AW876865 BE091581 BE080940 AI811189 AW868088 AW893127 BE080064 BE184254 AW998350 AW884228 AW992315 AW992364 BE091569 AW750680 BE066386 AA578227 BE091735 AW938830 BE078710 BE087253 BE084182 AW800859 AW801017 AW581371 BE088300 AW995341 BE090233 AW663786 BE091739 BE080113 AW578162 AW799799 AW992366 AW994673 BE185170 AW792778 AW663225 BE075590 BE080111 AA682934 BE090227 AI475441 BE085684 BE090223 AW581366 BE010705 AW898740 BE088170 AW992375 BE077833 BE083557 BE010688 AW998450 AW803434 BE083280 AW892655 AA506666 BE088288 BE005859 BE173856 BE001319 AA610814 BE011965 BE005855 BE005869 AA973929 BE185729 AW884298 BE185743 BE001342 BE005876 AI002988 AW799056 BE085411 AW841264 AW603110 BE006134 BE006139 BE006148 BE006147 BE006155 AA578273 BE008706 BE185440 AW946428 AA501940 AW603114 BE085757 AI460195 AA491145 AA772914 AA632730 AA508388 BE080196 BE185442 BE093446 AW946433 BE080119 BE001352 AW839003 BE006145 BE085405 BE008680 BE081428 AW581373 AW607246 BE094328 BE001336 AW868170 BE074119 AW884149 BE091734 BE008744 AI540867 BE185806 BE080193 BE185858 AA476398 BE081040 BE074724 BE085426 BE074725 AW998297 AW867606 BE185798 AW898734 BE076369 BE081672 BE088178 AA610264 BE088118 AA284217 AW578085 BE074518 BE001359 BE001328 AW820227 AW868196 AW868190 AW904548 BE008526 BE012037 BE079061 BE005870 AW867804 AW878433 BE008751 BE005875 BE008748 BE093440 BE183050 AA506676 BE001329 BE008803 BE080123 BE008041 AW994688 AW994675 AW994760 AW994691 AW994681 BE080189 BE080112 AW868173 AI768000 AW883094 AW868179 BE080201 AW665449 BE067473 BE008746 BE184053 BE076437 BE076376 BE076402 AA480395 BE082436 BE184134 BE185224 BE085428 BE008682 AW868181 AW998358 AW866102 BE083507 BE077974 BE008835 BE093439 BE076108 AI416987 BE008788 BE069909 BE093441 BE185502 BE183053 AW750669 BE011812 BE008672 BE081684 BE093445 AW868184 BE081839 BE008797 AW842067 BE008678 BE008670 BE551820 AW838974 BE081637 BE046696 BE008673 BE010328 BE083250 BE089614 BE082052 BE081424 BE001678 AW581368 AA503194 AW883721 AW883522 BE085564 AW868717 BE171078 BE078249 BE078194 AA555255 BE083486 AW842081 AW842080 AW868204 BE008717 AA484369 AI831719 AW997365 BE079327 AA503956 BE091999 AW793852 BE080251 BE078086 BE092515 BE170364 AW866193 AW067958 BE008042 BE008761 BE081681 BE081671 AW867400 BE082003 BE082253 BE081439 BE081486 BE081692 AW606020 AA501778 AW996417 BE045756 BE088394 AA491068 AW893099 AW578695 BE150440 BE006150 BE084684 AW992796 BE086891 AW866792 AW753605 BE082045 BE081106 BE008373 BE075399 AW996628 AW578707 BE084309 AW753604 BE185916 AW842220 BE185222 BE006152 BE008795 AW578706 BE080256 BE183984 AI934532 AA449648 AW578699 BE150514 AW883580 AA493568 BE085748 AW753601 BE150562 AW882677 BE091797 AW899123 BE081679 BE080121 AW606787 AW603410 BE001317 AW905799 BE150513 BE092206 AW996343 BE086922 BE008806 AW844759 AW606009 BE150487 AW750728 BE150491 BE150515 AW606010 BE150508 BE008718 AW578702 BE150509 AA436751 AW883918 BE183883 AW753607 BE008669 BE150446 AA533458 BE079219 AW838884 AW063806 AW063837 AW878479 BE078815 BE008802 AW992789 BE007925 AW802204 BE011825 BE092130 BE184059 BE079087 BE150568 BE185497 BE078308 AW883761 AW842295 BE161523 AA484796 AA480390 AW994667 BE073205 AW607316 BE083201 AW802265 AW578700 BE078715 AW860403 AW897456 AW996558 AW890602 AW860413 AA425412 BE008364 BE150438 AW602606 AI435236 AA574285 AI823745 AA501773 AI002987 AW832749 BE185491 AW996489 BE001442 AW946425 BE001586 AI524864 BE085556 AW867549 AW604038 BE079832 AI752160 AW999398 AW883904 AW882376 AW467098 BE080116 AW883984 AW883995 AA424095 BE074091 AW996348 AW860625 AW860633 AW946513 BE083485 AW860412 AW602207 BE075407 AW838972 AW607023 AW602201 AW799772 AW862452 AW862451 BE505041 BE161537 AW602206 AW860404 AW860555 BE007843 AW860632 AW862457 AW998019 AW860405 BE092062 AW603921 BE183386 AW868194 BE075664 BE078184 AI541202 AI204949 BE092451 AW603111 AA484587 AA484402 AW998675 AW896064 BE069923 AW867965 BE069919 BE092069 AA807842 AW605500 AW605501 BE085409 AA506738 BE080080 AW749523 AA493134 AW370137 AA491844 AA504425 AW605473 BE092456 BE010682 AW602608 BE079093 AA484911 BE010942 AI205087 AW794933 BE081848 BE011792 AW799897 BE174618 AW838848 AW821741 AW842724 BE008764 BE183962 AA501765 BE092513 BE183342 AW799806 AA442935 BE092268 AA580022 AW843219 BE093308 BE092275 BE087111 BE183392 AW842678 BE185597 BE183895 BE185278 BE082343 AW946219 BE079199 BE092272 AA586687 AW946109 AW946175 AW946184 BE008365 BE078172 BE085673 BE076240 BE083194 BE010604 BE079196 AW878636 AW799803 BE001348 BE077883 BE081835 AW992309 BE081012 BE078106 AW881899 BE008407 BE008410 AW842670 AW603738 BE083661 AA484571 AI799184 BE174545 BE001405 AA436967 AW995884 AW995785 AW896598 AW883999 BE075967 AA503938 BE092281 BE092279 BE087460 BE087569 BE081542 AI375386 AW843886 BE080115 BE171517 BE079898 AW882382 BE001450 BE076430 AW579377 BE008412 BE008790 BE182296 BE182297 BE078805 AW899132 BE078810 BE185867 BE087790 AA484928 AW578985 BE008400 BE074080 AW605101 BE076110 AW799904 AI205094 BE008370 BE182345 BE182373 BE008401 AA984441 BE182362 BE182372 BE008414 BE078186 BE009165 BE010266 BE009162 BE009167 BE011006 BE073335 BE182370 AW750556 BE182347 BE011000 AA484576 BE092982 BE183897 BE092973 AA573037 AW882317 BE081832 AA478471 AA551613 BE182366 AW838686 AW026827 BE008413 AW896605 AA503558 AA776622 BE084825 AA502971 BE081842 BE010628 AW802218 AI888924 AW867986 AW881775 BE079220 AI241060 AW802041 AW802005 BE011244 BE087051 AA984758 AA452997 AW992786 AW797500 BE077829 BE008402 AW881760 BE093516 AW802084 AW369007 BE185123 BE087775 AW801018 BE093443 AW867978 AW843271 BE173850 AW997859 BE010620 AW992516 AW843908 BE083200 BE164675 BE074340 AW880289 BE075433 BE008456 AW946438 BE066570 BE093547 AA508107 AW867992 BE076239 BE183881 AW617422 BE087717 AW899147 BE010608 AW992295 AA436737 BE075412 BE093011 AW581656 BE089529 BE008756 BE150494 AW903020 AW883102 BE076370 BE000625 BE166095 AW867979 BE182159 AW577501 AW577488 AW577491 BE010637 BE069910 BE093295 BE005243 AI620783 AW992550 AW890590 AW577496 AW577504 AW842725 AW842666 AW864691 AW997722 AW842662 BE009233 BE087809 BE083196 AA287768 AW939691 AW815631 BE001453 AW841903 BE077613 AW577500 BE081479 AW992558 BE011065 AW843187 AW867990 AW898296 BE074339 AA501697 AW749997 BE076249 AW867991 BE085718 AW994607 BE010678 BE075436 AW386825 AA484467 BE081144 AW577492 AW997932 AW899089 AW842706 AW890727 AW843175 BE075428 AW843155 AW842679 AW842708 BE069915 AW842721 AW438792 AI251478 BE069911 BE067054 BE079889 BE075453 BE069927 AA491920 BE170606 BE182305 BE080052 AW843406 BE011075 BE075969 AA525261 AW391518 BE079202 AA658195 BE076138 AW799901 AA493859 AW992510 BE011810 AA508724 BE075488 BE075661 AA258982 BE078726 BE069914 AA213698 BE075376 AA484600 AW580999 BE077872 AA503571 AW884724 AW880124 AW868454 AW577502 AW577489 AW799829 AW992545 BE075806 AW994606 BE350368 AA557836 BE077682 AW844660 AW883431 BE085872 AW838887 AW843890 AW868404 AA578417 BE074115 AW842680 AW277193 AW890728 AW605111 BE093940 AW890710 BE085560 AW868180 AW896778 BE069925 BE011054 BE075965 AW842668 AW868310 BE011071 BE075429 AW843152 AW905848 BE075397 AW842752 BE075402 BE077950 AW837810 BE079998 BE183965

BE075431 AW815917 AW998359 AW799883 AW603782 AA557480 AW841444 BE075915 AA548034 AW843393 AW391559 BE083265 AW939721 AW800857 AW079109 AW364901 AI435993 AA985526 AW799848 BE182463 AA776111 AW799915 BE008399 BE075377 AW577809 BE010272 BE182443 BE010296 AW577806 BE008415 BE184036 BE076597 AI817413 AW795053 AW896761 AW841433 BE182458 AW603796 AW842676 BE085455 AW884879 BE075414 AW838836 AW878273 AW998088 AW799778 AW899125 BE082247 AA774870 BE001401 BE001485 AW817297 AW796670 AW394063 BE001396 AW394070 AW603797 BE182447 AW582483 AW843283 AW749520 AW867449 AW899274 AW578232 AW603765 AW843919 AW578235 BE184139 AW997742 BE183923 BE084210 AW802033 AW748724 AW939018 AW997459 AW842742 AA213697 BE182308 BE011078 AW607702 AW882623 BE080016 AW580994 BE076531 AA443462 AW607407 AW883382 AW939399 AW605627 AW844615 AW939724 AW815931 AW883765 AA287421 BE075626 AW946171 AW841445 AW797994 AW815957 AA683300 AW369004 BE075368 BE081560 AW605626 AW939398 AA507280 AA506317 AW841230 AW992519 AA465332 AA425246 BE090234 BE090236 AA483259 AA451961 AA535566 AA506406 AA888571 AA503568 AA507130 AA532944 AA501672 BE168634 AA492022 AA507662 AW842286 AA494226 AA776038 AA442419 AW579900 BE171816 AA863065 AA491916 AA447490 AA461423 AA434543 AA243279 AW997466 AW603740 BE000295 AA658571

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400715	8118885	Minus	80151-80297
400736	8118985	Plus	143447-143851
401008	8117391	Minus	81421-81551,82364-82512,82862-82938
401069	3927852	Minus	45682-45831
401375	7417809	Minus	6121-6766
401405	7768126	Minus	69276-69452,69548-69958
401539	8072433	Minus	62028-62608
401557	8099866	Minus	112785-112924
401654	9097132	Minus	64695-64797
401940	3738108	Plus	153460-153592
402025	7547159	Plus	173835-173998
402442	9796503	Plus	141714-141842,142010-142122
402682	8138477	Minus	147522-147795
402796	3646083	Minus	6126-6265,6416-6689
402967	5360987	Minus	33518-34546
403038	7717439	Minus	290021-290284
403055	8748904	Minus	109532-110225
403310	8139936	Minus	183883-184026
403397	9438368	Minus	84481-84655
403839	4176355	Plus	21201-22223
404110	9212839	Minus	18344-18510
404495	8151634	Minus	59449-60477
404534	8247909	Minus	147853-148086
404630	9796665	Plus	74495-74715
404649	9796926	Minus	100027-100399
404680	9797204	Minus	159810-159979,160213-160321,161023-161304,162862-163140,164490-164644,166404-166530,166936-167083,167392-167522
404914	7341760	Plus	92603-92827
405417	4753290	Minus	50704-51499
405454	7656675	Plus	133807-134053
405510	7630909	Minus	101028-101174
405514	9454624	Plus	35953-36151
405536	9795661	Plus	164091-164162,164397-164516,166720-166790,167785-167935
406016	8272661	Plus	41341-41940
406410	9256394	Minus	115806-116104
406464	9789674	Plus	72161-72562
406562	7711584	Plus	37316-37426

TABLE 16A: 200 GENES DOWN-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 16A shows 200 genes down-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 15A, except that the numerator and denominator were switched, the median value amongst normal cervices was greater than or equal 40 units, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal cervix).

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigeneID	Unigene Title	R1
453596	AA441838	Hs.62905	hypothetical protein FLJ14834	18.1
443912	R37257	Hs.184780	ESTs	16.8
420923	AF097021	Hs.273321	differentially expressed in hematopoietic lineages	13.6
414422	AA147224	Hs.337232	Homeo box A13	13.1
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672	12.9
412639	AW961284	Hs.296235	ESTs	12.4

	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	12.4
	407938	AA905097	Hs.85050	phospholamban	11.3
	410544	AI446543	Hs.95511	ESTs	11.3
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	11.1
5	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]	11.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	10.9
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	10.6
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	10.5
	452106	AI141031	Hs.21342	ESTs	9.5
10	428780	AI478578	Hs.50636	ESTs	9.5
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	9.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PLACE1002968	9.0
	430468	NM_004673	Hs.241519	angiopoietin-like 1	9.0
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	8.7
15	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activin receptor inte	8.6
	401486	NA		C4000647*:gi|4758508|ref|NP_004253.1| airway trypsin-li	8.4
	417511	AL049176	Hs.82223	chordin-like	8.3
	429900	AA460421	Hs.30875	ESTs	8.2
	411908	L27943	Hs.72924	cytidine deaminase	8.0
20	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	8.0
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone DKFZp	8.0
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	8.0
	421666	AL035250	Hs.1408	endothelin 3	7.9
	450164	AI239923	Hs.30098	ESTs	7.9
25	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A; scatter factor	7.7
	425608	AA360486	Hs.92448	ESTs	7.6
	442748	AI016713	Hs.135787	ESTs	7.3
	415672	N53097	Hs.193579	ESTs	7.2
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	7.2
30	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	7.0
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nucleotide pyroph	6.7
	414214	D49958	Hs.75819	glycoprotein M6A	6.5
	436637	AI783629	Hs.26766	ESTs	6.5
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	6.5
35	432101	AI918950	Hs.123642	EphA3	6.3
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA, complete cds	6.3
	424153	AA451737	Hs.141496	MAGE-like 2	6.3
	420228	R25023	Hs.12369	ESTs	6.2
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myotilin)	6.1
40	444931	AV652066	Hs.75113	general transcription factor IIIA	6.1
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HEMBA1002970	6.1
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	6.1
	410425	BE278367	Hs.63510	KIAA0141 gene product	6.0
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	6.0
45	424973	X92521	Hs.154057	matrix metalloproteinase 19	6.0
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like 1	5.9
	429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	5.9
	440594	AW445167	Hs.126036	ESTs	5.9
	452768	AW069459	Hs.61539	ESTs	5.9
50	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 protein [H.sapiens	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
	425010	T16837	Hs.4241	ESTs	5.9
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.8
	437980	R50393	Hs.278436	KIAA1474 protein	5.8
55	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	5.7
	404097	NA		C5000242*:gi|9369379|gb|AAF87128.1|AC006434_24 (AC00643	5.7
	422546	AB007969	Hs.301478	KIAA0500 protein	5.7
	445872	AI681573	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458	5.7
	429999	AI761902	Hs.99597	ESTs	5.6
60	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492	5.6
	442082	R41823	Hs.7413	ESTs	5.5
	452073	AA625150	Hs.82098	ESTs	5.4
	430032	AW936136	Hs.99610	ESTs	5.4
	408767	AA057279	Hs.211928	ESTs	5.4
65	433234	AB040928	Hs.65366	KIAA1495 protein	5.3
	431708	AI698136	Hs.108873	ESTs	5.3
	421200	AA284811	Hs.264433	ESTs	5.2
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HEMBA1001008	5.2
	409643	AW450866	Hs.257359	ESTs	5.1
70	416676	AW392022	Hs.79507	KIAA0582 protein	5.1
	420357	U94333	Hs.97199	complement component C1q receptor	5.0
	417355	D13168	Hs.82002	endothelin receptor type B	5.0
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL06674	5.0
	430965	AA489732	Hs.154918	ESTs	4.9
75	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.9
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	4.8
	404485	NA		Target Exon	4.8
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB1001024	4.8
	417692	R09338	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC1000640	4.8
80	432304	AA932186	Hs.69297	ESTs	4.7
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.7
	448851	AI582207	Hs.177166	ESTs	4.7
	405523			C8001409*:gi|7441226|pir||S31212 collagen alpha 1(XIV)	4.7

450656	AA010539	Hs.18912	ESTs	4.6
422942	AF054839	Hs.122540	tetraspan 2	4.6
401479	T49304	Hs.110950	Rag C protein	4.6
444192	AW469413	Hs.151145	ESTs	4.6
439648	AW780192	Hs.267596	ESTs	4.5
410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member 4	4.5
444702	AI220122	Hs.326560	hypothetical protein MGC2780	4.5
410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX	4.5
452249	BE394412	Hs.202095	empty spiracles (Drosophila) homolog 2	4.5
430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	4.5
411037	BE145915	Hs.99472	ESTs	4.4
442803	AI675298	Hs.199917	ESTs	4.4
414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, be	4.4
400628	NA		C10001871*:gi|1705533|sp|P32018|CA1E_CHICK COLLAGEN ALP	4.3
414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage serine esterase	4.3
437110	AL049240	Hs.144995	ESTs	4.2
410646	W79408	Hs.50745	ESTs	4.2
456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens cDNA clone, mRN	4.2
401270			Target Exon	4.2
419447	BE092696	Hs.75928	ESTs	4.2
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	4.2
427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.2
434469	AA634806		gb:ab28c02.r1 Stratagene lung (937210) Homo sapiens cDN	4.1
444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR	4.1
418947	W52990	Hs.22860	ESTs	4.1
415434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.0
454736	BE184348		gb:CM0-HT0676-010500-355-e11 HT0676 Homo sapiens cDNA,	4.0
407945	X69208	Hs.606	ATPase, Cu transporting, alpha polypeptide (Menkes synd	4.0
447499	AW262580	Hs.147674	protocadherin beta 16	4.0
430686	NM_001942	Hs.2633	desmoglein 1	4.0
409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (cardiovascula	3.9
419047	AW952771	Hs.90043	ESTs	3.9
414272	AI651603	Hs.46988	ESTs	3.9
443808	AW377736	Hs.12420	ESTs	3.9
426883	H21520	Hs.35088	ESTs	3.9
410659	AI080175	Hs.68826	ESTs	3.9
431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.9
432181	AA527650	Hs.156037	ESTs	3.9
422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.8
453296	AA034413	Hs.62560	ESTs	3.8
400878	NA		Target Exon	3.8
401103	NA		C12001233:gi|7305361|ref|NP_038652.1| otogelin [Mus mus	3.8
436670	AI690021	Hs.201536	ESTs	3.7
432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface receptor	3.7
408793	BE258371	Hs.254660	ESTs	3.7
419093	AI804054	Hs.112885	spinal cord-derived growth factor-B	3.7
434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.7
450776	NM_007250	Hs.320861	Kruppel-like factor 8	3.7
437140	AA312799	Hs.283689	activator of CREM in testis	3.6
418421	R58620	Hs.85050	phospholamban	3.6
443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN	3.6
417194	N53793		gb:yz07a01.r1 Soares_multiple_sclerosis_2NbHMSP Homo sa	3.6
443567	AI077540	Hs.134090	ESTs	3.6
451879	AI821030		gb:yb52f11.y5 Stratagene ovary (937217) Homo sapiens cD	3.6
421013	M62397	Hs.1345	mutated in colorectal cancers	3.5
451896	AF196304	Hs.27197	SUMO-1-specific protease	3.5
413237	AI468574	Hs.171965	ESTs	3.5
424636	AA453734	Hs.10198	ESTs	3.5
432660	AI288430	Hs.64004	ESTs	3.5
414681	AL079440	Hs.74002	nuclear receptor coactivator 1	3.5
400802	NA		Target Exon	3.5
430015	AW768399	Hs.112157	ESTs	3.5
451978	AW813747	Hs.27371	Homo sapiens mRNA; cDNA DKFZp566J123 (from clone DKFZp5	3.5
449088	AI654048	Hs.196556	ESTs	3.5
425113	AI936992	Hs.154658	pleckstrin and Sec7 domain protein	3.5
458459	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone COL09609	3.5
420249	BE262895	Hs.276916	nuclear receptor subfamily 1, group D, member 1	3.5
401159	NA		Target Exon	3.5
442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQ	3.5
426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5 [H.sapiens]	3.4
407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC FINGER PROTEIN	3.4
423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	3.4
443178	AI631241	Hs.47312	ESTs	3.4
430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTONE H2B H [H.sap	3.4
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) homol	3.4
437950	U79244	Hs.112642	ESTs	3.3
419368	AI753518	Hs.209464	KIAA1604 protein	3.3
447335	BE617695	Hs.286192	hypothetical protein FLJ20940	3.3
451398	AI793124	Hs.144479	ESTs	3.3
452814	AI092790	Hs.334703	hypothetical protein FLJ14529	3.3
407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, expressed in pro	3.3
412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	3.3
447261	NM_006691	Hs.17917	extracellular link domain-containing 1	3.3

444216	D25303	Hs.222	integrin, alpha 9	3.3
418771	AA807881	Hs.25329	ESTs	3.3
433036	AA574091	Hs.105964	ESTs	3.2
404584			Target Exon	3.2
404195			NM_015718*:Homo sapiens NADPH oxidase 3 (NOX3), mRNA. V	3.2
428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
420833	R47948	Hs.188732	ESTs	3.1
413156	AA127133		gb:zl87e03.r1 Stratagene colon (937204) Homo sapiens cD	3.1
413607	T64741		gb:yc48f11.r1 Stratagene liver (937224) Homo sapiens cD	3.1
443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.1
428790	AF023456	Hs.193558	protein phosphatase, EF hand calcium-binding domain 2	3.1
434520	AA205273	Hs.177011	hypothetical protein	3.1
432247	AA531287	Hs.105805	ESTs	3.1
429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	3.1
439734	AC005013	Hs.149	cAMP response element-binding protein CRE-BPa	3.1
433546	AI075877	Hs.125461	hypothetical protein FLJ11539	3.0
430317	AB020645	Hs.239189	glutaminase	3.0
425130	AA448208	Hs.99163	ESTs	3.0
444195	AB002351	Hs.10587	KIAA0353 protein	3.0
409007	AL122107	Hs.49599	Homo sapiens mRNA; cDNA DKFZp434G0827 (from clone DKFZp	3.0
453773	AL133761		gb:DKFZp761C1413_r1 761 (synonym: hamy2) Homo sapiens c	3.0
442974	AI025670	Hs.109308	ESTs, Weakly similar to leucine-rich glioma-inactivated	3.0
446936	H10207	Hs.47314	ESTs	3.0
454086	AW885909	Hs.6975	PRO1073 protein	3.0
420271	AI954365	Hs.42892	ESTs	3.0
435545	AA687415	Hs.28107	ESTs	3.0
445175	AV652851	Hs.20255	ESTs	3.0

TABLE 16B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
413156	135116_1	AA127133 AA384396 AW958912 T72119
413607	1379911_1	T64741 BE158393 BE152805
417194	1657323_1	N53793 N53716 N53739
434469	387447_1	AA634806 C18732 AA729161 AA729860
451879	888642_1	AI821030 T47126 AI821318
453773	980699_1	AL133761 AL133767
454736	1232235_1	BE184348 AW817453 BE011068
456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101

TABLE 16C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400628	3818355	Plus	41851-41984
400802	8567867	Minus	174571-174856
400878	9864757	Plus	31493-32842
401103	8568122	Minus	98330-98449
401159	6067118	Minus	3180-3953
401270	9797168	Minus	141659-141813
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
404097	7770701	Plus	55512-55781
404195	3805917	Minus	39186-39332
404485	8096921	Plus	75166-75264,124036-124232
404584	9857511	Plus	138651-139153
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

TABLE 17A: 605 genes upregulated in testicular cancer relative to normal body tissues

Table 17A lists about 605 genes upregulated in cervical cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M,

likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 95th percentile of cervical cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1

408522; AI541214; Hs.46320; Small proline-rich protein SPRK [human, ; none,Cornifin; 33.942
422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; efhand,S_100;TM=M;SS=N; 33.05
424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 32.856
422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.604
433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recp;TM=M;SS=Y; 27.95054945
421948; L42583; Hs.334309; keratin 6A; filament,RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 26.778
446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 26.1133829
407242; M18728; ; gb:Human nonspecific crossreacting antig; ig;TM=M;SS=M; 23.382
424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2,hemopexin,Peptidase_M10;; 22.522
412719; AW016610; Hs.816; ESTs; none,none; 21.198
406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig;TM=M;SS=M; 20.028
402075; ; ; ENSP00000251056*:Plasma membrane calcium; none;; 19.038
431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin_C_term;TM=Y;SS=M; 17.92061281
412471; M63193; Hs.73946; endothelial cell growth factor 1 (platel; Glycos_transf_3,Glycos_trans_3N;TM=M;SS=M; 17.8978979
417308; H60720; Hs.81892; KIAA0101 gene product; none;TM=M;SS=N; 17.08333333
429259; AA420450; Hs.380088; Plakophilin; none,none; 17.08235294
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;; 16.91568628
439926; AW014875; Hs.137007; ESTs; none,none; 16.69
419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 16.365
413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD), kalinin; laminin_EGF,laminin_Nterm;; 15.75294118
413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;; 15.48600509
401781; ; ; Target Exon; filament;TM=M;SS=N; 15.43668831
420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobin;; 15.394
441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none;TM=M;SS=M; 15.12264151
452240; AI591147; Hs.61232; ESTs; none,none; 14.63
428957; NM_003881; Hs.194679; WNT1 inducible signaling pathway protein; tsp_1,vwc,IGFBP;TM=M;SS=M; 14.49772727
414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;SS=N; 14.4389313
432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none,none; 14.00909091
400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin,Peptidase_M10,Astacin;; 13.824
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.7754386
421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;; 13.74595843
400284; ; ; NM_000125*:Homo sapiens estrogen recepto; hormone_rec,zf-C4,Oest_recep;TM=M;SS=M; 13.31578947
428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 13.05294118
411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M;SS=N; 13.038
406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10;; 13.00311527
427666; AI791495; Hs.180142; calmodulin-like skin protein (CLSP); efhand;TM=M;SS=N; 12.79
400301; X03635; Hs.1657; estrogen receptor 1; F-box,hormone_rec,zf-C4,Oest_recep,adh_zinc,ketoacyl-synt,pp-binding,Acyl_transf,Thioesterase,ketoacyl-synt_C,AAA,E7,RFX_DNA_binding;TM=M;SS=N; 12.472
410001; AB041036; Hs.57771; kallikrein 11; trypsin;TM=M;SS=M; 12.47
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,ig; 12.28597122
430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;SS=N; 12.13379205
437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none;TM=M;SS=M; 12.04945055
418462; BE001596; Hs.85266; integrin, beta 4; fn3,integrin_B,Calx-beta,EGF;TM=M;SS=M; 11.95538462
443859; NM_013409; Hs.9914; follistatin; kazal;; 11.95467422
426350; NM_003245; Hs.2022; transglutaminase 3 (E polypeptide, prote; Transglutamin_N,Transglutamin_C,Transglut_core;TM=M;SS=N; 11.61
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;SS=N; 11.564
444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6,lactamase_B; 11.55285714
428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 11.47956989
418663; AK001100; Hs.41690; desmocollin 3; cadherin,Cadherin_C_term,none; 11.456
433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none;; 11.45352113
423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz_BPTI,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 11.32234432
428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3;TM=Y;SS=M; 11.28686327
424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none,none; 11.076
451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M;SS=N; 11.0381579
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 11
423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin,Peptidase_M10;TM=M;SS=M; 11
425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 10.93859649
437938; AI950087; Hs.369528; gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien; none,none; 10.78064516
425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 10.74825175
439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH; none,none; 10.542
437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 10.49538462
431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 10.48210736
411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 10.26714286
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 10.142
421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M;SS=N; 10.1
418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Reprolysin,Pep_M12B_propep,EGF;TM=Y;SS=M; 10.072
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisoIV,HATPase_c;; 9.996363636
414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibito; serpin;; 9.896825397
421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;SS=N; 9.888888889
407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 9.876056338
424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF;; 9.851635514
438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 9.840720222
413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT,none; 9.823170732
408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FliD,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M;SS=N; 9.812

409893; AW247090; Hs.57101; minichromosome maintenance deficient (S.; MCM,aldo_ket_red;TM=M;SS=N; 9.787878788
442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 9.637037037
425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin;TM=M;SS=M; 9.596
417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevi; WD40;TM=M;SS=N; 9.558
444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 9.55
421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 9.529085873
408591; AF015224; Hs.46452; mammaglobin 1; Uteroglobin;TM=M;SS=M; 9.506
444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 9.477961433
444006; BE395085; Hs.334762; type I transmembrane protein Fn14; Idl_recept_a,PKD,MHC_I;TM=M;SS=Y; 9.415151515
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;; 9.408
424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin-; ras;TM=M;SS=N; 9.36
429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M;SS=N; 9.315693431
421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 9.31
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.29
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh;; 9.264
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 9.241561181
445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 9.207272727
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 9.195167286
439223; AW238299; Hs.250618; UL16 binding protein 2; Idl_recept_a,PKD,MHC_I;TM=M;SS=Y; 9.108
428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA;TM=Y;SS=N; 9.028
421777; BE562088; Hs.108196; HSPC037 protein; none;TM=M;SS=N; 9.004
448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 9.001096491
418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 8.942
455601; AI368680; Hs.816; SRY (sex determining region Y)-box 2; HMG_box;; 8.87
429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin;TM=Y;SS=M; 8.77131783
456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M;SS=N; 8.738
430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 8.736
417034; NM_006183; Hs.80962; neurotensin; none;; 8.592
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 8.536
408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 8.49
439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 8.460655738
409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin_B,laminin_EGF;; 8.414
438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate_kin,PDZ,SH3; 8.376205788
439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 8.37
430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 8.364
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 8.266
417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 8.248314607
431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetase 2 (69-71; NTP_transf_2;TM=M;SS=N; 8.156
412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;SS=N; 8.142857143
448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitte; SNF;TM=Y;SS=N; 8.137559809
427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6,ET,PLA2_inh;; 8.043478261
424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase;; 8.038194444
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 8.024752475
453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none;TM=Y;SS=M; 8
424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibito; serpin;TM=M;SS=N; 7.982
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.973684211
413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.892
422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 7.824
452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 7.823874755
431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd_glycop,Integrin_A;TM=Y;SS=M; 7.758985201
432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 7.75887574
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 7.757751938
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 7.624
438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 7.605660377
427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;SS=N; 7.578
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 7.476
429299; AI620463; Hs.347408; hypothetical protein MGC13102; none;TM=Y;SS=N; 7.442528736
441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 7.442495127
446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.436781609
414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;; 7.435897436
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Recep_L_domain,YLP,none; 7.398360656
432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 7.394039735
431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subuni; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 7.383419689
416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 7.382
436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 7.327160494
409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 7.316
448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 7.315412186
428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.2984375
422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 7.28
451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 7.256802721
416819; U77735; Hs.80205; pim-2 oncogene; pkinase;; 7.234455959
421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 7.162534435
451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin_N;; 7.145454546
424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 7.126
414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 7.122413793
425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX ; Troponin,Exo_endo_phos,IQ;TM=M;SS=N; 7.106719368
430890; X54232; Hs.2699; glypican 1; Glypican;TM=M;SS=M; 7.088937093
407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 7.052
426514; BE616633; Hs.170195; bone morphogenetic protein 7 (osteogenic; TGF-beta,TGFb_propeptide;; 7.042
431241; AA496799; Hs.36958; ESTs; SH2,RasGEF,none; 7.03
437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 7.03
420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530I15; none,none; 7.026
439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none;TM=M;SS=N; 7.008

422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 6.991626794
416250; AA581386; Hs.73452; Kremen 2; kringle,CUB,WSC;; 6.972
430770; AA765694; Hs.123296; ESTs; none,none; 6.95
418869; AW516565; ; gb:xq01d05.x1 Soares_NHCeC_cervical_tumo; none,RasGAP,WW,IQ; 6.948
428953; AA306610; Hs.348183; tumor necrosis factor receptor superfami; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD;; 6.914
418283; S79895; Hs.83942; cathepsin K (pycnodysostosis); Peptidase_C1;; 6.876190476
419667; AU077005; Hs.92208; a disintegrin and metalloproteinase doma; disintegrin,Reprolysin,Pep_M12B_propep;TM=M;SS=M; 6.862970711
421143; AB024536; Hs.102171; immunoglobulin superfamily containing le; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.849056604
456181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9;TM=M;SS=N; 6.762
436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 6.721428571
411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 6.720348837
439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 6.717307692
450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 6.715240642
426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 6.688194444
439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig),; Sema,PSI,integrin_B;TM=Y;SS=N; 6.670553936
428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;; 6.662921348
456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM,PDZ,pkinase;; 6.653713299
425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;; 6.652671756
426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;SS=N; 6.639655172
438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 6.6
444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 6.6
408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 6.548148148
410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 6.532763533
414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 6.526951673
426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 6.512704174
420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B, ; Sulfotransfer;; 6.496
423031; AI278995; Hs.374579; ESTs; none,none; 6.447658402
421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.426666667
433933; AI754389; Hs.355397; Homo sapiens clone TCCCIA00164 mRNA sequ; none;NA;NA; 6.4
435094; AI560129; Hs.289008; EST; none,none; 6.312
432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanylate_kin,none; 6.276556777
427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 6.272727273
435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 6.269720102
418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 6.219081272
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin;TM=M;SS=N; 6.19
409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase_C,CARD;TM=M;SS=N; 6.188888889
449230; BE613348; Hs.356392; melanoma cell adhesion molecule; ig,isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 6.188046647
440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-li; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 6.15503876
450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb_propeptide;; 6.152
432314; AA533447; Hs.285173; ESTs; Xlink,none; 6.123040752
418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M;SS=N; 6.12
421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig,pkinase;TM=Y;SS=M; 6.095758355
422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial ; mito_carr;TM=M;SS=N; 6.089164786
452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 6.06284153
445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM;; 6.05513308
444309; U83236; Hs.10803; calcium and integrin binding protein (DN; efhand;; 6.04015544
414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPc,tsp_1,Ribosomal_S21,rvp;TM=M;SS=N; 6.009562842
438108; AI471795; Hs.287776; vanilloid receptor-related osmotically a; ank,ion_trans;TM=Y;SS=N; 6.004
413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 5.984536083
405484; ; ; C3002124*:gi|12737280|ref|XP_006682.2| k; none;; 5.978964401
414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M;; 5.978431373
419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;; 5.976
414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M;SS=N; 5.969387755
411756; BE294350; Hs.71891; discoidin domain receptor family, member; pkinase,F5_F8_type_C;TM=Y;SS=M; 5.95184136
424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 5.951550388
453459; BE047032; Hs.257789; ESTs; none,none; 5.95
456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=N; 5.938
429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin,Peptidase_M10;TM=M;SS=M; 5.917857143
414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 5.910455487
448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moi; NUDIX;TM=M;SS=M; 5.901886793
452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none,none; 5.868362832
418345; AJ001696; Hs.241407; serine (or cysteine) proteinase inhibito; serpin;TM=Y;SS=M; 5.842
452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 11; Euk_porin;TM=M;SS=M; 5.816363636
439625; AF086453; Hs.58611; ESTs; Fork_head,glycolytic_enzy,Na_sulph_symp; 5.811594203
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 5.81
422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 5.806
415198; AW009480; Hs.943; natural killer cell transcript 4; none;TM=M;SS=N; 5.804137931
431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep_L_domain,none; 5.8
457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 5.794
439335; AA742697; Hs.62492; NM_052863:Homo sapiens secretoglobin, fa; none;; 5.778588808
439246; AI498072; Hs.351474; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073;; 5.763492064
452461; N78223; Hs.108106; transcription factor; zf-C3HC4,ubiquitin,PHD,YDG_SRA;TM=M;SS=N; 5.728
414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 5.714634146
424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT_bind,STAT_prot,none; 5.701666667
419056; M89957; Hs.89575; CD79B antigen (immunoglobulin-associated; ig,ITAM;TM=Y;SS=M; 5.692
432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase,Sema,PSI,TIG,A4_EXTRA;TM=M;SS=M; 5.686
452696; AI826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate_kin,PDZ,SH3; 5.683673469
411030; BE387193; Hs.67896; 7-60 protein; none;TM=M;SS=N; 5.676767677
447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazaro; none;TM=Y;SS=N; 5.672977625
426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 5.666
407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfkB;TM=M;SS=N; 5.655616943

427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M;SS=N; 5.6485623
415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073;; 5.648
452690; AI536070; Hs.15085; ESTs; pou,homeobox,Ig_chan,ANF_receptor; 5.646
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;SS=N; 5.642405063
418703; NM_014448; Hs.87435; Rho guanine exchange factor (GEF) 16; SH3,PH,RhoGEF,Birna_VP3;TM=M;SS=N; 5.636
426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 5.635087719
424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;SS=N; 5.620930233
432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), cata; Metallophos;TM=M;SS=N; 5.608352145
417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3,pkinase;TM=M;SS=N; 5.596052632
430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.575112108
435017; AA336522; Hs.12854; angiotensin II, type I receptor-associat; none;TM=Y;SS=M; 5.556910569
439963; AW247529; Hs.6793; platelet-activating factor acetylhydrola; PAF-AH_lb,Lipase_GDSL;TM=M;SS=N; 5.556195965
415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3,pkinase;TM=M;SS=N; 5.555421687
424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 5.549751244
413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylin; SH2,SH3,C2,PH,PI-PLC-Y,PI-PLC-X,PDGF;; 5.541366907
406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 5.54076087
417700; M36542; Hs.1101; POU domain, class 2, transcription facto; homeobox,pou;TM=M;SS=N; 5.536
456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;SS=N; 5.52661597
436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 5.52638191
425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 5.519672131
412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF,sugar_tr,none; 5.516453382
417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 5.514964789
447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3,ig,Y_phosphatase,MAM;TM=Y;SS=M; 5.494202899
419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 5.471947195
410608; AI538438; Hs.159087; ESTs; ubiquitin,integrin_B,UBA,none; 5.465384615
448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin;TM=M;SS=N; 5.460076046
408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, ; UvrD-helicase,RNB,Runt;TM=M;SS=N; 5.450413223
426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2,BH4,none; 5.444805195
457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none,none; 5.444281525
422597; BE245909; Hs.118634; ATP-binding cassette, sub-family B (MDR/; ABC_tran,ABC_membrane,PRK;TM=Y;SS=N; 5.437931035
429191; AF065215; Hs.198161; phospholipase A2, group IVB (cytosolic); C2,PLA2_B,jmjC;TM=M;SS=N; 5.4375
449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain,none; 5.435211268
409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 5.433333333
443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase,RIO1;TM=M;SS=N; 5.429657795
434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.423322684
423189; M59371; Hs.171596; EphA2; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 5.421621622
452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisi; pkinase;TM=M;SS=N; 5.412
432527; AW975026; Hs.102754; ESTs; none,none; 5.40625
422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.405504587
410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3;TM=M;SS=N; 5.396
434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PL; 7tm_1,none; 5.391472868
438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ;; 5.389250814
439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004858.3 U1 sm; none,none; 5.382
437016; AU076916; Hs.5398; guanine monphosphate synthetase; PHD,SET,zf-CXXC,EGF,ank,notch,WW,FCH,GATase,GMP_synt_C,Occludin,YEATS,metalthio,EB,heme_1,RCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT;TM=M;SS=N; 5.373937677
424848; AI263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin,none; 5.36
452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN,sugar_tr;TM=Y;SS=M; 5.35971223
405932; ; ; C15000305:gi|3806122|gb|AAC69198.1| (AF0; ras;TM=M;SS=N; 5.349226804
416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; ig,ITAM,Zn_clus;TM=Y;SS=M; 5.346153846
453143; AA382234; Hs.356289; protein tyrosine phosphatase, receptor t; serpin;; 5.333667335
423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT;TM=M;SS=N; 5.33
408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none,none; 5.328
414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig;TM=Y;SS=M; 5.316
427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, r; ig;TM=Y;SS=M; 5.309638554
410165; BE560228; Hs.71869; apoptosis-associated speck-like protein ; PAAD_DAPIN,CARD;TM=M;SS=N; 5.293560606
415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 5.28
427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 5.278947368
431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 5.274746193
416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none;TM=Y;SS=M; 5.272222222
415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral_helicase1;TM=M;SS=N; 5.27
435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;SS=N; 5.251865672
409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 5.248
431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 5.232
422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2;; 5.212418301
436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;; 5.209259259
421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospha; Ribosomal_L20,Na_Pi_cotrans;TM=Y;SS=N; 5.202
425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M;SS=N; 5.19979716
437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC_tran,GTP_EFTU,ABC_membrane,none; 5.199074074
416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,vwc,TSPN;; 5.198224852
429556; AW139399; Hs.314807; ESTs; none;TM=M;SS=N; 5.192439863
427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head,IQ,zf-MYND;TM=M;SS=M; 5.190251572
400517; ; ; lengsin; none;TM=M;SS=N; 5.18
413436; AF238083; Hs.68061; sphingosine kinase 1; DAGKc;TM=M;SS=N; 5.172881356
423527; AI206965; Hs.105861; hypothetical protein FLJ13824; none;TM=M;SS=N; 5.165060241
419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR_ITPR,RyR,MIR;TM=Y;SS=N; 5.156976744
437809; AL137723; Hs.5855; Homo sapiens mRNA; cDNA DKFZp434D0818 (f; none,none; 5.154676259
452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 5.152360515
409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 5.144859813
442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra,DUF51,none; 5.142
434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;; 5.141534392
434808; AF155108; Hs.256150; NY-REN-41 antigen; none;TM=M;SS=N; 5.14
431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M;SS=N; 5.13968254

431685; AW296135; Hs.267659; vav 3 oncogene; CH,DAG_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 5.129476584
411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;SS=N; 5.121527778
433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type rece; 7tm_2,EGF,cadherin,laminin_EGF,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 5.107438017
433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,arf;TM=M;SS=M; 5.10251046
419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subu; CDK5_activator,PCI,none; 5.095194085
411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, ; inositol_P,ig;TM=M;SS=N; 5.092
435243; AW292886; Hs.348932; hypothetical protein dJ434O14.3; IRF,none; 5.092
434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f; DSPc,none; 5.091922006
415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 5.088932806
418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA;; 5.082840237
420030; BE503994; Hs.146233; KIAA0418 gene product; SH3,none; 5.080645161
444065; AW449415; Hs.10260; Homo sapiens cDNA FLJ11341 fis, clone PL; SH3;; 5.063953488
421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.056
411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;; 5.054133858
428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 5.054
423883; AF250238; Hs.134514; ATP-binding cassette, sub-family A (ABC1; ABC_tran,photoRC,SRP54,Ca_channel_B,Piterin_4a;TM=Y;SS=M; 5.051724138
421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_PI4_kinase,Pt3Ka;TM=M;SS=N; 5.051282051
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 5.047311828
410026; AI912061; Hs.55016; hypothetical protein FLJ21935; none,none; 5.04674221
426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 5.040298508
418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 5.039039039
444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC,death,TNFR_c6; 5.037151703
413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 5.034
446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 5.03030303
410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Topoisom_bac,Toprim;; 5.027985075
418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH;TM=M;SS=N; 5.014652015
415166; NM_003652; Hs.78068; carboxypeptidase Z; Zn_carbOpept,Dioxygenase,Fz;; 5.012269939
416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 5.001811594
410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;; 4.997983871
430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 4.994871795
409220; BE243323; Hs.51233; tumor necrosis factor receptor superfami; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.987135506
423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 4.985185185
423011; NM_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm_1;TM=Y;SS=M; 4.984
419577; L36531; Hs.91296; integrin, alpha 8; integrin_A,FG-GAP;TM=Y;SS=N; 4.968
402328; ; ; Target Exon; pkinase;TM=M;SS=N; 4.96728972
421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.966334165
435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.964491363
414203; BE262170; Hs.78629; ATPase, Na? transporting, beta 1 polypep; none,none; 4.961956522
409582; R27430; Hs.271565; ESTs; none,Neur_chan_LBD,Neur_chan_memb; 4.946
451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 4.943181818
453449; W16752; Hs.32981; sema domain, immunoglobulin domain (Ig),; ig,Sema,PSI;; 4.930508475
425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY,SAP,pkinase,fn3,ig; 4.925347222
425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10;; 4.92
422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB;TM=Y;SS=M; 4.912181303
442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.910224439
425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.909972299
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 4.904
409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;SS=N; 4.897338403
411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;SS=N; 4.894
446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1;TM=Y;SS=M; 4.886
423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 4.884
445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 4.876379691
448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG;; 4.876117497
427792; M63928; Hs.180841; tumor necrosis factor receptor superfami; SRP14,TNFR_c6;; 4.873684211
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M;SS=N; 4.872641509
421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 4.869318182
429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 4.868073879
458873; AW150717; Hs.345728; STAT induced STAT inhibitor 3; none,none; 4.861538462
437669; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none,pkinase,pkinase_C; 4.854651163
405545; ; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 4.85
424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 4.848387097
424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus; fn3,ig,IRK;TM=Y;SS=M; 4.846153846
425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.843694494
421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 4.842532468
418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_C,AT_hook,SNF2_N;TM=M;SS=N; 4.842
444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 4.841071429
417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 4.839464883
422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 4.837837838
434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.833333333
450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 4.821666667
453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion_trans;TM=Y;SS=M; 4.820936639
417949; AL049795; Hs.83004; interleukin 14; none,Armadillo_seg,IBB,WD40; 4.81443299
439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 4.81
432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.805063291
432194; AL040801; Hs.273219; breast cancer anti-estrogen resistance 1; SH3;; 4.803191489
431472; AK001023; Hs.256549; nucleotide binding protein 2 (E.coli Min; fer4_NifH,ParA,APS_kinase,ArsA_ATPase;TM=M;SS=N; 4.800990099
450690; AA296696; Hs.333418; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 4.795480881
448950; AF288687; Hs.9275; CGI-152 protein; E1-E2_ATPase,Hydrolase;TM=Y;SS=N; 4.776923077
427681; AB018263; Hs.284232; tumor necrosis factor receptor superfami; death,TNFR_c6,PH,Xlink,RhoGEF,Metallothio_5;TM=M;SS=M; 4.772196262
432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH,RhoGAP,SH3;TM=M;SS=N; 4.760115607
433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;; 4.751162791
419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.748
431657; AI345227; Hs.105448; ESTs, Weakly similar to B34087 hypotheti; pkinase,PA28_alpha,PA28_beta,Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3; 4.746

412958; BE391579; Hs.75087; Fas-activated serine/threonine kinase; none;; 4.736781609
414443; AU077268; Hs.76144; platelet-derived growth factor receptor,; ig,pkinase;TM=Y;SS=N; 4.733
419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1,BAH,zf-CXXC,DNA_methylase; 4.725454546
417903; NM_002342; Hs.1116; lymphotoxin beta receptor (TNFR superfam; TNFR_c6;TM=M;SS=M; 4.718858132
414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 4.718836565
426059; BE292842; Hs.166120; interferon regulatory factor 7; IRF;; 4.718543046
414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase;TM=M;SS=N; 4.708
407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC;TM=Y;SS=M; 4.707920792
448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX;TM=M;SS=N; 4.707671958
407143; C14076; Hs.332329; EST; none;TM=Y;SS=M; 4.682675815
428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 4.681818182
408806; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fis, clone C; SH3,PDZ,Guanylate_kin,none; 4.680440771
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP;TM=M;SS=M; 4.679841897
418836; AI655499; Hs.161712; ESTs; pkinase,Activin_recp,PDZ,ZU5,death; 4.679180887
425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,pkinase,Fz;TM=Y;SS=M; 4.675342466
414665; AA160873; Hs.356307; serum amyloid A1; zf-C2H2,BTB,K_tetra,none; 4.67447496
449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 4.673701299
428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (y; none;; 4.656756757
417088; M54915; Hs.81170; pim-1 oncogene; pkinase;TM=M;SS=N; 4.656190476
420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TiT3 com; ITAM;TM=M;SS=M; 4.65
425966; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C;TM=M;SS=N; 4.644
417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; ig,abhydrolase; 4.640384615
430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4,zf-RanBP,pkinase; 4.630653266
419273; BE271180; Hs.293490; ESTs, Weakly similar to I38022 hypotheti; none,none; 4.628
453880; AI803166; Hs.135121; ESTs, Weakly similar to I38022 hypotheti; HSP70,none; 4.619047619
459399; BE407712; Hs.153998; creatine kinase, mitochondrial 1 (ubiqui; none,none; 4.618577075
412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPc;; 4.616
433577; AW007080; Hs.284192; ESTs; none,none; 4.614
444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 4.612149533
408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2;TM=Y;SS=N; 4.602
450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin;; 4.596875
443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin,none; 4.587931035
433083; AL042759; Hs.191762; ESTs; SH3,PX;TM=M;SS=N; 4.586
407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, ; ig;TM=Y;SS=M; 4.58557047
412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C ; MARCKS;; 4.579087049
422009; AI742845; Hs.110713; DEK oncogene (DNA binding); SAP;; 4.576347305
412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin_c; 4.57312253
414561; AI054813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans;TM=Y;SS=N; 4.573015873
422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.570526316
459053; AI807052; Hs.97792; ESTs; none,7tm_2,GPS; 4.569230769
424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD_Synth,Idh,Idh_C,pkinase;; 4.566195373
439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like;TM=M;SS=N; 4.56056338
416178; AI808527; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.558
408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 4.552307692
421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; efhand,Idl_recept_a;; 4.547761194
439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1,LRR;TM=Y;SS=N; 4.547169811
426201; AW182614; Hs.128499; ESTs; SH3,none; 4.541666667
424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M;SS=N; 4.536
445229; BE276013; Hs.343828; Homo sapiens mRNA for FLJ00086 protein, ; G-alpha;TM=M;SS=N; 4.530588235
413109; AW389845; Hs.110855; ESTs; PHO4,none; 4.529761905
426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolo; EGF,cadherin,laminin_G;TM=Y;SS=M; 4.529710145
402330; ; ; Target Exon; pkinase,none; 4.528070175
439238; N47305; Hs.302161; EDG-8 (endothelial differentiation, sph; 7tm_1;TM=Y;SS=M; 4.524
433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20;; 4.523715415
413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenas; CBS,IMPDH_C,IMPDH_N,NPD;TM=M;SS=N; 4.522900763
431429; AF072813; Hs.252831; reticulon 3; Reticulon,Fz,ig,kringle,pkinase;TM=Y;SS=N; 4.512
424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB,none; 4.512
420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 4.51
449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 4.506
408157; AA047685; Hs.62946; ESTs; none,pkinase; 4.504
446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 4.50215208
431326; AW970580; Hs.198689; KIAA0728 protein; none,none; 4.501
428072; BE258602; Hs.182366; heat shock protein 75; HATPase_c,HSP90;TM=M;SS=N; 4.48828125
415149; X12451; Hs.78056; cathepsin L; Peptidase_C1;; 4.484375
421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypept; p450;TM=Y;SS=M; 4.48
445143; U29171; Hs.378918; casein kinase 1, delta; zf-C3HC4,Filamin,zf-B_box,NHL,pkinase,zf-MIZ;TM=M;SS=N; 4.478092784
421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen ; none;TM=Y;SS=M; 4.477337111
410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 4.476
438774; AA431620; Hs.379034; hypothetical protein MGC2745; none,none; 4.474874372
410726; AI623859; Hs.15936; ESTs; pkinase,pro_isomerase,none; 4.47
429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator,none; 4.468
426485; NM_006207; Hs.170040; platelet-derived growth factor receptor-; ig;; 4.464944649
433646; AA603319; Hs.155195; ESTs; pou,homeobox,lig_chan,ANF_receptor; 4.458
410293; AK000047; Hs.61960; hypothetical protein; K_tetra;TM=M;SS=N; 4.453020134
453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 4.448198198
410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galac; SH3,PDZ,Guanylate_kin,none; 4.446927374
441455; AJ271671; Hs.7854; zinc/iron regulated transporter-like; Zip;TM=Y;SS=M; 4.445010183
453064; R40334; Hs.89463; potassium large conductance calcium-acti; none,none; 4.436480187
443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 4.433411215
411825; AK000334; Hs.352415; solute carrier family 39 (zinc transport; SNF,Zip;TM=Y;SS=N; 4.432765152
428376; AF119665; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase;TM=M;SS=N; 4.428571429
429592; AB029041; Hs.209646; KIAA1118 protein; Troponin,Exo_endo_phos,IQ;TM=M;SS=N; 4.428
419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); ank,DAGKa,DAGKc,DAG_PE-bind;TM=M;SS=N; 4.426229508

427138; N77624; Hs.173717; phosphatidic acid phosphatase type 2B; PAP2,none; 4.4234375
414496; W73853; Hs.355424; ESTs; pkinase,F5_F8_type_C,adh_short,none; 4.42114094
429432; AI678059; Hs.202676; synaptonemal complex protein 2; none;TM=M;SS=N; 4.42
429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;SS=N; 4.419207317
446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L2; none;TM=M;SS=N; 4.418181818
435411; AW444619; Hs.138211; ESTs; none,pkinase; 4.414
414581; AA256213; Hs.72010; ESTs; none,Carn_acyltransf,Choline_kinase,SCO1-SenC,Glycos_transf_3,Glycos_trans_3N; 4.41
418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domai; death,DED;; 4.408523909
442259; AI690269; Hs.201345; ESTs; Acetyltransf,RhoGAP,FCH,SH3,Kelch,fn3; 4.406
415860; D56051; Hs.78888; diazepam binding inhibitor (GABA recepto; ACBP;TM=M;SS=N; 4.404678363
434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M;SS=N; 4.404
404440; ; ; NM_021048:Homo sapiens melanoma antigen,; MAGE;TM=M;SS=N; 4.4
435542; AA687376; Hs.351226; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.394
413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=N; 4.39028777
435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none,none; 4.38490566
427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1,none; 4.382129278
425749; AW328587; Hs.159448; surfeit 2; none;; 4.382
417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y;SS=N; 4.381422925
414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 4.380681818
431837; T79326; Hs.331967; olfactory receptor, family 2, subfamily ; none,7tm_3,sushi,ANF_receptor; 4.376
417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase;; 4.370247934
434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 4.37
430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans;TM=Y;SS=M; 4.367777778
403912; ; ; C5000394*:gi|12737280|ref|XP_006682.2| k; none;TM=M;SS=N; 4.367684478
426268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;; 4.366348449
434263; N34895; Hs.79187; ESTs; ig,none; 4.358527132
404760; ; ; Target Exon; cadherin;TM=M;SS=M; 4.356
413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;SS=N; 4.35472973
420757; X78592; Hs.99915; androgen receptor (dihydrotestosterone r; hormone_rec,zf-C4,Androgen_recep;TM=M;SS=N; 4.354
426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlo; none;TM=Y;SS=N; 4.353244838
431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV_H; 4.35
431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;SS=N; 4.347893916
447719; BE387402; Hs.19333; hypothetical protein FLJ10349; adenylatekinase,ATP-bind;TM=M;SS=N; 4.346007605
424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerev; Acetyltransf;TM=M;SS=N; 4.344
449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none,none; 4.334722222
411768; NM_013371; Hs.71979; interleukin 19; IL10;; 4.322
445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M;SS=N; 4.320359281
425964; AW889928; Hs.9071; progesterone membrane binding protein; homeobox,none; 4.318867925
450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm;TM=M;SS=N; 4.316573557
408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;; 4.316
400290; H18836; Hs.31608; hypothetical protein FLJ20041; none,Cys_knot; 4.314726682
438899; AF085833; Hs.135624; ESTs; none,PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 4.314084507
418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 4.312121212
419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4;TM=M;SS=N; 4.304407714
421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT;TM=M;SS=N; 4.304
430017; AA263172; Hs.35; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=M;SS=M; 4.302
447224; BE617125; Hs.142076; gb:601441664F1 NIH_MGC_65 Homo sapiens c; none;NA;NA; 4.302
425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;SS=N; 4.301639344
454042; H22570; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 4.30141844
446143; BE245342; Hs.306079; sec61 homolog; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 4.300872093
428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU S; none,rrm; 4.292620865
432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2;TM=M;SS=N; 4.290258449
432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.288405797
421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10_DDP,efhand,CH,spectrin,serpin;TM=M;SS=N; 4.284
448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK;; 4.28057554
453941; U39817; Hs.36820; Bloom syndrome; DEAD,helicase_C,HRDC;TM=M;SS=N; 4.28
437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyosin,pkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A;TM=M;SS=N; 4.277477478
417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;; 4.276162791
450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none,none; 4.273927393
438012; AA393254; Hs.43619; ESTs; Armadillo_seg,none; 4.273134328
409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG;TM=M;SS=N; 4.273109244
418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;SS=N; 4.272123894
415214; AI445236; Hs.125124; EphB2; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 4.268
438233; W52448; Hs.56147; ESTs; Neur_chan_LBD,Neur_chan_memb,MAGE; 4.26284585
429019; AA443280; Hs.279907; myosin IIIA; myosin_head,pkinase,PRK,IQ;TM=M;SS=N; 4.262
424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; Idh,Idh_C,SH3,pkinase,UBA;TM=M;SS=N; 4.258695652
453655; AW960427; Hs.342874; transforming growth factor, beta recepto; zona_pellucida,none; 4.257208766
417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB;; 4.251785714
453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M;SS=N; 4.249116608
424232; AB015982; Hs.143460; protein kinase C, nu; pkinase,DAG_PE-bind,PH;TM=M;SS=N; 4.247692308
404883; ; ; ENSP00000216009:Sodium-glucose cotranspo; SSF;TM=Y;SS=M; 4.242424242
412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 4.239285714
411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none,none; 4.237313433
436957; AA902488; Hs.122952; ESTs; none,DAGKc,DAGKa,RA,DAG_PE-bind; 4.236
452568; AA805634; Hs.300870; Homo sapiens mRNA; cDNA DKFZp547M072 (fr; PI3_PI4_kinase;TM=M;SS=M; 4.23537415
433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subunl; HEAT;TM=M;SS=N; 4.234793187
432728; NM_006979; Hs.278721; HLA class II region expressed gene KE4; Zip,Ig_chan;TM=Y;SS=M; 4.234545455
416350; AF188625; Hs.189507; phospholipase A2, group IID; phoslip;TM=M;SS=Y; 4.234
409533; AW969543; Hs.144609; mitogen-activated protein kinase kinase ; Peptidase_C48,none; 4.230666667
427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 4.228009259
403362; ; ; NM_001615*:Homo sapiens actin, gamma 2, ; actin;; 4.22688478
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;; 4.226388889

428897; AJ245719; Hs.194385; hypothetical protein FLJ20234; SH2;TM=M;SS=N; 4.224731183
425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinas; SH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.223684211
418566; C21220; Hs.321717; hypothetical protein FLJ10875; zf-C2H2,BTB,K_tetra,7tm_1; 4.222807018
454098; W27953; Hs.217493; Plakophilin; none,none; 4.22
424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); pkinase,FHA,DnaJ;TM=M;SS=N; 4.21875
419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 4.217130215
436756; Z18364; Hs.198298; v-src avian sarcoma (Schmidt-Ruppin A-2); none,none; 4.216
450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2;TM=M;SS=N; 4.215163934
416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;; 4.212041885
432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; none,DS,UPF0139,Glyco_hydro_38; 4.207407407
416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain,rrm;TM=M;SS=N; 4.206
432284; AA532807; Hs.287740; ESTs; pkinase,none; 4.205454546
418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;SS=N; 4.204142012
450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.202572347
412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep;TM=M;SS=N; 4.202061856
425394; AA356730; Hs.323949; kangai 1 (suppression of tumorigenicity ; transmembrane4,none; 4.195014663
449335; AW150717; Hs.345728; STAT induced STAT inhibitor 3; SH2;TM=M;SS=N; 4.192248062
415023; AA932146; Hs.355397; Homo sapiens clone TCCCIA00164 mRNA sequ; none;NA;NA; 4.192
443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 4.191878981
445330; R52656; Hs.21691; ESTs; 7tm_1,none; 4.189922481
430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y;SS=N; 4.188333333
434633; AI189587; Hs.120915; ESTs; SH3,PH,RhoGAP,none; 4.187106918
452908; AB001451; Hs.30965; neuronal Shc adaptor homolog; SH2,PID,Zn_carbOpept;TM=M;SS=N; 4.186885246
439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 3.930957684
432201; AI538613; Hs.298241; Transmembrane protease, serine 3; ldl_recept_a,trypsin;TM=Y;SS=M; 3.893103448
428969; AF120274; Hs.194689; artemin; TGF-beta;; 3.884030418
444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig;TM=Y;SS=M; 3.831669044
432305; M62402; Hs.274313; insulin-like growth factor binding prote; thyroglobulin_1,IGFBP,A2M_N;TM=M;SS=N; 3.742996346
405547; ; ; NM_018833*:Homo sapiens transporter 2, A; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.676
407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 3.634
426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 3.562
427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q,Collagen;; 3.49
405546; ; ; NM_018833*:Homo sapiens transporter 2, A; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.422661871
439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none,none; 3.402
404210; ; ; NM_005936:Homo sapiens myeloid/lymphoid ; FHA,PDZ,RA,DIL;TM=M;SS=N; 3.368807339
424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;; 3.213402062
418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); none;TM=M;SS=N; 3.084
451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc_N_term;TM=M;SS=N; 1.55

TABLE 17B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418869	12789_14	AA229762 AA230035

TABLE 17C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
405932	7767812	Minus	123525-123713
400517	9796686	Minus	49996-50346
402328	4464283	Minus	13758-13922,14558-14752
405545	1054740	Plus	118677-118807,119091-119296,121626-12182
402330	4464283	Minus	15325-15380,15484-15588,15842-15915
404440	7528051	Plus	80430-81581
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
404760	7767724	Plus	223266-223352,224472-224585
404883	5101762	Minus	94626-94730,96998-97069
403362	8571772	Plus	64099-64260
405547	1054740	Plus	124361-124520,124914-125050
405546	1054740	Plus	124010-124183
404210	5006246	Plus	169926-170121

Table 18A: 194 Up-Regulated Genes in Uterine Cancer Versus Normal Adult Tissues

Table 18A lists about 194 genes up-regulated in uterine cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" uterine cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" uterine cancer level was set to the 2nd highest amongst uterine cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst non-malignant tissues. In order to remove gene-specific background

levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	55.7
435094	AI560129	Hs.277523	EST	45.2
438817	AI023799	Hs.163242	ESTs	42.6
421478	AI683243	Hs.97258	ESTs	35.2
452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	27.3
450451	AW591528	Hs.202072	ESTs	26.0
428153	AW513143	Hs.98367	hypothetical protein FLJ22252	24.8
428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49) (HG38)	24.2
438993	AA828995	Hs.52620	integrin; beta 8	16.7
436775	AA731111	Hs.291891	ESTs	14.3
430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clo	13.5
441377	BE218239	Hs.202656	ESTs	13.5
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	12.3
400292	AA250737	Hs.72472	BMPR-Ib;bone morphogenetic protein receptor Ib	10.7
403899			predicted exon	10.1
442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA	10.0
447350	AI375572	Hs.1939	HER4 (c-erb-B4)	9.8
453964	AI961486	Hs.12744	ESTs	9.7
443830	AI142095	Hs.143273	ESTs	9.1
459325	AW088369	Hs.282184	ESTs	9.0
415245	N59650	Hs.27252	ESTs	8.9
446608	N75217	Hs.257846	ESTs	8.9
426635	BE395109	Hs.129327	ESTs	8.8
433426	H69125	Hs.133525	ESTs	8.7
437960	AI669586	Hs.222194	ESTs	8.5
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H	8.3
440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	7.3
447835	AW591623	Hs.164129	ESTs	7.2
440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO10	7.1
412925	AI089319	Hs.179243	ESTs	7.0
408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane receptor (robo2)	7.0
429272	W25140	Hs.110667	ESTs	6.9
453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAM	6.3
437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein	6.2
420610	AI683183	Hs.99348	distal-less homeo box 5	6.2
448672	AI955511	Hs.225106	ESTs	6.1
452461	N78223	Hs.108106	transcription factor	6.1
413335	AI613318	Hs.48442	ESTs	6.1
449611	AI970394	Hs.197075	ESTs	6.0
449260	AA741180	Hs.29879	ESTs	6.0
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	6.0
443715	AI583187	Hs.9700	cyclin E1	6.0
432113	AA935065	Hs.152385	ESTs	5.9
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.7
410658	AW105231	Hs.192035	ESTs	5.7
426465	AI758948		gb:ty16f07.x1 NCI_CGAP_Ut3 Homo sapiens cDNA	5.7
446704	AI337228	Hs.197083	ESTs	5.5
419503	AA243642	Hs.137422	ESTs	5.5
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	5.4
436076	AI193277	Hs.120954	ESTs	5.4
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.3
445258	AI635931	Hs.147613	ESTs	5.3
440901	AA909358	Hs.128612	ESTs	5.3
434636	AA083764	Hs.241334	ESTs	5.3
429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone LNG020	5.2
418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.2
459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapiens cDN	5.2
436787	AA908554	Hs.192756	ESTs	5.2
400301	X03635	Hs.1657	Estrogen receptor 1	5.1
428771	AB028992	Hs.193143	KIAA1069 protein	5.1
444929	AI685841	Hs.161354	ESTs	5.0
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
405609			predicted exon	5.0
410102	AW248508	Hs.279727	ESTs;	5.0
433283	BE041135	Hs.175622	ESTs	4.8
443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	4.8
410247	AF181721	Hs.61345	RU2S	4.7
422589	AA312735	Hs.179725	ESTs	4.7
452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat93620	4.7
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens cDNA	4.7
420440	NM_002407	Hs.97644	mammaglobin 2	4.6
451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	4.6

	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	4.6
	424115	AA335497	Hs.293965	ESTs	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	4.6
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	4.5
5	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	4.5
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG076	4.4
	458861	AI630223		PHD finger DNA binding protein isoform 1 (int	4.4
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	4.3
	420149	AA255920	Hs.88095	ESTs	4.3
10	433479	AW511459	Hs.249972	ESTs	4.3
	449416	AI651016	Hs.246311	ESTs	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone HEP106	4.3
	450109	AI539295	Hs.17967	ESTs	4.3
	436954	AA740151	Hs.130425	ESTs	4.3
15	415511	AI732617	Hs.182362	ESTs	4.3
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM40	4.3
	406411			predicted exon	4.2
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	4.2
	416456	H57052	Hs.176626	hypothetical protein EDAG-1	4.2
20	454692	AW813350		gb:MR3-ST0192-100100-024-g07	4.1
	452249	BE394412	Hs.61252	ESTs	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	4.1
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUB	4.1
	434988	AI418055	Hs.161160	ESTs	4.1
25	423515	AA327017	Hs.162204	ESTs	4.0
	435407	AI149774	Hs.117178	ESTs	4.0
	440886	AW511032	Hs.190516	ESTs	4.0
	444783	AK001468	Hs.62180	ESTs	4.0
	452039	AI922988	Hs.172510	ESTs	4.0
30	407300	AA102616	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT0614	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	4.0
	449433	AI672096	Hs.9012	ESTs	3.9
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP20	3.9
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518	3.9
35	453096	AW294631	Hs.11325	ESTs	3.9
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.9
	445034	AW293376	Hs.160323	ESTs	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	3.8
	422219	AW978073		gb:EST390182 MAGE resequences	3.8
40	440304	BE159984	Hs.125395	ESTs	3.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228	3.8
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK	3.8
	400250			predicted exon	3.8
	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	3.8
45	420092	AA814043	Hs.88045	ESTs	3.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	3.8
	437212	AI765021	Hs.210775	ESTs	3.8
	409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_52	3.7
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.7
50	427119	AW880562	Hs.114574	ESTs	3.7
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	3.7
	434539	AW748078	Hs.214410	ESTs	3.7
	424717	H03754	Hs.152213	wingless-type MMTV integration site family	3.7
	412078	X69699	Hs.73149	paired box gene 8 (PAX-8)	3.7
55	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAMILY J	3.7
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.7
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin)	3.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDNA clo	3.7
	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapiens c	3.6
60	441285	NM_002374	Hs.167	microtubule-associated protein 2	3.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	3.6
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	3.6
	441484	AA935481	Hs.58972	ESTs	3.6
	415802	AA169515	Hs.6006	ESTs	3.6
65	448112	AW245919	Hs.301018	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	3.6
	402606			predicted exon	3.6
	407905	AW103655	Hs.252905	ESTs	3.6
	424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone LNG025	3.6
70	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	3.6
	451842	AI820539	Hs.267087	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.6
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	3.6
	431731	BE266322	Hs.211374	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal sh	3.6
75	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	3.6
	406030			predicted exon	3.5
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA Libr	3.5
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.5
	437641	AA811452	Hs.291911	ESTs	3.5
80	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	3.4
	443450	N66045	Hs.133529	ESTs	3.4
	457438	NM_014053	Hs.270594	FLVCR protein	3.4
	451254	AI571016	Hs.172967	ESTs	3.4

419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.4
427778	AA412323	Hs.105323	ESTs	3.3
435031	AI632091	Hs.116877	ESTs	3.3
407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	3.3
417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187J11 on c	3.3
431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	3.2
432415	T16971	Hs.289014	ESTs	3.2
423126	AA322245	Hs.290165	ESTs	3.2
433420	AI674093	Hs.293961	ESTs	3.2
435174	AA687378	Hs.194624	ESTs	3.2
444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked molety X	3.2
452588	AA889120	Hs.110637	Homeo box A10	3.2
427304	AA761526	Hs.163853	ESTs	3.2
419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from cl	3.1
417728	AW136437	Hs.24790	KIAA1573 protein	3.1
419356	AI656166	Hs.7331	ESTs	3.1
458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [	3.1
435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase 1	3.1
416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone COL064	3.1
405174			predicted exon	3.1
403776			predicted exon	3.1
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily, m	3.1
431255	AA497043	Hs.115685	ESTs	3.1
442353	BE379594	Hs.49136	ESTs	3.1
456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (formerl	3.1
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.1
454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens cDNA c	3.1
406400			kallikrein 8 (neuropsin/ovasin)	3.0
439949	AW979197	Hs.292073	ESTs	3.0
430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186 Homo sapi	3.0
401517			predicted exon	3.0
417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	3.0
435267	N23797	Hs.110114	ESTs	3.0
426384	AI472078		ESTs	3.0
422797	AB033064	Hs.120908	KIAA1238 protein	3.0
428832	AA578229		gb:nl22b12.s1 NCI_CGAP_HSC1 Homo sapiens cDNA	3.0
449722	BE280074	Hs.23960	cyclin B1	3.0
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	3.0
422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	3.0

TABLE 18B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
409745	115237_1	AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
409867	1156530_1	AW502161 AW502587 AW502345
422219	213547_1	AW978073 AW978072 AA807550 AA306567
422689	219896_1	AW856665 AA315006 AW954733
426384	266211_1	AI472078 AA377209 AA865807
426465	267664_1	AI758948 AA379527 AA379948 AA379262 AW963933
428832	296144_1	AA578229 AA436432 AA481375 AA481363
430704	322217_1	AW813091 AW206655 AA484440
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438993	467651_1	AA828995 AA834879 AI926361
442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
443613	575391_1	AI079356 W23287
449034	794817_1	AI624049 AW117770 AI858360
451105	859083_1	AI761324 AW880941 AW880937
452771	930983_1	T05477 T07855 AI917711
454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
454692	1229118_1	AW813350 AW816082 AW813476 AW813383
455666	1349545_1	BE065813 BE065788 BE065889 BE065832
458154	491768_1	AW816379 AA888282 AA879046 AA879195
458861	798065_1	AI630223 AI630470

TABLE 18C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401517	7677912	Plus	29278-29770
402606	9909429	Minus	81747-82094
403776	7770611	Minus	1414-1513,1624-1756
403899	7381715	Minus	9144-9350
405174	7108030	Minus	102814-103063
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
406030	8312328	Minus	96123-96547
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406411	9256407	Plus	7400-7527

Table 19A: 225 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, UTERINE Cancer Versus Normal Adult Tissues

Table 19A lists about 225 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
PSDomain: Protein Structural Domain
R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	R1
452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	TM	27.3
438993	AA828995	Hs.52620	integrin; beta 8	SS,TM,integrin_B	16.7
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromo	SS,hemopexin	12.3
446608	N75217	Hs.257846	ESTs	TM	8.9
433426	H69125	Hs.133525	ESTs	TM	8.7
440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clo	TM,PAX	7.1
408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane	SS,TM,ig,fn3	7.0
420610	AI683183	Hs.99348	distal-less homeo box 5	TM,homeobox	6.2
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rab	TM,kinesin	6.0
443715	AI583187	Hs.9700	cyclin E1	TM,cyclin	6.0
432113	AA935065	Hs.152385	ESTs	TM	5.9
419503	AA243642	Hs.137422	ESTs	TM	5.5
444342	NM_014398	Hs.10887	similar to lysosome-associated memb	TM,Lamp	5.4
436076	AI193277	Hs.120954	ESTs	TM	5.4
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	TM,hemopexin	5.3
418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.2
459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo s	TM	5.2
400301	X03635	Hs.1657	Estrogen receptor 1	TM,hormone_rec,zf-C4	5.1
405609			predicted exon	TM,Myosin_tail,myosin_head	5.0
453922	AF053306	Hs.36708	budding uninhibited by benzimidazol	TM	5.0
410102	AW248508	Hs.279727	ESTs;	SS,TM,	5.0
433283	BE041135	Hs.175622	ESTs	TM	4.8
443270	NM_004272	Hs.9192	Homer, neuronal immediate early gen	TM	4.8
410247	AF181721	Hs.61345	RU2S	TM	4.7
422589	AA312735	Hs.179725	ESTs	TM	4.7
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sap	TM	4.7
420440	NM_002407	Hs.97644	mammaglobin 2	TM,Uteroglobin	4.6
453616	NM_003462	Hs.33846	dynein, axonemal, light intermediat	TM,Ribosomal_S27e	4.6
424115	AA335497	Hs.293965	ESTs	TM	4.6
414245	BE148072	Hs.75850	WAS protein family, member 1	TM,WH2	4.6
458861	AI630223		PHD finger DNA binding protein isof	TM,PHD	4.4
449416	AI651016	Hs.246311	ESTs	SS,TM,	4.3
420149	AA255920	Hs.88095	ESTs	TM	4.3
433479	AW511459	Hs.249972	ESTs	TM	4.3
457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, cl	TM	4.3
406411			predicted exon	TM,vwa,FG-GAP	4.2
416456	H57052	Hs.176626	hypothetical protein EDAG-1	TM	4.2
454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192	TM	4.1
436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	TM	4.1
434988	AI418055	Hs.161160	ESTs	TM	4.1
444783	AK001468	Hs.62180	ESTs	TM,PH	4.0
440886	AW511032	Hs.190516	ESTs	TM,FG-GAP	4.0
425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HU	TM,Glyco_transf_29,TEA	4.0
445034	AW293376	Hs.160323	ESTs	TM	3.8
418677	S83308	Hs.87224	SRY (sex determining region Y)-box	TM,HMG_box	3.8
400250			predicted exon	TM,Hist_deacetyl	3.8
428227	AA321649	Hs.2248	interferon-gamma induced protein	TM,IL8	3.8
415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 T	TM,Kunitz_BPTI,G-gamma	3.8
458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	TM,WW	3.7
421477	AI904743	Hs.104650	hypothetical protein FLJ10292	TM	3.7

413472	BE242870	Hs.75379	solute carrier family 1 (glial high	TM,SDF	3.7
447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SU	TM	3.7
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopon	TM,Osteopontin	3.7
453891	AB037751	Hs.36353	Homo sapiens mRNA full length inser	TM	3.7
441285	NM_002374	Hs.167	microtubule-associated protein 2	TM,tubulin-binding	3.6
409731	AA125985	Hs.56145	thymosin, beta, identified in neuro	TM,Thymosin	3.6
441484	AA935481	Hs.58972	ESTs	TM,fn3,ig,Y_phosphatase	3.6
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrily	SS,Peptidase_M10	3.6
407905	AW103655	Hs.252905	ESTs	SS,TM,Ephrin	3.6
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellula	SS,TM,	3.6
402606			predicted exon	TM	3.6
443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1	TM	3.6
437641	AA811452	Hs.291911	ESTs	TM	3.5
415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFA	TM,IQ,RIIa	3.4
443450	N66045	Hs.133529	ESTs	TM	3.4
457438	NM_014053	Hs.270594	FLVCR protein	TM	3.4
435031	AI632091	Hs.116877	ESTs	TM,RhoGEF,PH	3.3
417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-1	TM	3.3
435174	AA687378	Hs.194624	ESTs	TM,SPRY	3.2
444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linke	TM,mutT	3.2
433420	AI674093	Hs.293961	ESTs	TM	3.2
419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E23	TM	3.1
417728	AW138437	Hs.24790	KIAA1573 protein	TM	3.1
403776			predicted exon	SS,TM,IL8	3.1
426274	D38122	Hs.2007	tumor necrosis factor (ligand) supe	TM,TNF	3.1
416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, cl	TM,Ets	3.1
405174			predicted exon	TM	3.1
431255	AA497043	Hs.115685	ESTs	TM	3.1
456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog	TM,homeobox	3.1
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	TM,trypsin,pro_isomerase	3.1
454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapi	TM	3.1
406400			kallikrein 8 (neuropsin/ovasin)	TM,trypsin	3.0
401517			predicted exon	TM,HMG14_17	3.0
417830	AW504786	Hs.132808	epithelial cell transforming sequen	TM	3.0
435267	N23797	Hs.110114	ESTs	TM	3.0
449722	BE280074	Hs.23960	cyclin B1	TM,cyclin	3.0
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2	TM,ank	3.0
422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297	TM,SNF2_N	3.0
441794	AW197794	Hs.253338	ESTs	TM,ank	2.9
416658	U03272	Hs.79432	fibrillin 2 (congenital contractura	TM,EGF,TB	2.9
431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic pr	SS,wap	2.9
418113	AI272141	Hs.83484	ESTs	TM,HMG_box	2.9
402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome	TM,TEA	2.9
431989	AW972870	Hs.291069	ESTs	SS	2.9
400284			Estrogen receptor 1	TM,hormone_rec,zf-C4	2.9
438578	AA811244	Hs.164168	ESTs	TM,formyl_transf,AIRS,GARS	2.9
423513	AF035960	Hs.129719	transglutaminase 5	TM ,Transglutamin_N	2.8
448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 fis, clo	TM	2.8
431870	AW449902	Hs.105500	ESTs	TM,MHC_I,ig	2.8
409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276	TM	2.8
438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 [M.mus	TM	2.8
451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	2.8
433326	AI379486	Hs.159430	ESTs	TM	2.8
446221	BE622615		gb:601440775T1 NIH_MGC_72 Homo sapi	TM	2.8
448141	AI471598	Hs.197531	ESTs	TM,bZIP	2.8
456311	AA225632	Hs.190016	ESTs	TM,Sec7	2.8
405454			predicted exon	TM	2.8
459287	AL079369		gb:DKFZp564G2378_r1 564 (synonym: h	TM	2.8
438935	H40665	Hs.31564	ESTs	TM	2.7
421312	AA824627	Hs.291670	ESTs	TM,G-patch	2.7
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	TM,ABC_membrane,ABC_tran	2.7
424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clo	TM	2.7
417956	AA210704	Hs.190465	ESTs	SS,sushi	2.7
445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	2.7
448089	AI467945	Hs.173696	ESTs	SS,TM,	2.6
446643	AA194417	Hs.282060	ESTs	TM,Clat_adaptor_s	2.6
456671	AB011142	Hs.114293	KIAA0570 gene product	TM	2.6
457256	AA459443	Hs.231816	ESTs	SS	2.6
438986	AF085888	Hs.269307	ESTs	TM,Spin-Ssty	2.5
435313	AI769400	Hs.189729	ESTs	TM,MBD	2.5
417351	T90278	Hs.15049	ESTs	TM,CH	2.5
412198	AA937111	Hs.69165	ESTs	TM	2.5
413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	TM,ubiquitin	2.5
421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	TM,Na_Pi_cotrans	2.5
418092	R45154	Hs.106604	ESTs	TM,pkinase	2.5
410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (	TM,FG-GAP	2.5
420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH,I_LWEQ	2.5
431974	AW972689	Hs.200934	ESTs	TM,bZIP	2.5
438209	AL120659	Hs.6111	KIAA0307 gene product	TM,HLH,PAS	2.5
447578	AA912347	Hs.136585	ESTs	TM	2.5
414812	X72755	Hs.77367	monokine induced by gamma interfero	SS,IL8	2.5
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase	TM,Glyco_transf_29	2.4
416402	NM_000715	Hs.1012	complement component 4-binding prot	TM,sushi	2.4

439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HU	TM	2.4
428242	H55709	Hs.2250	leukemia inhibitory factor (choline	SS,LIF_OSM	2.4
417693	AW959741	Hs.40368	adaptor-related protein complex 1,	TM,Clat_adaptor_s	2.4
428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Hom	TM,HECT	2.4
436311	AA708958	Hs.168732	ESTs	TM	2.4
426920	AA393351	Hs.132121	ESTs	TM	2.4
426698	AA394104	Hs.97489	ESTs	TM	2.4
443426	AF098158	Hs.9329	Homo sapiens mRNA for fis353, compl	TM	2.4
406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate trans	TM,IPPT	2.4
434808	AF155108	Hs.256150	ESTs, Highly similar to NY-REN-41 a	TM	2.3
432441	AW292425	Hs.163484	EST	TM,Fork_head	2.3
435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	TM	2.3
402298			predicted exon	TM,zf-C2H2,KRAB	2.3
435542	AA687376	Hs.269533	ESTs	TM	2.3
442952	AI743261	Hs.131860	ESTs	TM	2.3
418203	X54942	Hs.83758	CDC28 protein kinase 2	TM,CKS	2.3
429228	AI553633	Hs.104985	ESTs	TM	2.3
418969	W33191	Hs.28907	hypothetical protein FLJ20258	TM,SH3	2.3
447570	AI868315	Hs.99669	ESTs	TM,PHD	2.3
405032			predicted exon	TM,FMO-like	2.3
416566	NM_003914	Hs.79378	cyclin A1	TM,cyclin	2.3
420900	AL045633	Hs.44269	ESTs	TM,FAD_binding_5	2.3
430563	AA481269	Hs.178381	ESTs	TM,ABC_membrane,p450	2.3
417372	T99755	Hs.290814	ESTs	TM	2.3
449083	AI948808	Hs.191144	ESTs	TM	2.3
410361	BE391804	Hs.62661	guanylate binding protein 1, interf	TM,GBP	2.3
434131	AI858275	Hs.143659	ESTs	TM	2.3
431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	2.3
425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific	TM	2.3
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	2.3
445870	AW410053	Hs.13406	syntaxin 18	TM	2.3
430639	AW025427	Hs.233552	ESTs	TM,pkinase	2.3
439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfam	SS,TM,	2.3
422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	SS,TM,Cu-oxidase	2.2
411558	AA102670	Hs.70725	"Human GABA-A receptor pi subunit m	TM,neur_chan	2.2
408380	AF123050	Hs.44532	diubiquitin	TM ,7tm_3,ANF_receptor	2.2
403721			predicted exon	TM	2.2
440711	AA904389	Hs.143511	ESTs	TM,rrm	2.2
457285	AI038658	Hs.228780	ESTs, Highly similar to AF199597 1	TM,efhand	2.2
422956	BE545072	Hs.122579	ESTs	TM	2.2
433482	AI953499	Hs.152617	ESTs	TM	2.2
431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, cl	TM	2.2
420777	AA280223	Hs.130865	ESTs	TM	2.2
446659	AI335361	Hs.226376	ESTs	TM	2.2
410227	AB009284	Hs.61152	exostoses (multiple)-like 2	TM	2.2
422282	AF019225	Hs.114309	apolipoprotein L	TM	2.2
431701	AW935490	Hs.14658	ESTs	TM,Occludin	2.2
426910	AA470023	Hs.190089	ESTs	TM,MMR_HSR1	2.2
405636		Hs.153595	predicted exon	SS,TM,EGF,ldl_recept_a	2.2
401933			predicted exon	TM,ion_trans	2.1
436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed pro	TM	2.1
451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 pr	TM	2.1
410664	NM_006033	Hs.65370	lipase, endothelial	SS,TM,Ribosomal_L22,lipase	2.1
449378	AW664026	Hs.59892	ESTs	TM	2.1
433345	AI681545	Hs.152982	EST cluster (not in UniGene)	TM	2.1
425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase	SS,TM,Branch	2.1
431832	AW276866	Hs.192715	ESTs	TM,Ets,SAM_PNT	2.1
448275	BE514434	Hs.20830	synaptic Ras GTPase activating prot	TM,kinesin ,abhydrolase_2	2.1
423049	X59373	Hs.188023	ESTs	TM,homeobox	2.1
427510	Z47542	Hs.179312	small nuclear RNA activating comple	TM	2.1
418076	R61388	Hs.6724	ESTs	TM	2.1
413670	AB000115	Hs.75470	hypothetical protein, expressed in	TM	2.1
429183	AB014604	Hs.197955	KIAA0704 protein	TM	2.1
439031	AF075079		gb:Homo sapiens full length insert	TM	2.1
431060	AF039307	Hs.249171	homeo box A11	TM,homeobox	2.1
451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HU	TM	2.1
419978	NM_001454	Hs.93974	forkhead box J1	TM,Fork_head	2.1
404535	Z25884	Hs.121483	chloride channel 1 , skeletal muscl	SS	2.1
445181	AW338972	Hs.147471	ESTs	TM	2.1
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM,Hydrolase	2.1
443591	AI078281	Hs.179240	ESTs	TM	2.1
448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN	TM,trypsin	2.1
424310	AA338648	Hs.50334	ESTs	TM	2.0
450193	AI916071	Hs.224623	ESTs	TM,pkinase	2.0
436009	H57130	Hs.120925	ESTs	SS,TM,Ephrin	2.0
453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, cl	TM	2.0
419833	AA251131	Hs.220697	ESTs	TM,WHEP-TRS	2.0
437555	AA759263	Hs.14041	ESTs	TM,Nramp	2.0
411828	AW161449	Hs.72290	wingless-type MMTV integration site	TM,wnt	2.0
440052	AI633744	Hs.195648	ESTs	TM,PAC	2.0
410718	AI920783	Hs.191435	ESTs	TM,SQS_PSY	2.0
404767			predicted exon	TM	2.0
447462	AW337214	Hs.158973	ESTs	TM	2.0

442255	AI701857	Hs.202388	ESTs	TM	2.0
410292	AA843087	Hs.124194	ESTs	TM	2.0
442748	AI016713	Hs.135787	ESTs	TM	2.0
458760	AI498631	Hs.111334	ferritin, light polypeptide	TM,HCO3_cotransp	2.0
409799	D11928	Hs.76845	phosphoserine phosphatase-like	TM,Hydrolase	2.0
401324			predicted exon	TM,myosin_head	2.0
432140	AK000404	Hs.272688	hypothetical protein FLJ20397	SS	2.0
447541	AK000288	Hs.18800	hypothetical protein FLJ20281	TM,zf-CCHC	2.0
421379	Y15221	Hs.103982	small inducible cytokine subfamily	SS,TM,IL8	2.0

TABLE 19B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
409457	1132521_1	AW818081 AW392887 AW514700 AW392881
410008	116812_1	AA079552 BE142525 BE142527
422689	219896_1	AW856665 AA315006 AW954733
428679	294049_1	AA431765 AA432015
438993	467651_1	AA828995 AA834879 AI926361
439031	46798_1	AF075079 H48601 H48795
448221	75534_-1	BE622615
454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
454692	1229118_1	AW813350 AW816082 AW813476 AW813383
458154	491768_1	AW816379 AA888282 AA879046 AA879195
458861	798085_1	AI630223 AI630470
459287	977129_1	AL079369 D81804

TABLE 19C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401324	9863791	Plus	234057-234174
401517	7677912	Plus	29278-29770
401933	3810668	Minus	48725-49057,51864-51955,52424-52589
402298	6598824	Plus	36758-37953
402606	9909429	Minus	81747-82094
403721	7528046	Minus	156647-157366
403776	7770611	Minus	1414-1513,1624-1756
404767	7882827	Minus	23244-23759
405032	7107731	Minus	131945-132224
405174	7108030	Minus	102814-103063
405454	7656675	Plus	133807-134053
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
405636	5123990	Plus	56384-56587
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406411	9256407	Plus	7400-7527

Table 20A: 56 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, Uterine Cancer Versus Normal Adult Tissues

Table 20A lists about 56 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g. pkinase, peptidase, isomerase, transporters). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
PSDomain: Protein Structural Domain
R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	R1
428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	7tm_1	24.2
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromoly	hemopexin	12.3
447350	AI375572	Hs.172634	HER4 (c-erb-B4)	kinase	9.8
420610	AI683183	Hs.99348	distal-less homeo box 5	homeobox	6.2
405609			predicted exon	Myosin_tail,myosin_head	5.0
458861	NM_007358	Hs.31016	PHD finger DNA binding protein	PHD	4.4
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone	NA	4.3

436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	NA	4.1
444783	AK001468	Hs.62180	ESTs	PH	4.0
418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	HMG_box	3.8
413472	BE242870	Hs.75379	solute carrier family 1	SDF	3.7
443613	AI079356	Hs.21807	gb:oz39b09.s1 Soares_NhHMPu_S1 Homo s	zf-C2H2	3.6
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	Peptidase_M10	3.6
443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 re	NA	3.6
435031	AI632091	Hs.116877	ESTs	RhoGEF,PH	3.3
417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187	NA	3.3
435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrola	NA	3.1
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	trypsin,pro_isomerase	3.1
406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	trypsin	3.0
418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	ank	3.0
441794	AW197794	Hs.253338	ESTs	ank	2.9
402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome de	TEA	2.9
423513	AF035960	Hs.129719	transglutaminase 5	Transglutamin_N	2.8
448141	AI471598	Hs.197531	ESTs	bZIP	2.8
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	guanylate_cyc	2.7
418862	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	ABC_membrane,ABC_tran	2.7
448435	BE293439	Hs.182278	calmodulin 2	NA	2.6
417351	T90278	Hs.15049	ESTs	CH	2.5
430372	AI206173	Hs.211375	ESTs	SH3,efhand,C2,PH	2.5
431974	AW972689	Hs.200934	ESTs	bZIP	2.5
428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hy	ank	2.4
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I	Glyco_transf_29	2.4
403095			predicted exon	homeobox,PAX	2.4
406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transfe	IPPT	2.4
435615	Y15065	Hs.4975	potassium voltage-gated channel	ion_channel	2.3
402298			predicted exon	zf-C2H2,KRAB	2.3
418203	X54942	Hs.83758	CDC28 protein kinase 2	CKS	2.3
430563	AA481269	Hs.178381	ESTs	ABC_membrane,p450	2.3
447570	AI868315	Hs.99669	ESTs	PHD	2.3
439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamil	NA	2.3
415539	AI733881	Hs.72472	BMPR-Ib;	bone morphogenetic protein NA	2.2
422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	Cu-oxidase	2.2
408380	AF123050	Hs.44532	diubiquitin	ANF_receptor,sushi,7tm_1	2.2
440711	AA904389	Hs.143511	ESTs	rrm	2.2
457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-	efhand	2.2
418506	AA084248	Hs.85339	G protein-coupled receptor 39	NA	2.2
410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22,lipase,PLAT	2.1
425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1	Branch	2.1
448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein	kinesin,PHD,abhydrolase_2	2.1
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-dom	rrm,NTF2	2.1
404535	Z25884	Hs.121483	chloride channel 1 , skeletal muscle	NA	2.1
448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2	trypsin	2.1
446342	BE298665	Hs.14846	Cationic amino acid transporter (ecto	NA	2.0
458760	AI498631	Hs.111334	ferritin, light polypeptide	HCO3_cotransp,zf-C3HC4	2.0
409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	2.0
401324			predicted exon	myosin_head	2.0

TABLE 20B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
443613	575391_1	AI079356 W23287
458861	798085_1	AI630223 AI630470

TABLE 20C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401324	9863791	Plus	234057-234174
402298	6598824	Plus	36758-37953
403095	8954339	Plus	150025-150240,151564-151690
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 21A: 270 Up-Regulated Genes, Uterine Cancer Versus Normal Uterus

Table 21A lists about 270 genes up-regulated in uterine cancer compared to normal uterus. These were selected as for Table 18A, except that the ratio was greater than or equal to 5.0, and the denominator was the median value for six non-malignant uterine specimens.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens	55.7
435094	AI560129	Hs.277523	EST	45.2
438461	AW075485	Hs.286049	phosphoserine aminotransferase	19.5
434779	AF153815	Hs.50151	potassium inwardly-rectifying channel	15.6
441633	AW958544	Hs.112242	ESTs	15.2
429183	AB014604	Hs.197955	KIAA0704 protein	14.6
436775	AA731111	Hs.291891	ESTs	14.3
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	14.0
446921	AB012113	Hs.16530	CC chemokine SCYA18 (MIP-4) (PARC)	13.0
413753	U17760	Hs.301103	Laminin, beta 3 (nicein (125kD), kalinin	12.9
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	12.2
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	12.0
453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	11.7
425196	AL037915	Hs.155097	carbonic anhydrase II	11.4
444863	AW384082	Hs.301323	ESTs	11.3
449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	11.1
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	10.9
449801	AA477355	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	10.3
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.3
414812	X72755	Hs.77367	monokine induced by gamma interferon	10.2
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	10.1
423645	AI215632	Hs.147487	ESTs	10.1
442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens	10.0
415786	AW419196	Hs.257924	ESTs	10.0
458017	AA813426	Hs.192034	ESTs, Weakly similar to KIAA0705 protein	10.0
435525	AI831297	Hs.123310	ESTs	9.9
413335	AI613318	Hs.48442	ESTs	9.7
420297	AI628272	Hs.88323	ESTs	9.6
452799	AI948829	Hs.213786	ESTs	9.6
434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	9.4
408243	Y00787	Hs.624	interleukin 8	9.3
430713	AA351647	Hs.2642	eukaryotic translation elongation factor	9.3
452092	BE245374	Hs.27842	hypothetical protein FLJ11210	9.2
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	9.2
443830	AI142095	Hs.143273	ESTs	9.1
442547	AA306997	Hs.268362	ESTs, Weakly similar to hypothetical pro	9.0
421633	AF121860	Hs.106260	sorting nexin 10	9.0
403381			0	8.9
426635	BE395109	Hs.129327	ESTs	8.8
440500	AA972165	Hs.150308	ESTs	8.7
436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulati	8.7
431668	AW969610	Hs.151179	ESTs	8.7
439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	8.7
424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino	8.6
425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	8.6
428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9	8.5
438986	AF085888	Hs.269307	ESTs	8.4
422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	8.4
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	8.3
415992	C05837	Hs.145807	Homo sapiens cDNA FLJ13593 fis, clone PL	8.2
431211	M86849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, co	8.2
409865	AW502208		gb:UI-HF-BR0p-aju-e-09-0-UI.r1 NIH_MGC_5	8.0
448158	AI627292	Hs.190877	ESTs	8.0
401519			0	7.9
441730	AI243276	Hs.149017	ESTs	7.9
432441	AW292425	Hs.163484	EST	7.8
448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	7.8
438424	AI912498	Hs.25895	ESTs, Weakly similar to PI-3 kinase [H.s	7.8
447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAMI	7.7
408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	7.7
423081	AF262992	Hs.123159	sperm associated antigen 4	7.6
414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	7.6
420931	AF044197	Hs.100431	small inductble cytokine B subfamily (Cy	7.6
459142	AI903396		gb:RC-BT029-120199-219_1 BT029 Homo sapi	7.5
411094	BE066142		gb:CM4-BT0320-221199-047-g10 BT0320 Homo	7.5
436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	7.5
452607	AI160029	Hs.61438	ESTs	7.5
443171	BE281128	Hs.9030	TONDU	7.4
459081	W07808		gb:zb03a12.r1 Soares_fetal_lung_NbHL19W	7.4
431195	AA503083	Hs.79742	ESTs	7.4
444459	AI680624	Hs.148676	ESTs	7.4

	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	7.3
	414918	AI219207	Hs.72222	Hypothetical protein FLJ13459	7.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	7.3
	448865	R35027		gb:yg60g02.r1 Soares infant brain 1NIB H	7.3
5	409219	AA393383	Hs.133331	ESTs	7.3
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	7.2
	403485			0	7.2
	408350	AW183350	Hs.250127	ESTs	7.2
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	7.1
10	400995			0	7.1
	406086			0	7.1
	403378			0	7.0
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	7.0
	422038	R39098	Hs.192028	ESTs	7.0
15	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	6.9
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.9
	427494	AI628365	Hs.130412	ESTs, Weakly similar to sre-2 [C.elegans	6.9
	429272	W25140	Hs.110667	ESTs	6.9
	427258	AA400091	Hs.39421	ESTs	6.9
20	449309	AW589823	Hs.224189	ESTs	6.9
	400104			0	6.9
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	6.8
	404767			0	6.8
	406690	M29540	Hs.220529	CEA (carcinoembryonic antigen-related ce	6.8
25	439750	AL359053	Hs.57664	ESTs	6.8
	403127	AI904493	Hs.99890	polymerase (DNA directed), delta 1, cata	6.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.8
	425858	AA364923		gb:EST75602 Pineal gland II Homo sapiens	6.8
	421712	AK000140	Hs.107139	hypothetical protein	6.7
30	456903	D49441	Hs.155981	mesothelin	6.7
	414564	AA164803	Hs.71994	ESTs	6.7
	457942	AW665665	Hs.153034	ESTs	6.7
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.7
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	6.7
35	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	6.7
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	6.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.6
	410664	NM_006033	Hs.65370	lipase, endothelial	6.6
	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibito	6.6
40	405400			kallikrein 8 (neuropsin/ovasin)	6.6
	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	6.5
	441460	AI962478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN I	6.5
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta pol	6.5
	424349	AF141289	Hs.145550	solute carrier family 7 (cationic amino	6.5
45	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.4
	445258	AI635931	Hs.147613	ESTs	6.4
	456032	AW957446	Hs.301711	ESTs	6.4
	404727			0	6.4
	422810	AA317400		gb:EST19374 Retina II Homo sapiens cDNA	6.4
50	440044	AW665167	Hs.259563	EST	6.4
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	6.4
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	6.4
	422170	AI791949	Hs.112432	anti-Mullerian hormone	6.4
	449611	AI970394	Hs.197075	ESTs	6.4
55	402539	AW502761	Hs.30909	KIAA0430 gene product	6.3
	456983	AI081687	Hs.170225	thymopoietin	6.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	6.3
	457887	AI240007	Hs.148812	ESTs	6.3
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	6.3
60	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR	6.2
	443494	T99719	Hs.270404	Homo sapiens cDNA: FLJ22389 fis, clone H	6.2
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	6.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	6.2
	413982	BE503035	Hs.279193	ESTs	6.2
65	458091	AF150286		gb:AF150286 Human mRNA from cd34+ stem c	6.2
	402104			0	6.2
	428771	AB028992	Hs.193143	KIAA1069 protein	6.1
	435313	AI769400	Hs.189729	ESTs	6.1
	441666	AI188346	Hs.301776	ESTs	6.1
70	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.1
	427308	D26067	Hs.174905	KIAA0033 protein	6.1
	423069	W15613	Hs.1613	adenosine A2a receptor	6.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.1
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.1
75	449409	AI650935	Hs.301694	ESTs	6.1
	400855			0	6.1
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192 Homo	6.0
	414869	AA157291	Hs.72163	ESTs	6.0
	439662	H97552	Hs.269060	ESTs	6.0
80	445181	AW338972	Hs.147471	ESTs	6.0
	437129	AL049327		gb:Homo sapiens mRNA; cDNA DKFZp564E016	6.0
	440128	AA962623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0

	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3	5.9
	405291			0	5.9
	432113	AA935065	Hs.152385	ESTs	5.9
	441236	AA923489	Hs.130432	ESTs	5.9
5	424418	BE503432	Hs.66170	HSKM-B protein	5.9
	453028	AB006532	Hs.31442	RecQ protein-like 4	5.8
	407137	T97307	Hs.199067	EST	5.8
	443462	AI064690	Hs.171176	ESTs	5.8
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens c	5.8
10	456311	AA225632	Hs.190016	ESTs	5.8
	446501	AI302616	Hs.150619	ESTs	5.8
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	5.8
	409615	AW444861		gb:UI-H-BI3-ajz-a-04-0-UI.s1 NCI_CGAP_Su	5.8
	459360	BE384526		gb:601277913F1 NIH_MGC_20 Homo sapiens c	5.8
15	403824			0	5.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	5.8
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
	426465	AI758948		gb:ty16f07.x1 NCI_CGAP_UI3 Homo sapiens	5.7
20	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retin	5.7
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.7
	405392			0	5.7
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	5.7
	449796	AA004321	Hs.194397	ESTs	5.7
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.7
	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3	5.7
	404220			0	5.6
	420973	AA743415	Hs.291368	ESTs	5.6
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	5.6
30	442549	AI751601	Hs.8375	TNF receptor-associated factor 4	5.6
	409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_5	5.6
	451110	AI955040	Hs.301584	ESTs	5.6
	418216	AA662240	Hs.283099	AF15q14 protein	5.6
	411897	AW875066		gb:RC6-PT0001-180100-021-F04 PT0001 Homo	5.6
35	456161	BE264645	Hs.282093	Homo sapiens cDNA: FLJ21918 fis, clone H	5.6
	406536			0	5.6
	432540	AI821517	Hs.105866	ESTs	5.6
	446315	NM_016293	Hs.14770	bridging integrator 2	5.6
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.6
40	451035	AU076785	Hs.430	plastin 1 (I isoform)	5.6
	406685	M18728		gb:Human nonspecific crossreacting antig	5.5
	454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HE	5.5
	402430			0	5.5
	446704	AI337228	Hs.197083	ESTs	5.5
45	435282	AA677428	Hs.189731	ESTs	5.5
	426062	N57014	Hs.44013	ESTs	5.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	5.5
	456002	AI628729	Hs.191450	ESTs, Weakly similar to type II membrane	5.5
	409613	AW444816	Hs.171537	Homo sapiens cDNA: FLJ21596 fis, clone C	5.5
50	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	5.5
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	5.5
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	5.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	5.4
	400379	NM_018432	Hs.283076	Homo sapiens ovarian cancer related prot	5.4
55	436076	AI193277	Hs.120954	ESTs	5.4
	432119	T80289		gb:yd03h04.r1 Soares infant brain 1NIB H	5.4
	417175	R44558	Hs.94002	ESTs	5.4
	445774	AI254165	Hs.145504	ESTs	5.4
	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	5.4
60	411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	5.4
	445262	AW205650	Hs.253503	ESTs	5.4
	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cD	5.4
	434756	AA827650	Hs.259307	ESTs	5.3
	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	5.3
65	439949	AW979197	Hs.292073	ESTs	5.3
	414995	C18200		gb:C18200 Human placenta cDNA (TFujiwara	5.3
	428071	AF212848	Hs.182339	transcription factor ESE-3B	5.3
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	5.3
	434283	AW235341	Hs.58715	mouse thiamin pyrophosphokinase homolog	5.3
70	447798	AI425049	Hs.119629	ESTs, Moderately similar to ALU1_HUMAN A	5.3
	401723			0	5.3
	406270			0	5.3
	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	5.3
	415757	AA830854	Hs.187810	ESTs	5.3
75	430051	AA464611	Hs.52515	transducin (beta)-like 2	5.2
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	5.2
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	5.2
	449009	BE044755	Hs.224812	ESTs	5.2
	424001	W67883	Hs.137476	KIAA1051 protein	5.2
80	409479	BE163800	Hs.136912	ESTs	5.2
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	5.2
	435928	H64345	Hs.183961	ESTs	5.2
	447397	BE247676	Hs.18442	E-1 enzyme	5.2

449183	AW445022	Hs.196985	Homo sapiens cDNA: FLJ21135 fis, clone C	5.2
410146	AW592655		gb:hf45f12.x1 Soares_NFL_T_GBC_S1 Homo s	5.2
458164	AI208666	Hs.192081	ESTs	5.2
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	5.1
439509	AF086332	Hs.58314	ESTs	5.1
422569	BE552132	Hs.118442	cyclin C	5.1
430664	AW969834		gb:EST381912 MAGE resequences, MAGK Homo	5.1
411231	AW833501		gb:QV4-TT0008-091199-025-e09 TT0008 Homo	5.1
412194	AW900282	Hs.115412	Homo sapiens cDNA FLJ13881 fis, clone TH	5.1
425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.1
417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.1
433279	AW971745		gb:EST383834 MAGE resequences, MAGL Homo	5.1
454112	NM_000885	Hs.301806	ESTs	5.1
423261	Z43509		gb:HSC1EA031 normalized infant brain cDN	5.1
434084	AI061640	Hs.192788	hypothetical protein PRO1905	5.1
446115	AI733075	Hs.292682	ESTs, Weakly similar to S69913 hypertens	5.1
416719	H79731		gb:yu81f12.r1 Soares fetal liver spleen	5.1
421462	AF016495	Hs.104624	aquaporin 9	5.1
424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	5.1
403383			0	5.1
430832	AI073913	Hs.100686	ESTs, Weakly similar to secreted cement	5.1
436070	AK000073		gb:Homo sapiens cDNA FLJ20066 fis, clone	5.0
416969	AI815443	Hs.283404	organic cation transporter	5.0
444929	AI685841	Hs.161354	ESTs	5.0
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
439031	AF075079		gb:Homo sapiens full length insert cDNA	5.0
414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	5.0
425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	5.0
449986	AW864502		gb:PM4-SN0016-120400-004-b12 SN0016 Homo	5.0
418717	AI334430	Hs.86984	ESTs	5.0
438769	AA830684	Hs.163426	ESTs	5.0
441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1	5.0
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase	5.0

TABLE 21B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
409615	1143425_1	AW444861 BE074994 BE074966 BE074992
409865	1156518_1	AW502208 AW502366 AW502148
409867	1156530_1	AW502161 AW502587 AW502345
410146	1178974_1	AW592655 R05927 R06916
411094	1231982_1	BE066142 AW817074
411231	1236356_1	AW833501 AW833506 AW833722 AW833332 AW833509 AW833511 AW833767 AW833339
411426	1245515_1	BE141714 AW845993 AW845989
411897	1264907_1	AW875066 AW875079 AW875075 AW875062 AW875061 AW875074
412323	1288770_1	AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173 AW937159 AW937139 AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179 AW937156 AW937140 AW937135 AW937170
412517	130281_1	BE271584 AA112511
414484	1452830_-1	BE314385
414539	1460320_1	BE379046 BE395459
414995	1511736_1	C18200 D78681 T82025
416719	1611345_1	H79731 H79732
422731	220507_1	AL138411 AL138412 AA315860
422810	221630_1	AA317400 AA434584
423261	226553_1	Z43509 H09001 AA375202 AW954383
425858	257265_1	AA364923 AW963483 BE182774 C21461
426465	267664_1	AI758948 AA379527 AA379948 AA379262 AW963933
430664	321423_1	AW969834 AA528493 AA483165 AW969842
432119	34170_1	T80289 AF052168
433279	361800_1	AW971745 AA581359 AA581358
433921	377350_1	AA618174 AI114549 R36464 R36465
434609	38950_1	R76593 AF147390 R76594
436070	41426_1	AK000073 AA380183 AA380181 AW963533
437129	43343_1	AL049327 AA847105
439031	46798_1	AF075079 H48601 H48795
442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
448865	78535_1	R35027 R12034 BE407120
449034	794817_1	AI624049 AW117770 AI858360
449986	821463_1	AW864502 AW864369 AI678780
454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
454692	1229118_1	AW813350 AW816082 AW813476 AW813383
455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
458091	472385_1	AF150286 AA835857
459081	889426_1	W07808 AI822066
459142	918906_1	AI903396 AI903361 AI903360

TABLE 21C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400855	1931571	Minus	17801-18228
400995	8099094	Plus	141186-141601
401519	6649315	Plus	157315-157950
401723	7656694	Plus	147273-147503
402104	8119072	Plus	122409-122600
402430	9796372	Minus	62382-62552
403378	9438244	Minus	44264-44443
403381	9438267	Minus	26009-26178
403383	9438267	Minus	119837-121197
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
403824	9798468	Plus	473-887
404220	6706820	Plus	46107-46439
404727	8081050	Plus	115534-115747
404767	7882827	Minus	23244-23759
405291	3845420	Plus	19999-20473,20672-21036,21147-21285,21378-21667
405392	6624069	Minus	116167-116289,118879-119030
406086	7107817	Plus	9418-9573
406270	7534217	Plus	13136-13591
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406536	7711478	Plus	25655-25782

TABLE 22A: 430 SIGNIFICANTLY DOWN-REGULATED GENES, UTERINE CANCER VERSUS NORMAL UTERUS

Table 22A lists about 430 genes significantly down-regulated in uterine cancer compared to normal uterus. These were selected as for Table 21A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 14 (i.e. 14-fold down-regulated in tumor vs. normal uterus).

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
414063	H26904	Hs.75736	apolipoprotein D	93.0
447990	BE048821	Hs.20144	small inducible cytokine subfamily A, member 14	75.7
407815	AW373860	Hs.301716	ESTs	68.7
452547	AA335295	Hs.74120	adipose specific 2	61.1
415165	AW887604	Hs.78065	complement component 7	55.1
453655	AW960427	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	54.0
429350	AI754634	Hs.131987	ESTs	52.6
407228	M25079	Hs.155376	hemoglobin, beta	52.0
425869	AA524547	Hs.160318	FXYD domain-containing ion transport regulato	51.6
416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	51.4
408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (from c	49.7
417542	J04129	Hs.82269	progestagen-associated endometrial protein (p	49.3
412295	AW088826	Hs.22971	ESTs	48.0
421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	47.0
452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (from c	46.7
429707	W76631	Hs.211819	matrix metalloproteinase 23B	45.7
416950	AL049798	Hs.80552	dermatopontin	45.6
408221	AA912183	Hs.47447	ESTs	44.6
406791	AI220684	Hs.272572	hemoglobin, alpha 2	43.0
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome	42.6
407938	AA905097	Hs.85050	phospholamban	41.1
410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	41.0
412524	AA417813	Hs.11177	ESTs	39.4
452426	AI904823	Hs.31297	Homo sapiens cDNA: FLJ23001 fis, clone LNG002	38.6
414290	AI568801	Hs.71721	ESTs	38.2
439627	BE621702	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone HEP018	38.0
400258		Hs.79064	deoxyhypusine synthase	37.0
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	36.1
410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	35.4
407663	NM_016429	Hs.37482	COPZ2 for nonclathrin coat protein zeta-COP	34.3
410286	AI739159	Hs.61898	DKFZP586N2124 protein	33.8
418986	AI123555	Hs.81796	ESTs	33.1
409060	AI815867	Hs.50130	necdin (mouse) homolog	33.1
436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	32.8
420674	NM_000055	Hs.1327	butyrylcholinesterase	32.6
417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, member	32.4
450810	BE207588	Hs.25511	transforming growth factor beta 1 induced tra	31.7
438150	AA037534	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	31.6

430468	NM_004673	Hs.130699	ESTs	31.5
453060	AW294092	Hs.21594	ESTs	31.3
424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vascular	30.8
422126	AW973784	Hs.112028	Misshapen/NIK-related kinase	30.5
406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (isoform	30.3
421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDNA clo	30.3
402520				29.9
418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase receptor	29.7
443906	AA348031	Hs.7913	ESTs	29.7
450958	AL137669	Hs.25700	Homo sapiens mRNA; cDNA DKFZp434M0435 (from c	29.4
418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-type 12-	29.4
412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob dise	29.4
429507	NM_003102	Hs.2420	superoxide dismutase 3, extracellular	29.2
400545				29.1
425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	29.1
429942	AI338993	Hs.134535	ESTs	28.9
438303	AB028998	Hs.6147	KIAA1075 protein	28.7
419971	AA400027	Hs.296234	ESTs, Highly similar to mitogen-activated pro	28.7
443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	28.7
452877	AI250789	Hs.32478	ESTs	28.6
412442	AI983730	Hs.26530	serum deprivation response (phosphatidylserin	28.6
424378	W28020	Hs.184367	GTPase activating protein-like	28.6
421823	N40850	Hs.28625	ESTs	27.9
447786	BE620810	Hs.39619	hypothetical protein LOC57333	27.6
400023			AFFX control: 18S ribosomal RNA	27.5
453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	27.2
414134	X60188	Hs.861	mitogen-activated protein kinase 3	27.1
428451	AW970451	Hs.98570	ESTs	26.9
435520	AA297990	Hs.9315	HNOEL-iso protein	26.6
437179	AA393508	Hs.171409	serologically defined colon cancer antigen 8	26.4
441481	AA935303	Hs.270553	ESTs	26.0
450227	BE388192	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone COL001	25.6
403731				25.5
452814	AI092790	Hs.55016	hypothetical protein FLJ21935	25.5
410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	25.5
416854	H40164	Hs.80296	Purkinje cell protein 4	25.4
418421	R58620	Hs.85050	phospholamban	25.4
407000	U12139		gb:Human alpha1(XI) collagen (COL11A1) gene,	25.3
421803	NM_012205	Hs.108441	3-hydroxyanthranilate 3,4-dioxygenase	25.3
445613	BE550889	Hs.158491	ESTs	25.1
432302	AA345857	Hs.274307	KIAA1442 protein	24.8
420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-associate	24.8
423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL021	24.7
417302	BE245812	Hs.8941	ESTs	24.6
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mimecan)	24.6
440130	AI083899	Hs.157527	ESTs	24.5
431967	AJ243653	Hs.283404	organic cation transporter	24.5
424580	AA446539	Hs.35092	ESTs	24.4
406907	Z25427		gb:H.sapiens protein-serine/threonine kinase	24.2
443745	AB039670	Hs.9728	ALEX1 protein	24.1
429101	AW452174	Hs.173780	ESTs	23.5
410691	AW239226	Hs.65450	reticulon 4	23.4
408853	AW291484	Hs.254967	ESTs	23.3
407979	AA046306	Hs.62927	ESTs	23.1
448619	AI867182	Hs.202255	ESTs	22.8
424585	AA464840		gb:zx43h11.r1 Soares_total_fetus_Nb2HF8_9w Ho	22.7
407891	AA486620	Hs.41135	Endomucin 2	22.6
407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma virus (FB	22.5
426990	AL044315	Hs.173094	Homo sapiens mRNA; cDNA DKFZp564H142 (from cl	22.5
450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelial cell)	22.1
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like	22.0
423690	AA329648	Hs.23804	ESTs	22.0
402865				21.9
417387	AW021102	Hs.21509	ESTs	21.9
456898	NM_001928	Hs.155597	D component of complement (adipsin)	21.9
459722			Homo sapiens cDNA: FLJ23449 fis, clone HSI058	21.8
422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	21.8
402195				21.7
418213	AW978753	Hs.127327	ESTs	21.6
440274	R24595	Hs.7122	scrapie responsive protein 1	21.6
455818	AI733747		gb:zn86d04.y5 Stratagene lung carcinoma 93721	21.4
420861	AI039044	Hs.88827	Homo sapiens mRNA for FLJ00033 protein, parti	21.4
405228				21.3
441292	AF131218	Hs.7765	chromosome 16 open reading frame 5	21.3
432553	AA553334	Hs.211095	ESTs	21.3
417098	AB017365	Hs.173859	frizzled (Drosophila) homolog 7	21.2
453642	AI370936	Hs.34074	dipeptidylpeptidase VI	21.2
405313				21.1
410243	D83402	Hs.289006	ESTs, Weakly similar to alternatively spliced	21.1
413186	AU077141	Hs.75231	solute carrier family 16 (monocarboxylic acid	21.1
425954	AK000633	Hs.164476	hypothetical protein FLJ20626	21.0
421770	AA374192	Hs.108124	ribosomal protein L41	21.0
435265	AA779958	Hs.185932	ESTs	20.8

430036	AL050284	Hs.227782	DKFZP586M1019 protein	20.7
430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (from c	20.7
436130	AA341497	Hs.31408	ESTs	20.7
434843	R43707	Hs.133159	ESTs, Weakly similar to PIHUSD salivary proli	20.7
429303	AW137635	Hs.44238	ESTs	20.6
442422	AI344415	Hs.156082	ESTs	20.5
410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific prot	20.5
435869	AF255910	Hs.54650	ESTs, Weakly similar to (defline not availabl	20.5
447384	AI377221	Hs.40528	ESTs	20.5
440610	AI733098	Hs.130800	ESTs	20.5
445806	AL137516	Hs.13323	hypothetical protein FLJ22059	20.4
433657	AI244368	Hs.8124	PH domain containing protein in retina 1	20.4
436467	AW450278	Hs.91681	ESTs	20.3
440191	AI990417	Hs.116107	Homo sapiens genomic DNA, chromosome 21q, sec	20.2
417511	AL049176	Hs.82223	chordin-like	20.2
406976	M60299		gb:Human alpha-1 collagen type II gene, exons	20.1
443547	AW271273	Hs.23767	ESTs	20.1
417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo sapi	20.1
419313	AA843387	Hs.87279	ESTs	20.1
408322	AW181985	Hs.249986	ESTs	20.0
448422	BE263813		gb:601194177F1 NIH_MGC_7 Homo sapiens cDNA cl	20.0
403121				19.9
424198	AB029010	Hs.143026	KIAA1087 protein	19.9
459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein D (AU	19.9
457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.sapiens	19.9
445029	AF196481	Hs.12256	midline 2	19.9
424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from c	19.8
417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal monoa	19.7
413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYDROXYP	19.6
435891	AW249394	Hs.5002	copper chaperone for superoxide dismutase	19.6
447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	19.6
400637				19.5
409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (car	19.4
430310	U60115	Hs.239069	four and a half LIM domains 1	19.4
402741				19.4
401703				19.3
409229	H60333	Hs.251928	nuclear pore complex interacting protein	19.3
453856	AA804789	Hs.19447	Homo sapiens mRNA for FLJ00106 protein, parti	19.3
430342	NM_005938	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (t	19.3
404033				19.2
411939	AI365585	Hs.146246	ESTs	19.2
431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	19.1
452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced	19.1
439698	AW779654	Hs.55876	ESTs	18.9
416253	BE250659	Hs.15463	ESTs	18.9
418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo sapien	18.9
408877	AA479033	Hs.130315	ESTs	18.9
415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24kD	18.9
417054	AF017060	Hs.174151	aldehyde oxidase 1	18.8
404654				18.8
420174	AI824144	Hs.23912	ESTs	18.8
400625				18.7
406150				18.7
457835	BE256338	Hs.192375	ESTs, Highly similar to dJ127B20.3 [H.sapiens	18.6
420105	AW015571	Hs.32244	ESTs	18.6
404619	BE514535	Hs.77171	minichromosome maintenance deficient (S. cere	18.5
423282	AL137563	Hs.126378	putative ABC transporter	18.5
424097	M13981	Hs.1734	inhibin, alpha	18.5
448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from c	18.5
427605	NM_000997	Hs.179779	ribosomal protein L37	18.4
406535				18.4
418947	W52990	Hs.22860	ESTs	18.4
414323	NM_014759	Hs.239500	KIAA0273 gene product	18.3
457111	AA482027	Hs.142569	ESTs	18.3
418373	AW750770	Hs.84344	CGI-135 protein	18.3
424461	D83542	Hs.148090	cadherin 15, M-cadherin (myotubule)	18.2
451565	NM_000897	Hs.456	leukotriene C4 synthase	18.2
407751	BE276096	Hs.38205	from HeLa cyclin-dependent kinase 2 interacti	18.2
432031	AF039196	Hs.284126	hairless (mouse) homolog	18.1
404608	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	18.1
451962	AW076832	Hs.226806	ESTs	18.1
424100	AI793080	Hs.123525	ESTs, Weakly similar to NGAL RAT NEUTROPHIL G	18.1
451509	AI969529	Hs.171637	Homo sapiens cDNA: FLJ21937 fis, clone HEP044	18.1
453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker protein	18.0
429924	W39693	Hs.226138	Homo sapiens mRNA; cDNA DKFZp566H2446 (from c	17.9
423780	AA352013		gb:EST59935 Infant brain Homo sapiens cDNA 5'	17.9
427030	AA397600	Hs.97531	ESTs	17.9
439872	T81058		gb:yd26c08.r1 Soares fetal liver spleen 1NFLS	17.9
407836	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone CAE112	17.9
451427	AI091441	Hs.26401	tumor necrosis factor (ligand) superfamily, m	17.9
424462	AU076666	Hs.148101	serum constituent protein	17.9
451533	NM_004657	Hs.26530	serum deprivation response (phosphatidylserin	17.8
422319	AW403342	Hs.115232	splicing factor 3a, subunit 2, 66kD	17.8

	400489				17.8
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein, parti	17.8
	449282	AL048056	Hs.23437	Homo sapiens cDNA FLJ13555 fis, clone PLACE10	17.7
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (from c	17.7
5	429790	AK001352	Hs.221737	hypothetical protein FLJ10490	17.7
	422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo sapi	17.7
	427980	AA418305		gb:zv96g05.s1 Soares_NhHMPu_S1 Homo sapiens c	17.6
	409543	AW410200		gb:fh05b12.x1 NIH_MGC_17 Homo sapiens cDNA cl	17.6
	440206	AI762232	Hs.46794	ESTs	17.6
10	455904	BE156173		gb:QV0-HT0367-201299-079-a02 HT0367 Homo sapi	17.5
	427707	NM_005578	Hs.180398	LIM domain-containing preferred translocation	17.5
	437140	AA312799	Hs.283689	activator of CREM in testis	17.5
	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB10	17.5
	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor type,	17.4
15	417808	AF177909	Hs.12828	tweety (Drosophila) homolog 1	17.4
	426232	Z70024	Hs.168157	nuclear transcription factor Y, gamma	17.4
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEOB	17.4
	415307	F05232	Hs.27495	prostate cancer associated protein 7	17.3
	407049	X72632		(NONE)	17.3
20	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT2RM40	17.3
	411085	AF022991	Hs.68398	period (Drosophila) homolog 1	17.3
	443104	AA088470	Hs.83135	p53-responsive gene 6	17.2
	424106	AA412442	Hs.98132	ESTs	17.2
	446716	AA436575	Hs.16602	ESTs	17.1
25	448677	AI560769	Hs.227051	ESTs	17.0
	434919	AI821740	Hs.116531	ESTs	17.0
	401171	AA360954	Hs.27268	Homo sapiens mRNA; cDNA DKFZp564N196 (from cl	17.0
	456804	AI421645	Hs.139851	caveolin 2	17.0
	453621	AW749983		gb:QV3-BT0537-280100-070-e04 BT0537 Homo sapi	16.9
30	413419	BE093686	Hs.48938	Homo sapiens cDNA: FLJ21802 fis, clone HEP007	16.9
	426515	BE394222	Hs.231444	ESTs	16.9
	428937	T82221	Hs.56729	lymphocyte-specific protein 1	16.9
	424562	AI420859	Hs.150557	basic transcription element binding protein 1	16.9
	444655	AF088886	Hs.11590	cathepsin F	16.9
35	447424	AI681105	Hs.181641	ESTs	16.8
	425439	D38024	Hs.157425	double homeobox, 2	16.8
	446707	AI591214	Hs.156336	ESTs	16.8
	405324				16.8
	434340	AI193043	Hs.128685	ESTs	16.8
40	422942	AF054839	Hs.122540	tetraspan 2	16.8
	421820	AW662990	Hs.108675	heme-binding protein	16.8
	420037	BE299598	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapiens]	16.7
	428818	AI131291	Hs.98866	ESTs	16.7
	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-like	16.7
45	404947				16.6
	412677	AW029608	Hs.17384	ESTs	16.6
	401551				16.6
	408053	AW139474	Hs.246862	ESTs	16.6
	425016	AA376049	Hs.154162	ADP-ribosylation factor-like 2	16.6
50	418179	X51630	Hs.1145	Wilms tumor 1	16.6
	418994	AA296520	Hs.89546	Selectin E (endothelial adhesion molecule 1)	16.5
	457514	AA775208	Hs.136423	ESTs	16.5
	426275	BE151551		gb:RC0-HT0297-201199-031-f12 HT0297 Homo sapi	16.5
	457924	AL390142	Hs.288697	Homo sapiens cDNA FLJ13861 fis, clone THYRO10	16.5
55	430712	AW044647	Hs.196284	ESTs	16.5
	455144	AW875942		gb:CM1-PT0013-131299-067-b10 PT0013 Homo sapi	16.4
	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory rece	16.4
	426712	AW173177	Hs.197755	ESTs	16.4
	429954	AI918130	Hs.21374	ESTs	16.4
60	446208	BE258323	Hs.225795	ESTs, Highly similar to OTX1_HUMAN HOMEOBOX P	16.4
	442792	AI352340	Hs.131194	ESTs	16.3
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effector b	16.3
	426767	AA384398	Hs.192491	ESTs	16.3
	436950	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	16.3
65	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	16.3
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo sapi	16.3
	433457	AA830194	Hs.199417	Homo sapiens mRNA for FLJ00027 protein, parti	16.2
	402316				16.2
	409736	AA078628		gb:7P07H07 Chromosome 7 Placental cDNA Librar	16.2
70	407964	AW130334	Hs.281111	ESTs	16.2
	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN ALU SU	16.2
	425507	AI684745	Hs.165983	hypothetical C2H2 zinc finger protein FLJ2250	16.2
	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT2RM40	16.2
	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB55Y Ho	16.1
75	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-induc	16.1
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	16.1
	442208	AW296984	Hs.255595	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	16.1
	402426				16.0
	412399	N53816	Hs.14394	hypothetical protein FLJ20157	16.0
80	413200	AA127395	Hs.222414	ESTs	16.0
	404597				15.9
	453143	AA382234	Hs.170121	protein tyrosine phosphatase, receptor type,	15.9
	455984	BE177442		gb:RC1-HT0595-200400-012-f01 HT0595 Homo sapi	15.9

	416193	T25400		gb:PTHI069 HTCDL1 Homo sapiens cDNA 5'/3' sim	15.9
	407065	Y10141		gb:H.sapiens DAT1 gene, partial, VNTR	15.9
	441785	AW138139	Hs.244598	ESTs	15.9
	413784	BE165819		gb:CM0-HT0486-220300-301-d12 HT0486 Homo sapi	15.9
5	429092	AI190864	Hs.178226	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.8
	408499	AW205323	Hs.253475	ESTs	15.8
	453754	AW972580	Hs.172753	ESTs	15.8
	450826	U43030	Hs.25537	cardiotrophin 1	15.8
	428486	AW583497	Hs.184604	pancreatic polypeptide	15.7
10	405895				15.7
	409108	AA339443	Hs.48793	ESTs	15.7
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	15.6
	422948	AW810824	Hs.21351	ESTs	15.6
	447852	AW504781		gb:UI-HF-BN0-aln-c-04-0-UI.r1 NIH_MGC_50 Homo	15.6
15	419084	AA496539	Hs.179902	transporter-like protein	15.6
	456771	AW016739	Hs.232201	ESTs	15.6
	438564	AA381553	Hs.198253	major histocompatibility complex, class II, D	15.6
	448705	H05072	Hs.124984	ESTs, Moderately similar to unnamed protein p	15.6
	454460	X66945	Hs.748	fibroblast growth factor receptor 1 (fms-rela	15.5
20	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.5
	426759	AI590401	Hs.21213	ESTs	15.5
	453769	R35261	Hs.24947	ESTs	15.4
	434179	AI743448	Hs.116177	ESTs	15.4
	404111				15.4
25	402056				15.4
	458602	AI262208	Hs.276489	ESTs	15.3
	427530	AA405093	Hs.126519	ESTs	15.3
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	15.3
	400632				15.3
30	443918	AA305475	Hs.22660	Homo sapiens cDNA FLJ11658 fis, clone HEMBA10	15.3
	432037	AW450592	Hs.300459	ESTs	15.3
	412921	BE009345	Hs.128942	ESTs	15.3
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H.sapi	15.3
	441704	AI458766	Hs.201988	ESTs	15.3
35	414272	AI651603	Hs.46988	ESTs	15.3
	448224	R48700	Hs.20733	EH-domain containing 2	15.2
	404611	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	15.2
	448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp434A1010 (from c	15.2
	454719	BE006547		gb:RC2-BN0130-040400-011-b03 BN0130 Homo sapi	15.2
40	446973	H95724	Hs.4283	ESTs	15.2
	457760	AA668123	Hs.134170	ESTs	15.2
	440144	AW082297	Hs.88523	ESTs	15.2
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1, parti	15.2
	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN ALU SU	15.2
45	404244				15.1
	402959				15.1
	435487	W07343	Hs.182538	phospholipid scramblase 4	15.1
	414213	BE297765		gb:601176246F1 NIH_MGC_17 Homo sapiens cDNA c	15.0
	455916	BE156710		gb:QV0-HT0368-310300-181-d01 HT0368 Homo sapi	15.0
50	448943	AI608810	Hs.193288	ESTs	15.0
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	15.0
	454082	AF283508	Hs.63168	cell death regulator aven	14.9
	453308	AW959731	Hs.32538	ESTs	14.9
	458823	AW207574	Hs.179501	ESTs	14.9
55	452532	AI905811	Hs.110757	DNA segment on chromosome 21 (unique) 2056 ex	14.9
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	14.9
	409473	AL137716	Hs.296567	Homo sapiens mRNA; cDNA DKFZp434D2030 (from c	14.8
	449779	AA004258	Hs.25218	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU C	14.8
	457546	AA568484	Hs.153632	ESTs	14.8
60	403368				14.8
	432163	AK000440	Hs.272799	hypothetical protein FLJ20433	14.8
	421531	AA713505	Hs.291769	ESTs	14.8
	428283	AI439096	Hs.25832	Homo sapiens mRNA; cDNA DKFZp564P116 (from cl	14.8
	443528	AK001778	Hs.9547	hypothetical protein FLJ10916	14.8
65	402399				14.8
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	14.8
	450300	AL041440	Hs.58210	ESTs	14.8
	403552				14.7
	406929	U04690		gb:Human olfactory receptor (OR17-210) gene,	14.7
70	436365	AW444548	Hs.163118	ESTs	14.7
	402550				14.7
	441782	AW140126	Hs.132357	ESTs	14.7
	415672	N53097	Hs.193579	ESTs	14.7
	430582	AI215509	Hs.143964	ESTs	14.7
75	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin	14.7
	432683	AW995441	Hs.10475	ESTs	14.7
	441871	AI306150	Hs.153450	ESTs, Weakly similar to 1909123A Na glucose c	14.6
	447481	AF052151	Hs.18686	Mouse Mammary Tumor Virus Receptor homolog	14.6
	405114				14.6
80	401082				14.6
	454316	AW366144		gb:QV0-HT0101-061099-032-b12 HT0101 Homo sapi	14.6
	421572	AA531607	Hs.125143	ESTs, Weakly similar to POL2 MOUSE RETROVIRUS	14.6
	424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	14.6

	441503	AW172263	Hs.185202	ESTs	14.6
	416199	R83537		gb:yq12a08.r1 Soares fetal liver spleen 1NFLS	14.6
	420360	U83171	Hs.97203	small inducible cytokine subfamily A (Cys-Cys	14.6
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	14.5
5	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, member	14.5
	405100				14.5
	454012	M76424	Hs.37014	carbonic anhydrase VII	14.5
	402457				14.5
	454613	AW810814		gb:MR2-ST0129-201099-004-e01 ST0129 Homo sapi	14.5
10	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (from cl	14.5
	431073	BE254470	Hs.249186	cone-rod homeobox	14.5
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing leucine	14.5
	401223				14.4
	438627	AI087335	Hs.123473	ESTs	14.4
15	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.4
	437217	AW779241	Hs.155316	ESTs	14.4
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G protein	14.4
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-biphosp	14.4
	413237	AI468574	Hs.171965	ESTs	14.4
20	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,	14.4
	426488	X03350	Hs.4	alcohol dehydrogenase 2 (class I), beta polyp	14.4
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	14.4
	405479				14.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	14.3
25	426316	NM_002430	Hs.301852	Human DNA sequence from clone 437G10 on chrom	14.3
	412171	AW897452		gb:CM0-NN0058-150400-337-b08 NN0058 Homo sapi	14.3
	447241	BE382838	Hs.19322	ESTs	14.3
	402100				14.2
	438286	AW139266	Hs.134807	Homo sapiens cDNA FLJ12057 fis, clone HEMBB10	14.2
30	407947	AI500332	Hs.102367	ESTs, Weakly similar to hTcf-4 [H.sapiens]	14.2
	402275				14.2
	402358				14.2
	439624	AA838771	Hs.124407	ESTs	14.2
	444455	AI149879	Hs.175024	Homo sapiens cDNA: FLJ23447 fis, clone HSI033	14.2
35	455314	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	14.2
	427872	AA835058	Hs.21111	ESTs	14.2
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	14.2
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene homolo	14.2
	442682	AI014545	Hs.231027	EST	14.1
40	457033	AF029674	Hs.173422	KIAA1605 protein	14.1
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	14.1
	401007				14.1
	458274	AF149297	Hs.8087	NAG-5 protein	14.1
	454106	D19687	Hs.245146	ESTs	14.1
45	432928	AA570454	Hs.186467	ESTs, Moderately similar to ALU1_HUMAN ALU SU	14.1
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin/ bet	14.1
	433887	AW204232	Hs.279522	ESTs	14.1
	434927	H46612	Hs.293815	ESTs, Weakly similar to PLM_HUMAN PHOSPHOLEMM	14.1
	404282				14.1
50	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor II	14.0
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	14.0
	408107	AA806754	Hs.62835	ESTs	14.0
	401577				14.0
	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-rich p	14.0
55	408104	AW972927	Hs.293968	ESTs	14.0
	404642				14.0
	400675				14.0
	406059				14.0
	448386	AB037750	Hs.21061	KIAA1329 protein	14.0
60	407287	AI678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	14.0

TABLE 22B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
408922	109017_1	R87388 R84328 AA058916
409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309
409736	115189_1	AA078628 R09051 AA078197 AA077334 AW748808 AW748807
412171	1280759_1	AW897452 Z20302 D55805 D52877 D60432
413784	1389150_1	BE165819 BE165853 W01386
414213	1426375_1	BE297765 BE262061 BE302686 T83915
416193	1577102_1	T25400 H26834 H44554 R73193
416199	1577561_1	R83537 W80940 H27368
417998	171375_1	AW967420 AA210915 AA236991 AA210916
418464	1759038_-2	R87580
418556	1767866_-1	T02850
422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361 T06241 AA326794 AL138130 AW407975 AW999277
423780	231952_1	AA352013 AA330878 AA339379 AW966303

424585	241151_1	AA464840 AA343628
426275	263712_1	BE151551 AA373783 BE182852 BE008826 BE008827 BE008781 BE008699
427980	285225_1	AA418305 AI264351
439872	47823_1	T81058 AL357200 T70270
442197	535550_1	AW837912 AW837934 AA984475 AW997490
447852	73973_1	AW504781 BE620394
448422	762770_1	BE263813 BE253504 AI500202 BE251145
453621	974526_1	AW749983 AL045823
454316	1109350_1	AW366144 AW366154 AW366142 AW366151 AW366140 AW366155 BE141715 BE141718 BE141698
454613	1226904_1	AW810814 AW810787 AW810854 AW810773 AW810735 AW810785 AW810660 AW810834 AW810874 AW810723 AW810881 AW810791 AW810644 AW810659 AW810676
454719	1230646_1	BE006547 AW815578 AW815311 AW856304
455144	1254914_1	AW875942 AW858234 AW875938 AW875941 AW858235 AW875958
455818	137219_1	AI733747 AA129802
455904	1382290_1	BE156173 BE156305 BE156196
455916	1382748_1	BE156710 BE156726 BE156712
455984	1397288_1	BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177433

TABLE 22C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400489	8954013	Plus	131475-131652
400545	9800107	Minus	124618-124881
400625	7228177	Minus	117266-117441
400632	3818355	Plus	72875-73447,75874-76425
400637	8894326	Plus	68901-69507
400675	8118750	Plus	11223-11816
401007	8117333	Minus	140821-141050
401082	3242744	Plus	22937-23494,27677-27966
401223	8099088	Plus	148940-150214
401551	8096896	Minus	189824-190728
401577	9280797	Minus	139377-139674,141195-141281,142217-142340
401703	4826475	Plus	135-1229
402056	8084234	Plus	207002-207288
402100	8117697	Plus	133649-133792
402195	7689778	Minus	147901-148884
402275	2935596	Minus	31065-31233,33680-33771,34345-34411,38890-39125,39779-39943
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
402358	8886976	Minus	131788-132729
402399	1905915	Minus	24502-24666,24986-25102
402426	9796361	Minus	73590-73824
402457	9796782	Minus	16513-16577,16838-16926
402520	7596899	Minus	171761-171996
402550	7652009	Minus	80413-80673
402741	9212200	Minus	18603-18760,19719-19890
402865	9716300	Plus	3197-3429,3722-3914,5795-5987,6802-6961,8653-8815,9292-9660
402959	9368493	Plus	36729-37084
403121	9180223	Plus	4059-4258
403368	4388738	Plus	70286-70429,75165-75258
403552	6862638	Minus	117504-117662
403731	7543752	Minus	144000-144618
404033	8122195	Plus	7976-8156
404111	9408736	Plus	161506-161781
404244	5672609	Minus	98173-98517
404282	2276311	Plus	61503-62205
404597	9958262	Minus	114369-114599
404642	9796810	Plus	102999-103145
404654	9797010	Plus	6275-6527
404947	7382205	Plus	29740-30105,30176-30412
405100	8076846	Plus	144114-144234
405114	8096938	Minus	97013-97560
405228	7248990	Plus	92234-95905
405313	3538954	Plus	68924-69093
405324	3342751	Minus	5475-5677
405479	6453391	Plus	1668-1844
405895	7677903	Minus	66990-67484
406059	9103984	Minus	13856-14004
406150	9886026	Minus	59331-59701
406535	7711477	Plus	83135-83362

TABLE 23A: 626 genes upregulated in uterine cancer relative to normal body tissues

Table 23A lists about 626 genes upregulated in uterine cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis

was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar accession number, GenBank accession number
UniGeneID:	UniGene number
Pred.Prot.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title:	UniGene gene title
R1	95th percentile of uterine cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1

428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10;; 35.11
420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobin;; 22.80
439335; AA742697; Hs.62492; NM_052863:Homo sapiens secretoglobin, fa; none;; 21.66
425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homolog 4; none;; 21.11
421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 20.20
437938; AI950087; Hs.369628; gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien; none,none; 19.83
406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10;; 17.68
446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin;; 17.60
418281; U09550; Hs.1154; oviductal glycoprotein 1, 120kD (mucin 9; Glyco_hydro_18;TM=M;SS=M; 17.48
431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey-acidic pr; wap;TM=M;SS=Y; 16.59
400301; X03635; Hs.1657; estrogen receptor 1; F-box,hormone_rec,zf-C4,Oest_recep,adh_zinc,ketoacyl-synt,pp-binding,Acyl_transf,Thioesterase,ketoacyl-synt_C,AAA,E7,RFX_DNA_binding;TM=M;SS=N; 16.11
419356; AI656166; Hs.7331; hypothetical protein FLJ22316; Asparaginase_2,none; 15.90
433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none,PHO4; 15.39
417931; W95642; Hs.82961; trefoil factor 3 (intestinal); trefoil;; 15.39
400284; ; ; NM_000125*:Homo sapiens estrogen recepto; hormone_rec,zf-C4,Oest_recep;TM=M;SS=M; 15.23
456662; NM_002448; Hs.1494; msh (Drosophila) homeo box homolog 1 (fo; homeobox,none; 15.04
438817; AI023799; Hs.163242; ESTs; none,none; 13.72
453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none;TM=Y;SS=M; 13.67
424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2,hemopexin,Peptidase_M10;; 13.51
458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (S; HMG_box;TM=M;SS=N; 13.44
410001; AB041036; Hs.57771; kallikrein 11; trypsin;TM=M;SS=M; 13.41
421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 13.27
449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp;TM=M;SS=M; 12.76
436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 12.59
450693; AW450461; Hs.203965; ESTs; Sema,Ig,none; 12.52
415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN,sugar_tr;TM=Y;SS=M; 12.46
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;; 12.23
431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 12.09
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 12.08
407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 11.91
444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 11.86
446608; N75217; Hs.175622; ESTs; Armadillo_seg,HEAT_PBS;TM=M;SS=M; 11.72
447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022 hypotheti; none,UQ_con; 11.59
420181; AI380089; Hs.158951; ESTs; none,Ig,pkinase,LRR,LRRCT; 11.49
451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 11.45
453968; AA847843; Hs.62711; High mobility group (nonhistone chromoso; HMG_box,none; 11.42
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP;TM=M;SS=M; 11.37
421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;; 11.08
452367; U71207; Hs.29279; eyes absent (Drosophila) homolog 2; Hydrolase;; 11.01
409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 10.95
415138; C18356; Hs.295944; tissue factor pathway inhibitor 2; Kunitz_BPTI,none; 10.91
416658; U03272; Hs.79432; fibrillin 2 (congenital contractural ara; EGF,TB,granulin,PSI,EB,TIL;TM=M;SS=M; 10.81
411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 10.72
438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.66
425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 10.66
430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior ; none,none; 10.52
451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF,WIF;; 10.50
421478; AI683243; Hs.97258; ESTs, Moderately similar to S29539 ribos; none,none; 10.50
409231; AA446644; Hs.692; GA733-2 antigen; epithelial glycoprotein; thyroglobulin_1;TM=Y;SS=M; 10.35
443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS protein; HLH,PAS;TM=M;SS=N; 10.34
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 10.34
431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 10.34
415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; pkinase,Activin_recp,PDZ,ZU5,death; 10.31
411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M;SS=N; 10.24
423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin,Peptidase_M10;TM=M;SS=M; 10.24
441377; BE218239; Hs.202656; ESTs; none,none; 10.17
400292; AA250737; Hs.72472; NAME OMITTED ... receptor kinase; pkinase,Activin_recp,PDZ,ZU5,death; 10.17
452594; AU076405; Hs.29981; solute carrier family 26 (sulfate transp; xan_ur_permease,Sulfate_transp,STAS,HMG_box; 10.12
429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, ; C2,PLA2_B;TM=M;SS=N; 9.87
413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT,none; 9.87
408562; AI436323; Hs.31141; roundabout (axon guidance receptor, Dros; Ig,fn3;TM=M;SS=N; 9.86
428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3;TM=Y;SS=M; 9.72
438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 9.68
411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none,none; 9.53
450451; AW591528; Hs.202072; ESTs; none,none; 9.53
456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none,none; 9.50

418113; AI272141; Hs.83484; SRY (sex determining region Y)-box 4; HMG_box,homeobox;TM=M;SS=N; 9.38
412791; AI131192; Hs.143199; ESTs, Weakly similar to S72481 probable ; pkinase,PBD,none; 9.36
432435; BE218886; Hs.282070; ESTs; none,none; 9.35
416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); trypsin;TM=M;SS=M; 9.32
439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23
445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM;; 9.19
410407; X66839; Hs.63287; carbonic anhydrase IX; carb_anhydrase;TM=M;SS=M; 9.19
417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 9.17
453459; BE047032; Hs.257789; ESTs; none,none; 9.14
431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV_H; 9.05
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.00
413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;; 8.93
436954; AA740151; Hs.130425; ESTs; none,none; 8.91
420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 8.89
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisoIV,HATPase_c;; 8.85
407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 8.80
451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN cDNA 2810; none,none; 8.79
422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 8.72
413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO;TM=M;SS=N; 8.70
444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B,Endonuclease,Phosphodiest;TM=Y;SS=M; 8.69
421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospha; Ribosomal_L20,Na_Pi_cotrans;TM=Y;SS=N; 8.67
437935; AW939591; Hs.5940; mucin 13, epithelial transmembrane; EGF,SEA;TM=Y;SS=M; 8.56
408692; AL040127; Hs.34074; dipeptidylpeptidase VI; DPPIV_N_term,Peptidase_S9,none; 8.55
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 8.53
428187; AI687303; Hs.285529; G protein-coupled receptor 49; 7tm_1,none; 8.49
448672; AI955511; Hs.374290; ESTs; lig_chan,ANF_receptor,SBP_bac_3;TM=Y;SS=M; 8.44
425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 8.40
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 8.40
452093; AA447453; Hs.27860; Homo sapiens mRNA; cDNA DKFZp586M0723 (f; 7tm_1,none; 8.33
407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase ; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 8.23
409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 8.21
419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 8.20
424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF;; 8.20
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;SS=N; 8.00
415752; BE314524; Hs.78776; putative transmembrane protein; none;TM=Y;SS=N; 7.99
422608; AW160644; Hs.118695; potassium voltage-gated channel, subfami; ion_trans,K_tetra;TM=Y;SS=N; 7.99
433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none;; 7.95
409649; AA159216; Hs.55505; hypothetical protein FLJ20442; Y_phosphatase,DSPc;TM=M;SS=N; 7.95
424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB,none; 7.86
432179; X75208; Hs.2913; EphB3; EPH_lbd,fn3,pkinase,SAM;TM=Y;SS=M; 7.85
424581; M62062; Hs.150917; catenin (cadherin-associated protein), a; Vinculin,DNA_ligase_ZBD;TM=M;SS=N; 7.84
420610; AI683183; Hs.99348; distal-less homeo box 5; homeobox;TM=M;SS=N; 7.81
436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 7.81
411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 7.80
407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagon; TGF-beta,DAN;; 7.78
424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 BT095 Homo ; none;TM=M;SS=M; 7.65
418836; AI655499; Hs.161712; ESTs; pkinase,Activin_recp,PDZ,ZU5,death; 7.64
435793; AB037734; Hs.4993; KIAA1313 protein; none;TM=M;SS=N; 7.61
426201; AW182614; Hs.128499; ESTs; SH3,none; 7.59
447400; AK000322; Hs.18457; hypothetical protein FLJ20315; zf-C3HC4;TM=Y;SS=M; 7.55
410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.55
453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 7.54
417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase;; 7.52
437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 7.38
443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 7.36
414617; AI339520; Hs.288617; ESTs, Moderately similar to N Chain N, M; hexokinase,hexokinase2;TM=Y;SS=N; 7.35
422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2;; 7.33
424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none,none; 7.30
409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none;TM=M;SS=M; 7.28
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;; 7.28
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 7.28
418506; AA084248; Hs.372651; Unknown protein for MGC:29643 (formerly ; none,none; 7.27
448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;SS=N; 7.26
409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 7.26
424317; AI865032; Hs.26017; ESTs; none,pkinase; 7.21
410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP,GBP_C;TM=Y;SS=M; 7.21
428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.14
438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT,MBOAT;TM=Y;SS=M; 7.05
423011; NM_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm_1;TM=Y;SS=M; 7.03
435021; AA922192; Hs.73962; ESTs; EPH_lbd,pkinase,fn3,SAM,none; 7.02
446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.01
447768; X86400; Hs.19520; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=M;SS=N; 7.00
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 6.99
451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin_N;; 6.99
450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb_propeptide;; 6.95
424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 6.93
432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA S-100 pro; none,none; 6.93
436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con;TM=M;SS=N; 6.92
419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 6.92
437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 6.87
418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.87

418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 6.86
410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; Ski_Sno;TM=M;SS=M; 6.86
425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10;; 6.85
453064; R40334; Hs.89463; potassium large conductance calcium-acti; none,none; 6.83
452046; AB018345; Hs.27657; KIAA0802 protein; none;TM=M;SS=N; 6.79
417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 6.79
422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glut; aldedh,aakinase;TM=M;SS=N; 6.77
431470; AA832417; Hs.139650; ESTs; none,ig,pkinase,LRR,LRRCT; 6.76
418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none,none; 6.75
418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2,none; 6.74
417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor,none; 6.72
412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C ; MARCKS;; 6.70
437960; AI669586; Hs.369312; ESTs; none,none; 6.68
428953; AA306610; Hs.348183; tumor necrosis factor receptor superfami; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD;; 6.66
444006; BE395085; Hs.334762; type I transmembrane protein Fn14; Idl_recept_a,PKD,MHC_I;TM=M;SS=Y; 6.65
413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex;TM=Y;SS=M; 6.64
449656; AA002008; Hs.188633; ESTs; PIP5K,none; 6.64
447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-induc; pyr_redox;TM=M;SS=N; 6.62
446063; AI720140; Hs.151079; ESTs; ISK_Channel,none; 6.61
424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none,none; 6.60
421554; AW137676; Hs.97775; ESTs; none,none; 6.59
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 6.55
424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M;SS=N; 6.54
448730; AB032983; Hs.21894; KIAA1157 protein; PP2C;TM=M;SS=N; 6.54
433577; AW007080; Hs.284192; ESTs; none,none; 6.53
422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 6.53
442133; AW874138; Hs.129017; ESTs; type Ia transmembrane protein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 6.52
430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 6.52
434263; N34895; Hs.79187; ESTs; ig,none; 6.49
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 6.48
419942; U25138; Hs.93841; potassium large conductance calcium-acti; CaKB;TM=Y;SS=M; 6.47
421064; AI245432; Hs.101382; tumor necrosis factor, alpha-induced pro; none;TM=M;SS=N; 6.47
432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 6.45
431685; AW296135; Hs.267659; vav 3 oncogene; CH,DAG_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 6.44
428832; AA578229; Hs.324239; ESTs, Moderately similar to ZN91_HUMAN Z; Osteopontin,none; 6.39
436775; AA731111; Hs.372225; ESTs; none,none; 6.39
424343; AW956360; Hs.4748; adenylate cyclase activating polypeptide; 7tm_2,HRM,none; 6.37
421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen ; none;TM=Y;SS=M; 6.37
438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear transl; HLH,PAS,IL8;TM=M;SS=N; 6.37
438993; AA828995; ; gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens ; EGF,metalthio,integrin_B,PSI,none; 6.27
406400; ; ; kallikrein 8 (neuropsin/ovasin) (KLK8); trypsin;TM=M;SS=M; 6.27
429556; AW139399; Hs.314807; ESTs; none;TM=M;SS=N; 6.26
409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-like; H5AR g; Steroid_dh;TM=Y;SS=M; 6.25
435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none,none; 6.24
439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,Ioxin_2;TM=Y;SS=M; 6.24
412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF,sugar_tr,none; 6.23
436961; AW375974; Hs.156704; ESTs; none,none; 6.23
434808; AF155108; Hs.256150; NY-REN-41 antigen; none;TM=M;SS=N; 6.22
440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-li; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 6.20
416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;; 6.20
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M;SS=N; 6.19
418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 6.19
452551; L27071; Hs.29877; TXK tyrosine kinase; Beach,WD40,SH2,SH3,pkinase;TM=M;SS=N; 6.14
418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 6.12
445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 6.11
456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM,PDZ,pkinase;; 6.11
449700; L02867; Hs.78358; paraneoplastic antigen; none;TM=M;SS=N; 6.10
428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 6.10
416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA;TM=M;SS=N; 6.09
433159; AB035898; Hs.150587; kinesin-like protein 2; bZIP,kinesin;; 6.08
432432; AA541323; Hs.115831; ESTs; ig,Sema,PSI,none; 6.07
409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG;TM=M;SS=N; 6.04
412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M;SS=N; 6.03
424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 6.03
409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.00
421143; AB024536; Hs.102171; immunoglobulin superfamily containing le; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.00
428677; AI657119; Hs.351582; troponin I, cardiac; none;TM=M;SS=N; 6.00
450098; W27249; Hs.8109; hypothetical protein FLJ21080; SET,zf-MYND;TM=M;SS=N; 6.00
410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, com; C1q,Collagen;; 5.99
419972; AL041465; Hs.182982; golgin-67; none,none; 5.99
421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;; 5.97
403362; ; ; NM_001615*:Homo sapiens actin, gamma 2, ; actin;; 5.95
451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M;SS=N; 5.95
420253; AI656055; Hs.96200; neighbor of A-kinase anchoring protein 9; none;NA;NA; 5.93
421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;SS=N; 5.93
450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 5.92
450747; AI064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 5.92
415211; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPc,tsp_1,Ribosomal_S21,rvp;TM=M;SS=N; 5.91
429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin) receptor; 7tm_1;TM=Y;SS=N; 5.90
447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazaro; none;TM=Y;SS=N; 5.89
437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none;TM=Y;SS=M; 5.89
446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 5.89

453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.87
426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 5.85
425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 5.85
426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 5.84
450502; T08065; Hs.118262; ESTs; ion_trans,ion_trans; 5.84
442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 5.83
424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none;TM=M;SS=N; 5.83
448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 5.82
422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;SS=N; 5.82
445133; AW157646; Hs.198689; ESTs; efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FliD,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AtP3;TM=M;SS=N; 5.79
426215; AW963419; Hs.155223; stanniocalcin 2; Stanniocalcin;; 5.78
414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 5.75
414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 5.74
452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 5.72
432201; AI538613; Hs.298241; Transmembrane protease, serine 3; ldl_recept_a,trypsin;TM=Y;SS=M; 5.72
429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 5.72
449458; AI805078; Hs.208261; ESTs; Frizzled,Fz,none; 5.72
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 5.71
418848; AI820961; Hs.193465; ESTs; PDZ,pkinase,none; 5.70
426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 5.69
411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;SS=N; 5.69
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin;TM=M;SS=N; 5.69
445136; AI348014; Hs.143949; ESTs, Weakly similar to Achaete-Scute ho; ion_trans,ion_trans; 5.69
409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2,SH3,RhoGAP,none; 5.67
430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y;SS=N; 5.66
429638; AI916662; Hs.211577; kinectin 1 (kinesin receptor); bZIP,Tropomyosin,spectrin,LBP_BPI_CETP,B56,M;TM=Y;SS=M; 5.65
450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 5.64
453950; AA156998; Hs.348037; eukaryotic translation initiation factor; none;; 5.64
425889; M57414; Hs.161305; tachykinin receptor 2; 7tm_1;TM=Y;SS=M; 5.64
432527; AW975028; Hs.102754; ESTs; none,none; 5.64
441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 5.63
419080; AW150835; Hs.18878; hypothetical protein FLJ21620; 2OG-FeII_Oxy;TM=M;SS=N; 5.63
447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 5.61
440422; AW452696; Hs.130760; myosin phosphatase, target subunit 2; BTB,Kelch,ank,none; 5.58
431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M;SS=N; 5.58
432805; X94630; Hs.3107; CD97 antigen; 7tm_2,EGF,GPS,FecCD;TM=Y;SS=M; 5.55
449230; BE613348; Hs.356392; melanoma cell adhesion molecule; ig,isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 5.55
441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,ig;TM=M;SS=N; 5.54
400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 5.54
434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.53
404210; ; ; NM_005936:Homo sapiens myeloid/lymphoid ; FHA,PDZ,RA,DIL;TM=M;SS=N; 5.53
408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 5.53
436726; AA324975; Hs.198689; ESTs, Weakly similar to T00079 hypotheti; efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FliD,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AtP3;TM=M;SS=N; 5.53
416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 5.52
428667; AI375550; Hs.346868; nucleolar protein p40; homolog of yeast ; none,none; 5.51
433907; AW296107; Hs.152686; ESTs; Armadillo_seg,none; 5.50
442821; BE391929; Hs.8752; transmembrane protein 4; none;; 5.50
422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB;TM=Y;SS=M; 5.49
439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none,none; 5.49
428771; AB028992; Hs.193143; KIAA1069 protein; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 5.48
452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI,7tm_1,none; 5.48
442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C1; none,none; 5.48
408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 5.47
422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 5.47
420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,TUDOR,none; 5.47
428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;; 5.46
424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT_bind,STAT_prot,none; 5.45
441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia vi; pkinase,Recep_L_domain,Furin-like,YLP,none; 5.44
414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 5.43
450402; BE218027; Hs.89969; ESTs; SH3,none; 5.42
428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 5.42
430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.42
412350; AI659306; Hs.73826; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ;TM=M;SS=N; 5.42
444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 5.41
448379; AI097463; Hs.21035; KIAA1130 protein; none,Zip; 5.41
410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rrm;TM=M;SS=N; 5.41
411817; BE302900; Hs.72241; mitogen-activated protein kinase kinase ; pkinase;TM=M;SS=M; 5.40
445413; AA151342; Hs.12677; CGI-147 protein; UPF0099;TM=M;SS=M; 5.39
451863; AL120634; Hs.331803; ATPase, Ca transporting, plasma membrane; cpn60_TCP1,E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase;; 5.38
442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra,DUF51,none; 5.38
439963; AW247529; Hs.6793; platelet-activating factor acetylhydrola; PAF-AH_lb,Lipase_GDSL;TM=M;SS=N; 5.36
450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin;; 5.34
441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 5.33
408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2;TM=Y;SS=N; 5.33
435391; AA704588; Hs.58934; ESTs; PIP5K,none; 5.33
411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK;; 5.33
422170; AI791949; Hs.112432; anti-Mullerian hormone; TGF-beta;; 5.32
447350; AI375572; Hs.172634; v-erb-a avian erythroblastic leukemia vi; pkinase,Recep_L_domain,Furin-like,YLP,none; 5.32
449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase;TM=M;SS=N; 5.31
426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 5.30
430407; H23551; Hs.30974; ESTs; pkinase,PBD,none; 5.29

416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3;TM=M;SS=N; 5.27
425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,pkinase,Fz;TM=Y;SS=M; 5.27
424596; AB020639; Hs.151017; estrogen-related receptor gamma; hormone_rec,zf-C4;TM=M;SS=N; 5.27
428013; AF151020; Hs.181444; hypothetical protein; none;TM=Y;SS=M; 5.26
447384; AI377221; Hs.40528; ESTs; SH3,Sorb,none; 5.26
441824; AB007871; Hs.7977; KIAA0411 gene product; SH3,RhoGAP;TM=M;SS=N; 5.26
438493; AI130740; Hs.6241; phosphoinositide-3-kinase, regulatory su; SH2,SH3,RhoGAP;TM=M;SS=N; 5.26
428579; NM_005756; Hs.184942; G protein-coupled receptor 64; 7tm_2,GPS;TM=Y;SS=M; 5.25
414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadherin (osteob; cadherin,Cadherin_C_term;TM=Y;SS=M; 5.25
426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 5.24
427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 5.24
423685; BE350494; Hs.49753; uveal autoantigen with coiled coil domai; ank,bZIP,M,DUF164,AIP3;; 5.23
452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN,sugar_tr;TM=Y;SS=M; 5.23
427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;SS=N; 5.23
417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF;; 5.23
412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 5.23
426770; AI948618; Hs.150178; ESTs; Sulfate_transp,STAS;TM=Y;SS=N; 5.23
422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha;TM=M;SS=N; 5.22
414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 5.22
448093; AW977382; Hs.15898; 2,4-dienoyl CoA reductase 2, peroxisomal; adh_short;; 5.21
443646; AI085198; Hs.164226; Thrombospondin 1; EGF,tsp_1,vwc,TSPN,tsp_3,none; 5.18
457916; BE085271; Hs.8834; ring finger protein 3; pkinase,none; 5.18
433933; AI754389; Hs.355397; Homo sapiens clone TCCCIA00164 mRNA sequ; none;NA;NA; 5.18
436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;; 5.17
433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,arf;TM=M;SS=M; 5.17
450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_tail,EGF; 5.16
409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 no; none;TM=M;SS=N; 5.15
454438; AA224053; Hs.172405; cell division cycle 27; SPRY,7tm_3,ANF_receptor; 5.14
413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 5.14
422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial ; milo_carr;TM=M;SS=N; 5.14
415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial ; milo_carr;TM=M;SS=N; 5.14
411704; AI499220; Hs.71573; hypothetical protein FLJ10074; pkinase;TM=M;SS=N; 5.13
422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.13
454128; AL031259; Hs.367900; programmed cell death 2; zf-MYND;TM=M;SS=N; 5.13
431322; AW970622; Hs.376626; gb:EST382704 MAGE resequences, MAGK Homo; none,none; 5.13
444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 5.12
422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3,EGF;; 5.12
416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 5.11
436494; AA720997; Hs.128295; ESTs; none,CAP_GLY,HCO3_cotransp,Glyco_hydro_63,PH; 5.11
419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetas; WHEP-TRS,tRNA-synt_1b,none; 5.10
453387; AI990741; Hs.252809; ESTs; Na_Ca_Ex,none; 5.07
413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;SS=N; 5.07
456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M;SS=N; 5.07
438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate_kin,PDZ,SH3; 5.07
448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX;TM=M;SS=N; 5.06
413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap_PNP;; 5.06
407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none,Ribosomal_S13,Galactosyl_T,Zip,adh_short,zf-C3HC4; 5.06
421369; NM_005089; Hs.171909; U2 small nuclear ribonucleoprotein auxil; rrm,zf-CCCH,lectin_c,integrin_B;TM=M;SS=N; 5.06
412170; D16532; Hs.73729; very low density lipoprotein receptor; ldl_recept_a,ldl_recept_b,EGF;TM=M;SS=M; 5.06
442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 5.05
421109; L32832; Hs.101842; AT-binding transcription factor 1; HMG14_17,homeobox,zf-C2H2;TM=M;SS=M; 5.05
453880; AI803166; Hs.135121; ESTs, Weakly similar to I38022 hypotheti; HSP70,none; 5.05
431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh,ldh_C,SH3,pkinase,UBA;TM=M;SS=N; 5.05
435411; AW444619; Hs.138211; ESTs; none,pkinase; 5.04
419088; AI538323; Hs.367688; integrin, beta 8; integrin_B,none; 5.04
425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX ; Troponin,Exo_endo_phos,IQ;TM=M;SS=N; 5.04
428376; AF119665; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase;TM=M;SS=N; 5.03
413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 5.03
436415; BE265254; Hs.343258; proliferation-associated 2G4, 38kD; Peptidase_M24,Furin-like,pkinase,Recep_L_domain,efhand; 5.01
449674; AW444937; Hs.233482; ESTs; C2,PI-PLC-Y,PI-PLC-X,none; 5.01
445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,arf,TK;; 5.01
412133; U83460; Hs.104557; solute carrier family 31 (copper transpo; none;TM=Y;SS=N; 5.01
446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;; 5.00
449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT,pkinase,UCH-2,UCH-1,rrm,zf-C2H2,zf-RanBP,G-patch; 5.00
416365; U15131; Hs.79265; suppression of tumorigenicity 5; DENN,dDENN,uDENN;TM=M;SS=N; 5.00
421351; AU076667; Hs.103755; receptor-interacting serine-threonine ki; CARD,pkinase;TM=M;SS=N; 4.99
413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 4.98
442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rrm,IRK;; 4.95
441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT; none,none; 4.95
426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; 7tm_1;TM=Y;SS=M; 4.95
457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase,pkinase; 4.94
408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;SS=N; 4.94
427541; AI798983; Hs.375835; solute carrier family 35 (CMP-sialic aci; none,none; 4.94
452792; AB037765; Hs.30652; KIAA1344 protein; thiored;TM=M;SS=M; 4.93
430713; AA351647; Hs.2642; eukaryotic translation elongation factor; GTP_EFTU,GTP_EFTU_D3,GTP_EFTU_D2;; 4.93
444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 4.93
440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin (neuronal; HNH,cadherin,Cadherin_C_term;TM=M;SS=N; 4.92
421302; T34462; Hs.103291; neuritin; none;TM=M;SS=Y; 4.91
452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisi; pkinase;TM=M;SS=N; 4.91
408657; AA782601; Hs.378649; ESTs; B56,none; 4.91
439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 4.91
421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 4.90
424503; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin receptor,; integrin_A,FG-GAP;TM=Y;SS=N; 4.89

438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig,MHC_II_alpha,none; 4.89
427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 4.88
434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.88
414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig;TM=Y;SS=M; 4.88
424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; perilipin;; 4.88
410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD,helicase_C,PRK,AIP3;TM=M;SS=N; 4.87
417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage_CLC,CBS,none; 4.86
429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-; Phosphodiest,Somatomedin_B,Endonuclease,none; 4.86
417666; AI345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M;SS=N; 4.86
453864; AW021407; Hs.21068; hypothetical protein; none,none; 4.86
453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion_trans;TM=Y;SS=M; 4.85
413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo_endo_phos;; 4.85
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;; 4.85
435652; N32388; Hs.334370; uncharacterized hypothalamus protein HBE; none;TM=M;SS=N; 4.84
419355; AA428520; Hs.90061; progesterone binding protein; heme_1;TM=Y;SS=M; 4.83
431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 4.83
408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran,ABC_membrane,PRK,Bac_export_3;TM=Y;SS=N; 4.83
425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 4.82
435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 4.81
424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;SS=N; 4.81
425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.81
453354; W55946; Hs.234863; Homo sapiens cDNA FLJ12082 fis, clone HE; transmembrane4,none; 4.81
450883; NM_001348; Hs.25619; death-associated protein kinase 3; pkinase;TM=M;SS=N; 4.79
429736; AF125304; Hs.212680; tumor necrosis factor receptor superfami; TNFR_c6;TM=M;SS=M; 4.79
431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 4.79
409960; BE261944; Hs.355264; hexokinase 1; none,none; 4.78
422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1,kazal,A2M,A2M_N;TM=Y;SS=M; 4.78
423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1,7tm_2;TM=Y;SS=M; 4.78
429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4;TM=Y;SS=M; 4.78
427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M;SS=N; 4.77
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 4.76
444672; Z95636; Hs.11669; laminin, alpha 5; laminin_EGF,laminin_G,EGF,TNFR_c6,laminin_B,laminin_Nterm,metalthio,Tropomyosin,DUF164,p450;TM=M;SS=N; 4.76
407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfkB;TM=M;SS=N; 4.75
438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 4.75
410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;; 4.75
411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;; 4.75
425548; AA890023; Hs.1906; prolactin receptor; fn3;TM=Y;SS=M; 4.73
434158; T86534; Hs.14372; ESTs; adenylatekinase,none; 4.73
459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypotheti; none,SH3,myosin_head,IQ; 4.73
409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 4.73
434503; T96231; Hs.17762; ESTs; SH3,Sorb,none; 4.73
446342; BE298665; Hs.14846; solute carrier family 7 (cationic amino ; none;TM=M;SS=N; 4.72
427418; AA402587; Hs.356667; LAT1-3TM protein; none,none; 4.71
449433; AI672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-bindi; Frizzled,Fz,Frizzled,Fz; 4.71
418910; Z25821; Hs.89466; Homo sapiens, Similar to dodecenoyl-Coen; ECH;; 4.70
414907; X90725; Hs.77597; polo (Drosophia)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M;; 4.70
442199; BE277633; Hs.372542; etoposide-induced mRNA; none;TM=Y;SS=M; 4.69
418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 4.69
453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 ; none;; 4.69
418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domai; death,DED;; 4.68
434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.68
443323; BE560621; Hs.9222; estrogen receptor binding site associate; none;TM=M;SS=M; 4.68
400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor,; integrin_A,FG-GAP;TM=Y;SS=N; 4.68
418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiest;TM=Y;SS=M; 4.67
417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;; 4.67
425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 4.66
407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 4.66
450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2;; 4.66
420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530I15; none,none; 4.65
404287; ; ; FGENESH predicted novel CUB-domain conta; none,none; 4.64
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 4.63
426680; AA320160; Hs.171811; adenylate kinase 2; adenylatekinase;TM=M;SS=N; 4.63
430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 4.63
447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of ; SH3,PH;TM=M;SS=N; 4.63
414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;SS=N; 4.62
429126; AW172356; Hs.99083; ESTs; 7tm_1,none; 4.61
429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 4.60
409220; BE243323; Hs.51233; tumor necrosis factor receptor superfami; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.60
421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10_DDP,efhand,CH,spectrin,serpin;TM=M;SS=N; 4.60
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 4.59
400290; H18836; Hs.31608; hypothetical protein FLJ20041; none,Cys_knot; 4.59
430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans;TM=Y;SS=M; 4.59
409645; AI142265; Hs.55498; geranylgeranyl diphosphate synthase 1; polyprenyl_synt;TM=M;SS=N; 4.59
427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M;SS=N; 4.58
437212; AI765021; Hs.210775; ESTs; UDPGT,none; 4.58
430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;; 4.57
452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 4.56
416041; AA345547; Hs.53263; hypothetical protein FLJ13287; WD40;; 4.55
434511; R28982; Hs.18106; ESTs; pkinase,Glyco_hydro_39; 4.55
410174; AA306007; Hs.59461; DKFZP434C245 protein; none,DSPc; 4.55
418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;SS=N; 4.55
451367; AA923729; Hs.26322; cell cycle related kinase; pkinase;TM=M;SS=N; 4.54

417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 4.54
411296; BE207307; Hs.10114; growth suppressor 1; 2OG-FeII_Oxy;TM=M;SS=M; 4.53
439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like;TM=M;SS=N; 4.53
431992; NM_002742; Hs.2891; protein kinase C, mu; pkinase,DAG_PE-bind,PH;TM=M;SS=M; 4.53
443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 4.53
428005; AW302245; Hs.181390; casein kinase 1, gamma 2; pkinase;TM=M;SS=N; 4.52
407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.52
435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.51
447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HE; none,none; 4.51
405484; ; ; C3002124*:gi|12737280|ref|XP_006682.2| k; none;; 4.50
443605; H06865; Hs.134131; ESTs; efhand,ion_trans,none; 4.50
431738; AW237726; Hs.288549; hypothetical protein FLJ14710; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 4.50
422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;; 4.49
418869; AW516565; ; gb:xq01d05.x1 Soares_NHCeC_cervical_tumo; none,RasGAP,WW,IQ; 4.48
447898; AW969638; Hs.112318; 6.2 kd protein; none,none; 4.48
450607; AL050373; Hs.25213; hypothetical protein; SH3;TM=M;SS=N; 4.48
418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 4.48
424823; NM_006226; Hs.153322; phospholipase C, epsilon; C2,PH,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 4.48
426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlo; none;TM=Y;SS=N; 4.47
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Recep_L_domain,YLP,none; 4.47
435615; Y15065; Hs.4975; potassium voltage-gated channel, KQT-lik; ion_trans,KCNQ1_channel;TM=Y;SS=N; 4.47
427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6,ET,PLA2_inh;; 4.47
428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4,LIM;TM=M;SS=N; 4.46
412760; AW379030; Hs.41324; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 4.46
409093; BE243834; Hs.50441; CGI-04 protein; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M;; 4.46
434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin;; 4.46
447434; R16890; Hs.137135; ESTs; pkinase,fn3,ig,pkinase,fn3; 4.45
422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 4.45
414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;SS=N; 4.44
457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 4.44
409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC_tran,ABC_membrane;TM=M;SS=M; 4.44
408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 4.44
436823; AW749865; Hs.117077; ESTs, Weakly similar to I38022 hypotheti; aa_permeases,zf-C2H2,KRAB,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN,TFIIS;TM=M;SS=N; 4.44
450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg;TM=M;SS=N; 4.43
437915; AI637993; Hs.202312; Homo sapiens clone N11 NTera2D1 teratoca; none,none; 4.43
417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR;TM=M;SS=M; 4.43
445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 4.43
411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, ; inositol_P,ig;TM=M;SS=N; 4.43
452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.43
422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK,PH,Oxysterol_BP;; 4.42
416202; AW964492; Hs.169624; ESTs; none;TM=M;SS=N; 4.42
441518; AW161697; Hs.294150; ESTs; Y_phosphatase,DSPc,none; 4.42
441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg;TM=M;SS=N; 4.42
431429; AF072813; Hs.252831; reticulon 3; Reticulon,Fz,ig,kringle,pkinase;TM=Y;SS=N; 4.42
453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP,integrin_A,NIF; 4.41
421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.41
456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;SS=N; 4.41
419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death,ZU5;; 4.41
432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M;SS=N; 4.41
413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=N; 4.41
458097; AW341135; Hs.58104; ESTs; none,SH3,PID; 4.40
458248; BE407379; Hs.108082; ESTs, Weakly similar to T31636 hypotheti; C1q,Collagen;TM=M;SS=Y; 4.40
427681; AB018263; Hs.284232; tumor necrosis factor receptor superfami; death,TNFR_c6,PH,Xlink,RhoGEF,Metallothio_5;TM=M;SS=M; 4.40
443693; AI344782; Hs.9683; DnaJ (Hsp40) homolog, subfamily C, membe; rrm,DnaJ,TPR;TM=M;SS=N; 4.40
437162; AW005505; Hs.5464; thyroid hormone receptor coactivating pr; bromodomain;TM=M;SS=N; 4.39
453891; AB037751; Hs.301242; Homo sapiens mRNA full length insert cDN; none,none; 4.39
442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.39
427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, r; ig;TM=Y;SS=M; 4.37
445817; NM_003642; Hs.13340; histone acetyltransferase 1; none;TM=M;SS=N; 4.37
444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC,death,TNFR_c6; 4.37
408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 4.37
432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanylate_kin,none; 4.37
418283; S79895; Hs.83942; cathepsin K (pycnodysostosis); Peptidase_C1;; 4.37
445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; ig,tsp_1,ZU5,Nucleoside_tran; 4.37
417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y;SS=N; 4.36
400257; ; Hs.76366; ENSP00000000452:BAD protein (BCL-2 bindi; none;TM=M;SS=N; 4.36
431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT;; 4.36
416178; AI808527; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.36
456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 4.36
427716; L38951; Hs.180446; karyopherin (importin) beta 1; Armadillo_seg,HEAT;TM=M;SS=N; 4.35
425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding,PAH,BAH,bromodomain,PHD,SET;TM=M;SS=N; 4.35
420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms; pkinase,ig,pkinase,ig,p450,SET,PWWP; 4.35
445926; AF054284; Hs.334826; splicing factor 3b, subunit 1, 155kD; none;TM=M;SS=N; 4.35
410726; AI623859; Hs.15936; ESTs; pkinase,pro_isomerase,none; 4.35
433996; AW135357; Hs.192374; ESTs; HSP90,HATPase_c,UDG; 4.34
433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) ; none;TM=M;SS=N; 4.34
437103; AW139408; Hs.152940; ESTs; Choline_kinase,none; 4.34
410068; AI633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3;TM=M;SS=N; 4.34
427349; AA360154; Hs.177415; Finkel-Biskis-Reilly murine sarcoma viru; ubiquitin;TM=M;SS=N; 4.33
439807; AA376417; Hs.374608; hypothetical protein MGC:5244,; abhydrolase_2;TM=M;SS=M; 4.33
453308; AW959731; Hs.323099; ESTs; none,pkinase,Activin_recp; 4.33
424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OV; SAM;; 4.33

444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-S; DSPc;TM=M;SS=N; 4.33
429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,ig,none; 4.32
409121; AA902256; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR,none; 4.32
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 4.32
423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbon; HCO3_cotransp;TM=Y;SS=M; 4.29
425654; AB033022; Hs.158654; KIAA1196 protein; zf-C2H2;TM=M;SS=N; 4.29
457500; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase;TM=M;SS=N; 4.29
427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 4.29
447191; NM_014521; Hs.17667; SH3-domain binding protein 4; SH3;TM=M;SS=N; 4.29
408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc;TM=M;SS=N; 4.29
441130; AI160734; Hs.267604; Homo sapiens PNAS-129 mRNA, complete cds; BTB,Kelch,K_tetra,DSPc;TM=M;SS=N; 4.28
430057; AW450303; Hs.2534; bone morphogenetic protein receptor, typ; Activin_recp,pkinase;TM=Y;SS=M; 4.28
430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 4.28
406774; AW518383; Hs.177592; ribosomal protein, large, P1; 60s_ribosomal;; 4.28
413809; L25851; Hs.851; integrin, alpha E (antigen CD103, human ; vwa,integrin_A,FG-GAP;TM=M;SS=Y; 4.27
443960; AI093577; Hs.255416; hypothetical protein FLJ21986; TTL;TM=M;SS=N; 4.27
427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE;TM=M;SS=N; 4.27
412204; AI125507; Hs.24937; ESTs; ig,rrm,none; 4.26
439506; AI361238; Hs.41136; ESTs; MAM,pkinase,Nucleoplasmin,none; 4.26
451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene ; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.26
452488; N74921; Hs.184389; ESTs; none;TM=M;SS=N; 4.26
450973; AF012072; Hs.25732; eukaryotic translation initiation factor; W2,MA3,MIF4G;TM=M;SS=N; 4.26
452437; AA026237; Hs.181272; ESTs; efhand,ion_trans,none; 4.26
438204; AI589645; Hs.128690; ESTs; none,7tm_1; 4.25
424756; AW504557; Hs.152931; lamin B receptor; ERG4_ERG24,FKBP;TM=Y;SS=N; 4.25
430570; AI417881; Hs.292464; ESTs; 7tm_2,Fz,Frizzled,none; 4.25
445709; H02592; Hs.74280; ESTs; PDZ,none; 4.25
428134; AA421773; Hs.161008; ESTs; Armadillo_seg,none; 4.24
434149; Z43829; Hs.244624; hypothetical protein MGC5469; none;TM=M;SS=M; 4.24
425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M;SS=N; 4.24
433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;; 4.24
447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA sequence; none,pkinase; 4.24
450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig;TM=Y;SS=M; 4.23
435542; AA687376; Hs.351226; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.23
426224; BE085860; Hs.374468; karyopherin (importin) beta 2; Armadillo_seg,HEAT;TM=M;SS=N; 4.23
413284; AU077055; Hs.289107; baculoviral IAP repeat-containing 2; zf-C3HC4,CARD,BIR,death,ig;TM=M;SS=N; 4.22
421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_PI4_kinase,PI3Ka;TM=M;SS=N; 4.22
431239; AL039971; Hs.251216; hypothetical protein DKFZp434A196; SH2,ank,WH2;; 4.22
419685; W76083; Hs.134185; ESTs; none;TM=M;SS=N; 4.22
431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 4.22
425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;; 4.21
422219; AW978073; Hs.1010; regulator of mitotic spindle assembly 1; pkinase,none; 4.21
450746; D82673; Hs.278589; general transcription factor II, i; none,SH3,PX; 4.21
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 4.21
416907; W60909; ; gb:zd29g10.s1 Soares_fetal_heart_NbHH19W; ion_trans,none; 4.21
411768; NM_013371; Hs.71979; interleukin 19; IL10;; 4.21
425262; D87119; Hs.155418; GS3955 protein; pkinase;; 4.21
430035; NM_003463; Hs.227777; protein tyrosine phosphatase type IVA, m; Y_phosphatase,DSPc;TM=M;SS=N; 4.21
411789; AF245505; Hs.72157; Adlican; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 4.15
416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 4.14
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 4.13
431745; AW972448; Hs.163425; Novel FGENESH predicted cadherin repeat ; none,none; 4.10
416965; N25223; Hs.160436; MDAC1; none;NA;NA; 3.94
426890; AA393167; Hs.41294; ESTs; none,none; 3.88
442438; AA995998; Hs.370007; gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens; none,DNA_pol_B,DNA_pol_B_exo; 3.86
412314; AA825247; Hs.356084; downstream of: G protein-coupled recepto; 7tm_1;TM=Y;SS=M; 3.84
448243; AW369771; Hs.367688; integrin, beta 8; integrin_B,none; 3.64
439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 3.61
415999; AA172179; Hs.294029; ESTs; none,none; 3.60
429466; M85835; Hs.12827; ESTs; none,none; 3.45
407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 3.34
400517; ; ; lengsin; none;TM=M;SS=N; 3.17
439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.88
426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.84
414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigeni; DAN;TM=M;SS=M; 2.81
424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;; 2.70
438167; R28363; Hs.24286; chemokine binding protein 2 (CCBP2), mRN; none;TM=Y;SS=M; 2.68
418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestin; cadherin;TM=Y;SS=M; 2.17

TABLE 23B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
438993	2580163_1	AI926361 AA834879 AA828995

418869	12789_14	AA229762 AA230035
416907	1112245_1	W60909 W61051 M78905 BG959483

TABLE 23C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404287	2326514	Plus	53134-53281
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
400517	9796686	Minus	49996-50346

TABLE 24A: 571 GENES UP-REGULATED IN HEAD AND NECK TUMORS COMPARED WITH NORMAL BODY TISSUES

Table 24A lists about 571 genes up-regulated in head and neck tumors compared with normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 70th percentile of AI for head and neck cancer samples vs. the 80th percentile of the AI for normal body tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
421155	H87879	Hs.102267	lysyl oxidase	166.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	156.00
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	80.00
438274	AI918906	Hs.55080	ESTs	28.00
401486				121.00
446999	AA151520	Hs.334822	hypothetical protein MGC4485	126.00
423887	AL080207	Hs.134585	DKFZP434G232 protein	13.00
419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	98.00
428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00
420602	AF060877	Hs.99236	regulator of G-protein signalling 20	35.00
445019	AI205540	Hs.281295	ESTs	93.00
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	270.62
449722	BE280074	Hs.23960	cyclin B1	9.81
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	373.00
424086	AI351010	Hs.102267	lysyl oxidase	200.00
447078	AW885727	Hs.301570	ESTs	184.00
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	177.00
409506	NM_006153	Hs.54589	NCK adaptor protein 1	170.00
426471	M22440	Hs.170009	transforming growth factor, alpha	158.00
413268	AL039079	Hs.75256	regulator of G-protein signalling 1	155.00
419948	AB041035	Hs.93847	NADPH oxidase 4	140.00
451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	139.00
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	111.00
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	109.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	106.00
416283	NM_005429	Hs.79141	vascular endothelial growth factor C	95.00
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	92.00
449101	AA205847	Hs.23016	G protein-coupled receptor	92.00
442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	86.00
438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	85.68
414132	AI801235	Hs.48480	ESTs	85.00
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	83.00
402047	AK001921	Hs.169575	hypothetical protein MGC2550	80.00
414972	BE263782	Hs.77695	KIAA0008 gene product	74.00
452943	BE247449	Hs.31062	hypothetical protein FLJ10525	74.00
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	71.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	70.19
449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	66.25
418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	66.00
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	64.00
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14436 fis, clone HE	63.00
432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	60.00
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	58.00
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	57.00
418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	57.00
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	54.00
452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	54.00
423020	AA383092	Hs.1608	replication protein A3 (14kD)	49.00

	422426	W79117	Hs.58559	ESTs	49.00
	406747	AI925153	Hs.217493	annexin A2	46.00
	445828	F05802	Hs.81907	ESTs	46.00
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	44.00
5	452909	NM_015368	Hs.30985	pannexin 1	43.95
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	43.00
	458027	L49054	Hs.85195	myeloid leukemia factor 1	43.00
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	43.00
	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	42.00
10	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	40.00
	433859	AW896758	Hs.273789	ESTs	38.00
	426753	T89832	Hs.170278	ESTs	37.00
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	36.00
	402034				35.00
15	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	34.00
	458424	AI084049	Hs.206761	ESTs	34.00
	435159	AA668879	Hs.116649	ESTs	33.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	32.00
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	31.00
20	439128	AI949371	Hs.153089	ESTs	29.20
	420795	AA323037	Hs.128645	sorting nexin 16	26.00
	422505	AL120862	Hs.124165	ESTs	25.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	24.00
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	22.10
25	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	19.00
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	19.00
	414869	AA157291	Hs.21479	ubinuclein 1	17.37
	453049	BE537217	Hs.30343	ESTs	16.00
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	14.00
30	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	13.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	10.00
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	9.60
	414231	AI468004	Hs.278956	hypothetical protein FLJ12929	9.00
35	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	8.09
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	8.07
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.07
	417791	AW965339	Hs.111471	ESTs	8.04
	436486	AA742221	Hs.120633	ESTs	7.23
40	432731	R31178	Hs.287820	fibronectin 1	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	5.18
	435039	AW043921	Hs.130526	ESTs	5.00
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.25
	457001	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	4.24
45	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	3.74
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	3.19
	458531	AA367718	Hs.159083	ESTs	3.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.53
	411388	X72925	Hs.69752	desmocollin 1	1.00
50	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	1.00
	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	1.00
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	1.00
	449467	AW205006	Hs.197042	ESTs	1.00
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00
55	453637	NM_002589	Hs.34073	BH-protocadherin (brain-heart)	1.00
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	517.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	616.00
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	226.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	278.00
60	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	56.11
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	264.00
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	124.00
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.00
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	1.00
65	415511	AI732617	Hs.182362	ESTs	1.00
	406467				141.00
	422330	D30783	Hs.115263	epiregulin	98.00
	452461	N78223	Hs.108106	transcription factor	159.00
	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	1.00
70	413324	V00571	Hs.75294	corticotropin releasing hormone	1.00
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (	7.60
	443211	AI128388	Hs.143655	ESTs	99.00
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00
	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	3.00
75	439926	AW014875	Hs.137007	ESTs	2.79
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	94.00
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	1.22
	448062	AW295923	Hs.255472	KIAA1843 protein	1.00
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.27
80	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00
	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	89.00
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	1.00

449773	R76294	Hs.302383	ESTs	1.00
443054	AI745185	Hs.8939	yes-associated protein 65 kDa	90.00
432097	X51730	Hs.2905	progesterone receptor	1.00
453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	0.38
430184	AB013802	Hs.234790	contactin 5	1.00
432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.23
415025	AW207091	Hs.72307	ESTs	1.00
416575	W02414	Hs.38383	ESTs	1.00
443171	BE281128	Hs.9030	TONDU	0.92
424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	20.30
400844				0.60
409402	AF208234	Hs.695	cystatin B (stefin B)	1.96
412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.38
435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.60
400751				1.34
436361	AA825814	Hs.149065	ESTs	0.92
455612	BE042896	Hs.274848	ESTs	0.81
447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	1.55
404148				0.77
431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	1.00
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.47
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.92
442994	AI026718	Hs.16954	ESTs	0.40
415327	H22769		gb:ym54c02.r1 Soares infant brain 1NIB H	0.47
418624	AI734080	Hs.104211	ESTs	1.90
452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	0.54
401747			Homo sapiens keratin 17 (KRT17),	7.22
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.10
418259	AA215404	Hs.137289	ESTs	1.28
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	8.13
403381				21.00
420923	AF097021	Hs.273321	differentially expressed in hematopoieti	0.00
418216	AA662240	Hs.283099	AF15q14 protein	11.29
444649	AW207523	Hs.197628	ESTs	0.10
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	4.64
402230				1.64
412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.97
447334	AA515032	Hs.91109	ESTs	0.62
432829	W60377	Hs.57772	ESTs	0.86
418686	Z36830	Hs.87268	annexin A8	8.44
421508	NM_004833	Hs.105115	absent in melanoma 2	2.68
410553	AW016824	Hs.255527	hypothetical protein MGC14128	2.22
419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	78.00
425721	AC002115	Hs.159309	uroplakin 1A	0.86
420370	Y13645	Hs.97234	uroplakin 2	0.87
417720	AA205625	Hs.208067	ESTs	5.83
437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.07
431753	X76029	Hs.2841	neuromedin U	7.00
402075				286.00
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitb	363.00
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.81
405064				1.00
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	2.00
441233	AA972965	Hs.135568	ESTs	1.00
456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.23
414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	0.65
412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1.00
405494				1.00
407189	AA598927		gb:ae37e03.s1 Gessler Wilms tumor Homo s	1.00
403085				1.00
408633	AW963372	Hs.46677	PRO2000 protein	2.46
435257	AA677026	Hs.191217	ESTs	1.00
410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00
445182	AW189787	Hs.147474	ESTs	0.50
417275	X63578	Hs.295449	parvalbumin	1.00
418406	X73501	Hs.84905	cytokeratin 20	1.00
421110	AJ250717	Hs.1355	cathepsin E	1.00
406081				2.13
449448	D60730	Hs.57471	ESTs	123.00
451668	Z43948	Hs.326444	cartilage acidic protein 1	0.37
408243	Y00787	Hs.624	interleukin 8	3.35
436246	AW450963	Hs.119991	ESTs	51.00
440304	BE159984	Hs.125395	ESTs	1.00
402778				1.00
406117				1.00
406360				71.00
435347	AW014873	Hs.116963	ESTs	1.00
445550	AI242754	Hs.137306	ESTs	1.00
451359	H85334	Hs.336623	ESTs	1.00
419559	Y07828	Hs.91096	ring finger protein	1.00
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	58.00
425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00
402901				0.85

	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	0.87
	417715	AW969587	Hs.86366	ESTs	5.12
	442577	AA292998	Hs.163900	ESTs	2.19
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.54
5	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.11
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	1.27
	414683	S78296	Hs.76888	hypothetical protein MGC12702	0.67
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.03
	403903				0.87
10	405033				0.13
	422262	AF019225	Hs.114309	apolipoprotein L	2.13
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.59
	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.69
15	459702	AI204995			1.00
	446082	AI274139	Hs.156452	ESTs	0.60
	400843				0.76
	417409	BE272506	Hs.82109	syndecan 1	1.78
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	1.20
20	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.50
	404875				0.80
	436293	AI601188	Hs.120910	ESTs	1.40
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.03
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.94
25	404977			Insulin-like growth factor 2 (somatomedi	0.99
	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.10
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	0.85
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.20
	420876	AA918425	Hs.177744	ESTs	0.85
30	422119	AI277829	Hs.111862	KIAA0590 gene product	0.71
	400846			sortilin-related receptor, L(DLR class)	0.75
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	4.01
	430152	AB001325	Hs.234642	aquaporin 3	1.74
	402777				0.70
35	417151	AA194055	Hs.293858	ESTs	0.99
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.48
	405034	AL035754	Hs.2474	toll-like receptor 1	1.00
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	18.68
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.94
40	453134	AA032211	Hs.118493	ESTs	0.70
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.19
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	0.25
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.74
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.07
45	438315	R56795	Hs.82419	ESTs	0.65
	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	1.18
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	0.85
	444444	AI149332	Hs.14855	ESTs	0.59
	407581	R46402	Hs.173508	P3ECSL	0.82
50	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	0.92
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	0.62
	446024	AB040946	Hs.284227	KIAA1513 protein	0.92
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.42
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.68
55	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	1.57
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.08
	446009	AI989885	Hs.231926	ESTs	1.00
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	0.98
	415949	H10562	Hs.21691	ESTs	0.61
60	420281	AI623693	Hs.191533	ESTs	7.01
	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	0.72
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.21
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	0.99
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	0.54
65	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.06
	426900	AW163564	Hs.142375	ESTs	0.48
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	0.83
	402305				0.89
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.04
70	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	0.65
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	0.63
	405932				1.76
	401760				2.61
75	452240	AI591147	Hs.61232	ESTs	453.00
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.04
	421373	AA808229	Hs.167771	ESTs	17.00
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.16
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.68
80	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.19
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.73
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00
	454789	BE156314		gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1.00

434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	0.06
424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.45
418067	AI127958	Hs.83393	cystatin E/M	1.41
441801	AW242799	Hs.86366	ESTs	140.00
423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	2.45
410153	BE311926	Hs.15830	hypothetical protein FLJ12691	58.00
400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	1.17
452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	0.86
427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	0.91
451161	AA211329	Hs.26006	hypothetical protein FLJ10559	1.00
453204	R10799	Hs.191990	ESTs	1.13
437240	AA747537		gb:nx85c05.s1 NCI_CGAP_GCB1 Homo sapiens	1.00
405531				0.92
440249	AI246590	Hs.337275	ESTs	1.32
426783	Z19084	Hs.172210	MUF1 protein	1.17
434192	AW387314	Hs.34371	ESTs	1.00
407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	87.14
402001				37.00
433967	AF113018	Hs.284302	PRO1621 protein	1.00
451592	AI805416	Hs.213897	ESTs	10.00
422170	AI791949	Hs.112432	anti-Mullerian hormone	0.67
408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	1.00
452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.99
441940	AW298115	Hs.128152	ESTs	0.88
425048	H05468	Hs.164502	ESTs	0.33
444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.01
421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.06
423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.45
407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.62
410348	AW182663	Hs.95469	ESTs	1.00
419078	M93119	Hs.89584	insulinoma-associated 1	0.04
414907	X90725	Hs.77597	polo (Drosophia)-like kinase	1.04
441795	N58115	Hs.21137	AD024 protein	10.00
418583	AA604379	Hs.86211	hypothetical protein	1.22
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	106.67
413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.30
441495	AW294603	Hs.127039	ESTs	0.44
417933	X02308	Hs.82962	thymidylate synthetase	2.48
412661	N32660	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.00
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.44
430034	X60155	Hs.227767	zinc finger protein 41	1.00
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.87
454417	AI244459	Hs.110826	trinucleotide repeat containing 9	0.54
429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	2.27
417599	AA204688	Hs.136201	ESTs	1.01
438366	AA805760	Hs.303567	ESTs	1.00
438746	AI885815	Hs.184727	ESTs	1.47
409691	T89983	Hs.246042	Homo sapiens, clone MGC:5437, mRNA, comp	1.00
408827	AW275730	Hs.254825	ESTs	1.00
414735	BE468016	Hs.281904	ESTs	1.00
422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	5.21
412719	AW016610	Hs.129911	ESTs	494.00
417034	NM_006183	Hs.80962	neurotensin	1.00
430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	23.36
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.98
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	7.50
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	9.77
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	445.00
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	13.93
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	12.77
452838	U65011	Hs.30743	preferentially expressed antigen in mela	45.00
418663	AK001100	Hs.41690	desmocollin 3	10.89
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.29
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	0.88
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	38.31
421948	L42583	Hs.334309	keratin 6A	36.81
431846	BE019924	Hs.271580	uroplakin 1B	1.37
424098	AF077374	Hs.139322	small proline-rich protein 3	8.85
453964	AI961486	Hs.12744	ESTs	0.40
446856	AI814373	Hs.164175	ESTs	1.16
443648	AI085377	Hs.143610	ESTs	2.15
408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	4.39
431384	BE158000		gb:MR2-HT0377-150200-202-e03 HT0377 Homo	1.18
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.22
435505	AF200492	Hs.211238	interleukin-1 homolog 1	164.00
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	9.85
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	5.59
441020	W79283	Hs.35962	ESTs	5.76
423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.97
448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.09
444371	BE540274	Hs.239	forkhead box M1	2.44
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.39

	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.53
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	1.67
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	2.30
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.04
5	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.11
	401781				11.07
	401780				9.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	1.12
10	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	947.00
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.79
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.16
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.08
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	5.20
15	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	2.53
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	72.00
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	19.96
	409103	AF251237	Hs.112208	XAGE-1 protein	0.47
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	0.66
20	428471	X57348	Hs.184510	stratifin	3.39
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.61
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.31
	451541	BE279383	Hs.26557	plakophilin 3	1.82
	418203	X54942	Hs.83758	CDC28 protein kinase 2	5.60
25	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.78
	437016	AU076916	Hs.5398	guanine monphosphate synthetase	2.01
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.18
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.58
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.63
30	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.25
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	11.88
	430677	Z26317	Hs.94560	desmoglein 2	1.38
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.09
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.09
35	422963	M79141	Hs.13234	ESTs	2.28
	418462	BE001596	Hs.85266	integrin, beta 4	1.40
	450832	AW970602	Hs.105421	ESTs	13.31
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.25
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.89
40	458933	AI638429	Hs.24763	RAN binding protein 1	1.54
	439394	AA149250	Hs.56105	ESTs	3.89
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.77
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.52
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.11
45	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	0.61
	439606	W79123	Hs.58561	G protein-coupled receptor 87	303.00
	453884	AA355925	Hs.36232	KIAA0186 gene product	10.55
50	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.38
	451743	AW074266	Hs.23071	ESTs	2.90
	413129	AF292100	Hs.104613	RP42 homolog	2.38
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	5.92
55	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.18
	416819	U77735	Hs.80205	pim-2 oncogene	1.01
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	0.67
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.19
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.55
60	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	3.06
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.64
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	7.04
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	203.00
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33
65	430337	M36707	Hs.239600	calmodulin-like 3	1.32
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	81.00
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.03
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	28.00
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.24
70	425245	AI751768	Hs.155314	KIAA0095 gene product	1.40
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.55
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00
	418678	NM_001327	Hs.167379	cancer/testis antigen	0.82
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00
75	427335	AA448542	Hs.251677	G antigen 7B	0.91
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	6.53
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	1.35
	421917	AB028943	Hs.109445	KIAA1020 protein	0.94
	404440				38.57
80	409582	R27430	Hs.271555	ESTs	3.19
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.45
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.61
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	1.95

	408380	AF123050	Hs.44532	diubiquitin	7.23
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.35
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	0.81
	446102	AW168067	Hs.252956	ESTs	1.03
5	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	137.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.91
	423761	NM_006194	Hs.132576	paired box gene 9	36.00
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.35
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	207.00
10	440659	AF134160	Hs.7327	claudin 1	3.06
	434360	AW015415	Hs.127780	ESTs	3.89
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.28
	438898	AI819863	Hs.106243	ESTs	1.73
	441553	AA281219	Hs.121296	ESTs	1.47
15	418379	AA218940	Hs.137516	fidgetin-like 1	40.42
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	14.25
	429413	NM_014058	Hs.201877	DESC1 protein	5.17
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.95
	415380	F07953	Hs.16085	putative G-protein coupled receptor	0.18
20	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.09
	429538	BE182592	Hs.11261	small proline-rich protein 2A	6.14
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	44.00
25	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	149.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	127.00
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	20.00
	404996				147.00
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00
30	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	54.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	139.00
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR	22.00
	438702	AI879064	Hs.54618	ESTs	1.00
	444378	R41339	Hs.12569	ESTs	1.00
35	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	41.00
	407839	AA045144	Hs.161566	ESTs	7.50
	439223	AW238299	Hs.250618	UL16 binding protein 2	3.39
	409041	AB033025	Hs.50081	KIAA1199 protein	245.00
	429228	AI553633	Hs.337139	ESTs	10.89
40	409757	NM_001898	Hs.123114	cystatin SN	3.19
	411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	0.78
	436511	AA721252	Hs.291502	ESTs	0.23
	449207	AL044222	Hs.23255	nucleoporin 155kD	1.68
	453331	AI240665	Hs.8895	ESTs	5.21
45	409935	AW511413	Hs.278025	ESTs	0.75
	428969	AF120274	Hs.194689	artemin	1.17
	445443	AV653838	Hs.322971	ESTs	1.00
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	11.42
	401785				2.76
50	412723	AA648459	Hs.335951	hypothetical protein AF301222	107.00
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	2.17
	405770				2.42
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.24
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	4.50
55	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.95
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.44
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.33
	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1.11
60	427441	AA412605	Hs.178053	SPANX family, member C	5.00
	403478				0.78
	400842				0.16
	441525	AW241867	Hs.127728	ESTs	0.79
	452865	AI924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	1.50
65	405646				1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	0.79
	431413	AA504777	Hs.105293	ESTs	1.00
	401994				3.25
	402420				0.05
70	404298				0.64
	404927				88.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	0.96
	436961	AW375974	Hs.156704	ESTs	3.58
	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	0.92
75	426067	AW664691	Hs.97053	ESTs	0.97
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	0.66
	426897	AW976570	Hs.97387	ESTs	1.29
	443892	AI889572	Hs.134791	ESTs	1.00
	413223	AI732182	Hs.191866	ESTs	0.79
80	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.51
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	2.59
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.39
	420758	AW297536	Hs.33053	ESTs	0.89

423816	AL031985	Hs.133034	hypothetical protein	1.00
447534	AW953935	Hs.30837	ESTs	1.88
451919	W05086	Hs.114256	ESTs, Weakly similar to I78885 serine/th	0.11
409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell	0.92
403715				0.89
428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00
425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	37.00
436839	AA767346	Hs.291614	ESTs	1.00
413582	AW295647	Hs.71331	hypothetical protein MGC5350	59.00
413573	AI733859	Hs.149089	ESTs	78.00
430686	NM_001942	Hs.2633	desmoglein 1	127.08
438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	1.00
448243	AW369771	Hs.52620	integrin, beta 8	133.00
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	232.00
426427	M86699	Hs.169840	TTK protein kinase	66.00
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	148.00
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	40.75
453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.00
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	106.00
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	159.00
415989	AI267700	Hs.317584	ESTs	196.00
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	32.44
453160	AI263307	Hs.239884	H2B histone family, member L	7.00
409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.13
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	45.00

TABLE 24B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accessions: Genbank accession numbers

Pkey	CAT number	Accessions
411880	1263110_1	AW872477 BE088101 T05990
412296	1288043_1	AW936233 AW936272
413804	1390710_1	T64682 BE168190 BE168256
414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
415327	1534137_1	H22769 R35182 Z43545 F05783 N92089 H71928
427260	276598_1	AA663848 AA400100 AA401424
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
431384	33264_1	BE158000 BE157999 H75671 H70965 C18895 BE386512 BE385815 BE390298 AI341995 BE074534 AA055592 AA132265 AI733757 AA134504 BE145037 AA055887 BE070191 R66492 AW858018 AW858058 AW817057 AW862031 AW861688 AW862029 AW858805 AW858792 AW862028 AW858017 AW819164 AW853698 AI522161 AW854789 AW817408 BE152005 AI732411 AA133084
432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
437214	434730_1	BE092336 BE092259 BE092497 BE092051 AA746882 AI336378
437240	435139_1	AA747537 BE089068 BE089070
438993	467651_1	AA828995 AA834879 AI926361
439780	47673_1	AL109688 R23665 R26578
444163	593658_1	AI126098 AI184746 AI148521
451844	888230_1	T61430 AI820546 AI821336
453823	982526_1	AL137967 BE064160 BE064186
454789	1234742_1	BE156314 BE156316 AW820750
456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 24C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400751	7331445	Minus	35395-35533
400842	1927148	Plus	90462-90673
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400846	9188605	Plus	39310-39474
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402001	9501818	Plus	68052-68223

402034	7684482	Minus	86227-86451
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
402305	7328724	Plus	40832-41362
402420	9796339	Plus	129750-129919
402777	9588235	Plus	126786-126948
402778	9588235	Plus	128560-128702
402901	8894222	Minus	175426-175667
403085	8954241	Plus	165035-165334,165420-165713
403381	9438267	Minus	26009-26178
403478	9958258	Plus	116458-116564
403715	7239669	Plus	85128-85292
403903	7710671	Minus	101165-102597
404148	9863703	Plus	78218-78418,79571-79709
404298	9944263	Minus	73591-73723
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
404927	7342002	Plus	68690-69563
404977	3738341	Minus	43081-43229
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405033	7107731	Minus	142358-142546
405064	7658416	Plus	81207-81416
405494	8050952	Minus	70284-70518
405531	9665194	Plus	35602-35803
405646	4914350	Plus	741-969
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713
406081	9123861	Minus	38115-38691
406117	9142932	Plus	54304-54584
406360	9256107	Minus	7513-7673
406467	9795551	Plus	182212-182958

TABLE 25A: 691 genes upregulated in head and neck cancer relative to normal body tissues

Table 25A lists about 691 genes upregulated in head and neck cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar accession number, GenBank accession number
UniGeneID:	UniGene number
Pred.Prot.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title:	UniGene gene title
R1	85th percentile of head and neck cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1

422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; efhand,S_100;TM=M;SS=N; 46.25
408522; AI541214; Hs.46320; Small proline-rich protein SPRK [human, ; none,Cornifin; 40.37
417366; BE185289; Hs.1076; small proline-rich protein 1B (cornifin); Cornifin;TM=M;SS=N; 38.94
401781; ; ; Target Exon; filament;TM=M;SS=N; 29.74
422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.54
401760; ; ; NM_005557*:Homo sapiens keratin 16 (foca; filament,filament; 28.58
424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 28.55
421948; L42583; Hs.334309; keratin 6A; filament,RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 25.74
428471; X57348; Hs.184510; stratifin; 14-3-3;TM=M;SS=N; 23.65
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;; 21.02
421574; AJ000152; Hs.105924; defensin, beta 2; Defensin_beta;TM=M;SS=M; 20.83
409601; AF237621; Hs.80628; keratin 1 (epidermolytic hyperkeratosis); filament,bZIP,UvrD-helicase,TBCA;TM=M;SS=N; 20.72
433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recp;TM=M;SS=Y; 19.63
446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 19.53
420783; AI659838; Hs.99923; lectin, galactoside-binding, soluble, 7 ; Gal-bind_lectin;TM=M;SS=N; 19.12
407788; BE514982; Hs.38991; S100 calcium-binding protein A2; efhand,S_100,S_100,efhand; 17.93
416091; AF295370; Hs.283082; defensin, beta 3; Defensin_beta;TM=M;SS=M; 17.63
431211; M86849; Hs.323733; gap junction protein, beta 2, 26kD (conn; connexin;TM=Y;SS=M; 16.94
429259; AA420450; Hs.380088; Plakophilin; none,none; 14.92
417515; L24203; Hs.82237; ataxia-telangiectasia group D-associated; zf-B_box,zf-UBR1;TM=M;SS=N; 14.75
423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none;TM=M;SS=M; 14.45
418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase_M10,Astacin,PG_binding_1;; 13.02
409632; W74001; Hs.55279; serine (or cysteine) proteinase inhibito; serpin;; 12.82
406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 12.81
431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin_C_term;TM=Y;SS=M; 12.45
446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8;; 11.71
401760; ; ; Target Exon; none,bromodomain; 11.68
407839; AA045144; Hs.161566; ESTs; cadherin,cadherin; 11.65
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh;; 11.56
444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6,lactamase_B; 11.31

453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none;TM=Y;SS=M; 11.03
424012; AW368377; Hs.137569; tumor protein 63 kDa with strong homolog; SAM,P53;TM=M;SS=N; 10.75
430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;SS=N; 10.58
419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 10.30
411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M;SS=N; 10.25
441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none;TM=M;SS=M; 9.84
446989; AK001898; Hs.16740; hypothetical protein FLJ11036; none;TM=Y;SS=N; 9.74
402075; ; ; ENSP00000251056*:Plasma membrane calcium; none;; 9.50
444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 9.50
431009; BE149762; Hs.48956; gap junction protein, beta 6 (connexin 3; connexin;TM=Y;SS=M; 9.48
439310; AF086120; Hs.102793; ESTs; casein_kappa,pkinase,ig,none; 9.43
414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;SS=N; 9.33
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.14
408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FliD,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M;SS=N; 9.12
451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M;SS=N; 9.11
425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin;TM=M;SS=M; 8.66
452240; AI591147; Hs.61232; ESTs; none,none; 8.57
429228; AI553633; Hs.356828; ESTs; none,none; 8.46
400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin,Peptidase_M10,Astacin;; 8.44
425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 8.15
407242; M18728; ; gb:Human nonspecific crossreacting antig; ig;TM=M;SS=M; 8.05
407944; R34008; Hs.239727; desmocollin 2; cadherin,Cadherin_C_term,Hanta_G2;TM=Y;SS=M; 7.90
413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;; 7.82
428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10;; 7.82
417308; H60720; Hs.81892; KIAA0101 gene product; none;TM=M;SS=N; 7.77
413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD), kalinin; laminin_EGF,laminin_Nterm;; 7.76
423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz_BPTI,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 7.71
430686; NM_001942; Hs.2633; desmoglein 1; cadherin,Cadherin_C_term;TM=Y;SS=M; 7.69
412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;SS=N; 7.54
428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 7.53
418663; AK001100; Hs.41690; desmocollin 3; cadherin,Cadherin_C_term,none; 7.30
452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide,TGF-beta,none; 7.28
429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin;TM=Y;SS=M; 7.26
412719; AW016610; Hs.816; ESTs; none,none; 7.17
446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin;; 7.10
423961; D13666; Hs.136348; periostin (OSF-2os); Fasciclin;TM=M;SS=M; 7.09
427666; AI791495; Hs.180142; calmodulin-like skin protein (CLSP); efhand;TM=M;SS=N; 7.08
431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 7.06
423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin,Peptidase_M10;TM=M;SS=M; 7.03
401747; ; ; Homo sapiens keratin 17 (KRT17); none,bromodomain; 7.01
413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT,none; 6.98
429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M;SS=N; 6.96
432239; X81334; Hs.2936; matrix metalloproteinase 13 (collagenase; hemopexin,Peptidase_M10;; 6.87
417715; AW969587; Hs.86366; ESTs; none,none; 6.72
422440; NM_004812; Hs.116724; aldo-keto reductase family 1, member B10; aldo_ket_red,ROK;TM=M;SS=N; 6.50
429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin,Peptidase_M10;TM=M;SS=M; 6.39
418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M;SS=N; 6.38
420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B, ; Sulfotransfer;; 6.38
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisoIV,HATPase_c;; 6.35
442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 6.30
409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin_B,laminin_EGF;; 6.28
424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin-; ras;TM=M;SS=N; 6.27
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 6.23
424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2,hemopexin,Peptidase_M10;; 6.22
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 6.21
428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3;TM=Y;SS=M; 6.12
423017; AW176761; Hs.227948; serine (or cysteine) proteinase inhibito; serpin;; 6.08
424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none,none; 6.08
426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 6.04
439335; AA742697; Hs.62492; NM_052863:Homo sapiens secretoglobin, fa; none;; 5.81
439223; AW238299; Hs.250618; UL16 binding protein 2; Idl_recept_a,PKD,MHC_I;TM=M;SS=Y; 5.77
418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 5.72
454098; W27953; Hs.217493; Plakophilin; none,none; 5.71
417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevi; WD40;TM=M;SS=N; 5.70
435505; AF200492; Hs.211238; interleukin-1 homolog 1; IL1;TM=M;SS=N; 5.69
406685; M18728; ; gb:Human nonspecific crossreacting antig; ig;TM=M;SS=M; 5.67
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 5.63
430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 5.61
449722; BE280074; Hs.23960; cyclin B1; cyclin,cyclin_C;TM=M;SS=N; 5.61
439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 5.60
452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like and metallo; Pep_M12B_propep,tsp_1,Reprolysin,none; 5.58
433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,arf;TM=M;SS=M; 5.57
411296; BE207307; Hs.10114; growth suppressor 1; 2OG-FeII_Oxy;TM=M;SS=M; 5.55
433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carbOpept,Propep_M14;; 5.54
416819; U77735; Hs.80205; pim-2 oncogene; pkinase;; 5.48
428368; BE440042; Hs.83326; matrix metalloproteinase 3 (stromelysin ; hemopexin,Peptidase_M10,Astacin;; 5.47
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 5.46
444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 5.42
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;; 5.35
445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 5.28
418462; BE001596; Hs.85266; integrin, beta 4; fn3,integrin_B,Calx-beta,EGF;TM=M;SS=M; 5.26

429554; NM_012275; Hs.207224; interleukin 1, delta; IL1;TM=M;SS=N; 5.14
421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M;SS=N; 5.13
439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none;TM=M;SS=N; 5.11
427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosophila, mous; NHL;TM=M;SS=N; 5.11
426227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 5.08
436396; AI683487; Hs.152213; wingless-type MMTV integration site fami; wnt,none; 5.07
406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig;TM=M;SS=M; 5.05
453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M;SS=N; 5.04
414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibito; serpin;; 5.00
413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 4.96
421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;SS=N; 4.93
412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkines; kinesin,Tropomyosin;TM=M;SS=N; 4.92
445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM;; 4.91
428953; AA306610; Hs.348183; tumor necrosis factor receptor superfami; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD;; 4.90
436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 4.89
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 4.84
430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 4.81
439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH; none,none; 4.80
444371; BE540274; Hs.239; forkhead box M1; Fork_head;TM=M;SS=N; 4.75
428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 4.74
419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc;; 4.69
431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 4.69
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,ig; 4.68
418067; AI127958; Hs.83393; cystatin E/M; cystatin;; 4.66
414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;; 4.64
456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM,PDZ,pkinase;; 4.62
410418; D31382; Hs.63325; transmembrane protease, serine 4; ldl_recept_a,trypsin;TM=Y;SS=M; 4.60
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;; 4.60
438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 4.60
418140; BE613836; Hs.83551; microfibrillar-associated protein 2; none;TM=M;SS=M; 4.57
408380; AF123050; Hs.44532; diubiquitin; ubiquitin;TM=M;SS=N; 4.55
422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.50
425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10;; 4.50
418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domai; death,DED;; 4.49
408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 4.48
414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPc,tsp_1,Ribosomal_S21,rvp;TM=M;SS=N; 4.47
416178; AI808527; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.47
411789; AF245505; Hs.72157; Adlican; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 4.47
414561; AI064813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans;TM=Y;SS=N; 4.47
422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 4.45
427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6,ET,PLA2_inh;; 4.43
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 4.42
409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none;TM=M;SS=M; 4.41
406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gen; none,none; 4.40
450701; H39960; Hs.288467; hypothetical protein XP_098151 (leucine-; none,LRRCT,LRR; 4.40
409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;SS=N; 4.38
429500; X78565; Hs.289114; hexabrachion (tenascin C, cytotactin); EGF,fn3,fibrinogen_C,toxin_2,Keratin_B2;TM=M;SS=Y; 4.38
448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 4.32
423725; AJ403108; Hs.132127; hypothetical protein LOC57822; none;TM=M;SS=N; 4.32
411573; AB029000; Hs.70823; KIAA1077 protein; Sulfatase;TM=M;SS=N; 4.31
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;SS=N; 4.31
418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none,none; 4.30
437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 4.29
424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD_Synth,ldh,ldh_C,pkinase;; 4.29
414621; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig;TM=Y;SS=M; 4.29
404996; ; ; Target Exon; Peptidase_C1;TM=M;SS=M; 4.29
416539; Y07909; Hs.79368; epithelial membrane protein 1; PMP22_Claudin,oxidored_q5_N;TM=Y;SS=M; 4.28
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 4.25
421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT;TM=M;SS=N; 4.25
424503; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin receptor,; integrin_A,FG-GAP;TM=Y;SS=N; 4.24
414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 4.24
439720; AI935202; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 4.23
437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none;TM=M;SS=M; 4.23
409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb_propeptide,Tub;; 4.20
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 4.20
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 4.19
407137; T97307; ; gb:ye53h05.s1 Soares fetal liver spleen ; GDA1_CD39,none; 4.18
419235; AW470411; Hs.288433; neurotrimin; none,none; 4.18
410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 4.18
456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M;SS=N; 4.17
448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked mol; NUDIX;TM=M;SS=M; 4.17
400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor,; integrin_A,FG-GAP;TM=Y;SS=N; 4.14
409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 4.13
445417; AK001058; Hs.12680; a disintegrin-like and metalloprotease w; fsp_1,Reprolysin,Pep_M12B_propep,none; 4.12
433895; AI287912; Hs.3628; mitogen-activated protein kinase kinase ; pkinase,zf-C4,CNH,ERM;TM=M;SS=N; 4.12
424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;SS=N; 4.09
419121; AA374372; Hs.89626; parathyroid hormone-like hormone; none,none; 4.08
416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,vwc,TSPN;; 4.07
424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 4.07
427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;SS=N; 4.06
427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M;SS=N; 4.03
439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig),; Sema,PSI,integrin_B;TM=Y;SS=N; 4.02

414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 4.02
413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=M; 4.01
418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 4.01
406906; Z25424; ; gb:H.sapiens protein-serine/threonine ki; none,none; 3.98
450375; AA009647; Hs.352537; a disintegrin and metalloproteinase doma; Reprolysin,Pep_M12B_propep,disintegrin,Reprolysin,Pep_M12B_propep,disintegrin; 3.98
410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;; 3.96
410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM;TM=Y;SS=M; 3.95
425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase,pkinase_C;TM=M;SS=M; 3.95
417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 3.95
427792; M63928; Hs.180841; tumor necrosis factor receptor superfami; SRP14,TNFR_c6;; 3.93
407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 3.91
424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF;; 3.91
415989; AI267700; Hs.351201; ESTs; none,none; 3.90
423189; M59371; Hs.171596; EphA2; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 3.90
443859; NM_013409; Hs.9914; follistatin; kazal;; 3.89
429612; AF062649; Hs.252587; pituitary tumor-transforming 1; none;; 3.89
419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death,ZU5;; 3.88
450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig;TM=Y;SS=M; 3.88
428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 3.86
413441; AI929374; Hs.75367; Src-like-adapter; SH2,SH3;TM=M;SS=N; 3.84
437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 ; TIMP,pkinase,DAG_PE-bind,RBD; 3.83
436291; BE568452; Hs.344037; protein regulator of cytokinesis 1; none;TM=M;SS=N; 3.82
417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD;TM=Y;SS=M; 3.81
427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis, clone KA; none,pkinase; 3.80
431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 3.80
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2,none; 3.80
430378; Z29572; Hs.2556; tumor necrosis factor receptor superfami; IL2;; 3.79
428157; AI738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 3.78
409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase_C,CARD;TM=M;SS=N; 3.78
417720; AA205625; Hs.208067; ESTs; none,none; 3.77
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Recep_L_domain,YLP,none; 3.77
449029; N28989; Hs.22891; solute carrier family 7 (cationic amino ; aa_permeases;TM=Y;SS=M; 3.76
413436; AF238083; Hs.68061; sphingosine kinase 1; DAGKc;TM=M;SS=N; 3.75
416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; ig,ITAM,Zn_clus;TM=Y;SS=M; 3.74
413281; AA861271; Hs.222024; transcription factor BMAL2; HLH,PAS;; 3.74
436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con;TM=M;SS=N; 3.74
431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subuni; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 3.74
424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; perilipin;; 3.73
426471; M22440; Hs.170009; transforming growth factor, alpha; EGF;TM=M;SS=M; 3.72
422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; EGF,vwd,AMOP;; 3.72
450125; AA005418; Hs.158186; ESTs; CIDE-N,7tm_1,none; 3.71
427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, r; ig;TM=Y;SS=M; 3.70
444006; BE395085; Hs.334762; type I transmembrane protein Fn14; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 3.70
422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 3.70
418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 3.69
415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 3.68
443759; BE390832; Hs.134729; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 3.68
452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp,STAS;; 3.68
439625; AF086453; Hs.58611; ESTs; Fork_head,glycolytic_enzy,Na_sulph_symp; 3.66
426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 3.66
452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q,Collagen;; 3.65
447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (; SH3,PH,RhoGEF;TM=M;SS=N; 3.64
418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 3.64
438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT,MBOAT;TM=Y;SS=M; 3.64
422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetase-like; ubiquitin;; 3.63
449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN cDNA 5730; none;TM=M;SS=N; 3.62
438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate_kin,PDZ,SH3; 3.62
446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 3.62
452696; AI826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate_kin,PDZ,SH3; 3.60
407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc; Galactosyl_T;TM=M;SS=Y; 3.59
423575; C18863; Hs.163443; intron of periostin (OSF-2os); Fasciclin,none; 3.59
421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig,none; 3.58
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 3.58
419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (; SH3,PH,RhoGEF;TM=M;SS=N; 3.58
431457; NM_012211; Hs.256297; integrin, alpha 11; FG-GAP,vwa;TM=Y;SS=M; 3.57
430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans;TM=Y;SS=M; 3.55
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 3.55
441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E coli Re; none;; 3.53
426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;SS=N; 3.53
429556; AW139399; Hs.314807; ESTs; none;TM=M;SS=N; 3.52
449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 3.52
432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 3.51
433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 3.51
452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 3.49
425566; AW162943; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 3.48
402447; ; ; C1000201:gi|204416|gb|AAA02627.1| (L0519; none;TM=Y;SS=M; 3.48
431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 3.48
448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptc; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 3.48
415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 3.48
425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX ; Troponin,Exo_endo_phos,IQ;TM=M;SS=N; 3.47
424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 3.44
446051; BE048061; Hs.37054; ephrin-A3; Ephrin,A_deamin,dsrm,z-alpha; 3.43
418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Reprolysin,Pep_M12B_propep,EGF;TM=Y;SS=M; 3.42

417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;; 3.42
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin;TM=M;SS=N; 3.42
430044; AA464510; Hs.152812; ESTs; none,none; 3.42
425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;; 3.39
425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 3.39
428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino a; eIF6,SDF;TM=M;SS=N; 3.39
443648; AI085377; Hs.143610; ESTs; Fork_head,none; 3.39
418869; AW516565; ; gb:xq01d05.x1 Scares_NHCeC_cervical_tumo; none,RasGAP,WW,IQ; 3.38
432179; X75208; Hs.2913; EphB3; EPH_lbd,fn3,pkinase,SAM;TM=Y;SS=M; 3.38
418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 3.38
414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 3.37
408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, ; UvrD-helicase,RNB,Runt;TM=M;SS=N; 3.37
457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 3.37
422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 3.37
421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 3.36
400298; AA032279; Hs.61635; six transmembrane epithelial antigen of ; none;TM=Y;SS=N; 3.35
428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;; 3.33
400261; ; Hs.1802; Eos Control; ig,MHC_II_beta;TM=Y;SS=M; 3.33
410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3;TM=M;SS=N; 3.32
412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin_c; 3.32
416065; BE267931; Hs.78996; proliferating cell nuclear antigen; PCNA,PCNA_C;TM=M;SS=N; 3.31
426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 3.31
426840; BE244217; Hs.172690; diacylglycerol kinase, alpha (80kD); efhand,DAG_PE-bind,DAGKa,DAGKc,DC1;TM=M;SS=N; 3.31
434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M;SS=N; 3.31
418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;SS=N; 3.31
424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 3.31
423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT;TM=M;SS=N; 3.30
421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig,pkinase;TM=Y;SS=M; 3.30
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M;SS=N; 3.28
423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 3.28
426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2;TM=M;SS=N; 3.28
435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 3.27
431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;SS=N; 3.27
430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 3.27
425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_PI4_kinase,FAT,FATC;TM=M;SS=N; 3.26
446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 3.26
444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 3.25
422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 3.25
405932; ; ; C15000305:gi|3806122|gb|AAC69198.1| (AF0; ras;TM=M;SS=N; 3.25
400205; ; Hs.81848; NM_006265*:Homo sapiens RAD21 (S. pombe); DUF173;; 3.25
432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 3.24
412942; AL120344; Hs.75074; mitogen-activated protein kinase-activat; pkinase;TM=M;SS=N; 3.23
435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig;TM=M;SS=M; 3.22
439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 3.22
410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 3.22
427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 3.22
436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.22
428698; AA852773; Hs.334838; KIAA1866 protein; none;NA;NA; 3.22
448388; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;SS=N; 3.22
415149; X12451; Hs.78056; cathepsin L; Peptidase_C1;; 3.21
423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M;SS=N; 3.21
424618; L29472; Hs.1802; major histocompatibility complex, class ; ig,MHC_II_beta;TM=Y;SS=M; 3.20
438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig,MHC_II_alpha,none; 3.20
456181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9;TM=M;SS=N; 3.20
418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH;TM=M;SS=N; 3.19
440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP;TM=M;SS=N; 3.18
415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073;; 3.16
419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;; 3.16
450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin,ldl_recept_a,none; 3.16
426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 3.15
412939; AW411491; Hs.75069; eukaryotic translation elongation factor; none,none; 3.15
433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;; 3.15
410668; BE379794; Hs.159651; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 3.15
431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 3.15
432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface ; none;TM=M;SS=M; 3.15
407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 3.14
408634; AW407254; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none,none; 3.14
423061; AI290473; Hs.44807; ESTs; integrin_B,Sema,PSI,TIG,none; 3.14
438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ;; 3.13
431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 3.13
425394; AA356730; Hs.323949; kangai 1 (suppression of tumorigenicity ; transmembrane4,none; 3.13
429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIB (25-hy; p450;; 3.13
449230; BE613348; Hs.356392; melanoma cell adhesion molecule; ig,isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 3.13
429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4;TM=Y;SS=M; 3.12
419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;SS=N; 3.12
417386; AL037228; Hs.301957; D123 gene product; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 3.11
419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR_ITPR,RyR,MIR;TM=Y;SS=N; 3.11
440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-li; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 3.10
406467; ; ; Target Exon; efhand,Acyltransferase,none; 3.10
422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell transformi; BRCT,RhoGEF;TM=M;SS=N; 3.10
417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 3.09
437016; AU076916; Hs.5398; guanine monphosphate synthetase; PHD,SET,zf-CXXC,EGF,ank,notch,WW,FCH,GATase,GMP_synt_C,Occludin,YEATS,metalthio,EB,heme_1,RCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT;TM=M;SS=N; 3.09

441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 3.09
416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 3.09
416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 3.09
426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 3.08
414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 3.08
402233; ; ; NM_030760*:Homo sapiens endothelial diff; 7tm_1;TM=Y;SS=M; 3.07
430066; AI929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR_synt; 3.07
425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 3.06
434263; N34895; Hs.79187; ESTs; Ig,none; 3.06
443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding prc; none;TM=M;SS=Y; 3.05
409378; U42387; Hs.54426; pancreatic polypeptide receptor 1; 7tm_1;TM=Y;SS=M; 3.05
410165; BE560228; Hs.71869; apoptosis-associated speck-like protein ; PAAD_DAPIN,CARD;TM=M;SS=N; 3.05
440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; fn3;; 3.05
449003; X76342; Hs.389; alcohol dehydrogenase 7 (class IV), mu o; adh_zinc;TM=M;SS=N; 3.05
420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank;; 3.05
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2;; 3.05
421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 3.04
415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;SS=N; 3.03
425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M;SS=N; 3.03
449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp;TM=M;SS=M; 3.03
413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 3.02
442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra,DUF51,none; 3.02
436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 3.02
446269; AW263155; Hs.14559; hypothetical protein FLJ10540; none;TM=M;SS=N; 3.02
418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 3.01
421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 3.00
421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 3.00
409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF;; 2.99
429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator,none; 2.99
430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 2.98
418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 2.97
410026; AI912061; Hs.55016; hypothetical protein FLJ21935; none,none; 2.97
448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitte; SNF;TM=Y;SS=N; 2.97
432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2;TM=M;SS=N; 2.97
453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (; none,none; 2.97
427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 2.97
431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep_L_domain,none; 2.96
441389; AF134838; Hs.7835; endocytic receptor (macrophage mannose r; fn2,lectin_c;TM=Y;SS=M; 2.95
412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF,sugar_tr,none; 2.94
427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1,none; 2.94
402558; ; ; C1000201:gi|204416|gb|AAA02627.1| (L0519; none;TM=Y;SS=M; 2.94
425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death,TNFR_c6;TM=Y;SS=M; 2.94
442080; AW444761; Hs.72901; ESTs; ank;; 2.94
450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 2.93
444809; BE207568; Hs.208219; oculospanin; transmembrane4;TM=Y;SS=N; 2.93
449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 2.93
416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 2.93
453768; BE382670; Hs.198511; Homo sapiens mRNA; cDNA DKFZp761I177 (fr; arf,G-alpha,none; 2.92
414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 2.92
421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-li; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 2.92
434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 2.91
451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 2.91
422127; AW504286; Hs.112049; SET binding factor 1; dDENN,DENN,GRAM,PH;; 2.91
419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 2.90
430451; AA836472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase;; 2.90
424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibito; serpin;TM=M;SS=N; 2.89
414907; X90725; Hs.77597; polo (Drosophia)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M;; 2.89
429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 2.89
413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone H; none,none; 2.89
417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3,pkinase;TM=M;SS=N; 2.89
422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 2.89
405556; ; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;SS=N; 2.89
423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 2.89
425262; D87119; Hs.155418; GS3955 protein; pkinase;; 2.88
422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK,PH,Oxysterol_BP;; 2.88
452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 2.88
414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 2.87
444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 2.86
413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 2.86
458039; AA835884; Hs.130685; leukotriene b4 receptor (chemokine recep; CIDE-N,none; 2.86
434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f; DSPc,none; 2.86
425802; Y14838; ; chemokine-like receptor 1; 7tm_1,none; 2.86
403112; ; ; Target Exon; efhand,C2,PH,PI-PLC-Y,PI-PLC-X;; 2.86
435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=N; 2.85
442117; AW664964; Hs.128899; ESTs; hypothetical protein for IMAGE:447; none,none; 2.84
457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none,none; 2.84
456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 2.83
408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none,none; 2.83
446947; AF146747; Hs.232165; polycythemia rubra vera 1; cell surface ; none;TM=M;SS=M; 2.83
448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 2.82
427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head,IQ,zf-MYND;TM=M:SS=M; 2.82
407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC;TM=Y;SS=M; 2.82

459707; AA631362; Hs.120866; gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens; 7tm_1,none; 2.82
422699; BE410590; Hs.119257; ems1 sequence (mammary tumor and squamou; SH3,HS1_rep;TM=M;SS=N; 2.82
438108; AI471795; Hs.287776; vanilloid receptor-related osmotically a; ank,ion_trans;TM=Y;SS=N; 2.82
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 2.82
448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.81
423598; BE247600; Hs.377968; ESTs; 7tm_1;TM=Y;SS=M; 2.81
412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPc;; 2.81
414198; AW505308; Hs.75812; phosphoenolpyruvate carboxykinase 2 (mit; PEPCK;; 2.81
436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 2.81
432314; AA533447; Hs.285173; ESTs; Xlink,none; 2.81
416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none;TM=Y;SS=M; 2.80
446985; AL038704; Hs.156827; ESTs, Weakly similar to ALU1_HUMAN ALU S; SAM,SH3,HS1_rep; 2.80
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L;
aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 2.80
432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;SS=N; 2.80
426006; R49031; Hs.22627; ESTs; pkinase,TBC; 2.79
414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 2.79
411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;; 2.79
450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 2.78
424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 2.78
421448; AF033850; Hs.104519; phospholipase D2; PH,PLDc,PX;TM=M;SS=N; 2.78
410226; AI831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;SS=N; 2.78
433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subuni; HEAT;TM=M;SS=N; 2.78
442503; AF147078; Hs.375031; p53-responsive gene 5; K_tetra,ion_trans,none; 2.77
413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/H; TPR,PDZ,WW,Guanylate_kin;TM=M;SS=N; 2.77
454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;SS=N; 2.77
440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 2.77
449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain,none; 2.76
422667; H25642; Hs.132821; ESTs; FMO-like,FMO-like; 2.76
415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3,pkinase;TM=M;SS=N; 2.76
402316; ; ; NM_013447:Homo sapiens egf-like module c; 7tm_2,GPS;TM=M;SS=M; 2.75
425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 2.75
447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), ma; PP2C;TM=M;SS=N; 2.75
438629; AI187380; Hs.257170; ESTs, Weakly similar to T12515 hypotheti; TNFR_c6,none; 2.75
451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme; HATPase_c,none; 2.74
408543; N78098; Hs.44289; ESTs; none;TM=M;SS=N; 2.74
429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 2.74
407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfkB;TM=M;SS=N; 2.73
420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 2.73
407217; AA477136; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 2.73
414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M;SS=N; 2.73
410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 2.73
411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 2.73
438022; AW517524; Hs.135201; NOD2 protein; LRR,CARD,GTP_CDC,Viral_helicase1;TM=M;SS=N; 2.72
420929; AI694143; Hs.326248; programmed cell death 4; MA3;TM=M;SS=N; 2.72
421155; H87879; Hs.102267; lysyl oxidase; Lysyl_oxidase,Aldose_epim,Epimerase;; 2.72
448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK;; 2.71
449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain,none; 2.71
444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig;TM=Y;SS=M; 2.71
412259; AI560292; Hs.279909; protein phosphatase 2 (formerly 2A), reg; WD40;TM=M;SS=N; 2.71
419569; AI971651; Hs.91143; jagged 1 (Alagille syndrome); DSL,EGF,laminin_EGF,vwc,metalthio;TM=M;SS=M; 2.71
452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB;; 2.71
458190; BE561793; Hs.21446; KIAA1716 protein; ASC,Galactosyl_T,none; 2.70
432126; AA865239; Hs.37196; ESTs; 7tm_1;TM=Y;SS=M; 2.70
422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;SS=N; 2.70
424717; H03754; Hs.152213; wingless-type MMTV integration site fami; wnt,none; 2.70
414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;SS=N; 2.70
446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 2.70
416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 2.69
427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 2.69
404891; ; ; Target Exon; none,none; 2.69
432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 2.69
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;SS=N; 2.68
425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,pkinase,Fz;TM=Y;SS=M; 2.68
414443; AU077268; Hs.76144; platelet-derived growth factor receptor,; ig,pkinase;TM=Y;SS=N; 2.68
427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 2.68
436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 2.68
437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (f; SH2,SH3,BTB; 2.67
450690; AA296696; Hs.333418; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 2.67
452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 2.67
445330; R52656; Hs.21691; ESTs; 7tm_1,none; 2.67
452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 2.67
419754; H52299; Hs.308467; Homo sapiens mRNA; cDNA DKFZp586I0523 (f; none;TM=M;SS=N; 2.67
434237; AF119908; Hs.235516; hypothetical protein PRO2955; none;; 2.67
445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; ig,tsp_1,ZU5,Nucleoside_tran; 2.66
446696; AF279265; Hs.298476; solute carrier family 26, member 6; Sulfate_transp,STAS,xan_ur_permease;TM=Y;SS=N; 2.66
439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 2.66
413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap_PNP;; 2.66
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 2.66
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 2.66
449030; AI365582; Hs.57100; Homo sapiens mRNA for FLJ00016 protein, ; transmembrane4;TM=Y;SS=M; 2.66
434979; AI953054; Hs.89643; transketolase (Wernicke-Korsakoff syndro; ASC,transketolase,transket_pyr,transketolase_C,pkinase; 2.66
406137; ; ; NM_000179*:Homo sapiens mutS (E. coli) h; MutS_C,PWWP,MutS_N;TM=M;SS=N; 2.66

412935; BE267045; Hs.75064; tubulin-specific chaperone c; none;; 2.66
408633; AW963372; Hs.222088; PRO2000 protein; bromodomain,AAA,Sigma54_activat;; 2.66
412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep;TM=M;SS=N; 2.65
452682; AA456193; Hs.374574; progesterone membrane binding protein; homeobox,none; 2.65
401752; ; ; RAN binding protein 3; SH2,STAT,STAT_bind,STAT_prot,ion_trans,PAC,PAS,Orexin; 2.65
450747; AI064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 2.65
425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 2.64
452701; NM_005110; Hs.30332; glutamine-fructose-6-phosphate transamin; GATase_2,SIS;TM=M;SS=N; 2.64
433933; AI754389; Hs.355397; Homo sapiens clone TCCCIA00164 mRNA sequ; none;NA;NA; 2.64
421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 2.64
436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;; 2.64
423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 2.64
435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;SS=N; 2.64
437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyosin,pkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A;TM=M;SS=N; 2.63
458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 2.63
447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 2.63
445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 2.63
425075; AA506324; Hs.1852; acid phosphatase, prostate; acid_phosphat;TM=Y;SS=M; 2.63
405588; ; ; NM_000299*:Homo sapiens plakophilin 1 (e; Armadillo_seg;TM=M;SS=N; 2.63
438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.63
448243; AW369771; Hs.367688; integrin, beta 8; integrin_B,none; 2.63
452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA_topoisoIV,K-box;TM=M;SS=N; 2.63
412182; AA205588; Hs.73737; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr;; 2.63
423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y;SS=N; 2.63
417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 2.62
413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo_endo_phos;; 2.62
414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 2.62
417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi;TM=M;SS=M; 2.62
429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;SS=N; 2.62
401812; ; ; sorting nexin 14; AAA,NB-ARC,APS_kinase,cdc48_N,cdc48_2,none; 2.61
417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor,none; 2.61
457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substra; SH3;TM=M;SS=N; 2.61
428512; AI018187; Hs.375624; Human DNA sequence from clone RP11-243J1; none;; 2.61
426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase;TM=M;SS=N; 2.61
454042; H22570; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 2.61
421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;SS=N; 2.60
420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M;SS=N; 2.60
416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain,rrm;TM=M;SS=N; 2.60
417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF;; 2.60
411133; AW819204; ; gb:CM1-ST0283-071299-061-h03 ST0283 Homo; ANF_receptor,none; 2.60
405602; ; ; Target Exon; pkinase;; 2.60
400440; X83957; Hs.83870; nebulin; SH3,Nebulin;; 2.60
424848; AI263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin,none; 2.59
432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase;TM=M;SS=N; 2.59
452690; AI536070; Hs.15085; ESTs; pou,homeobox,lig_chan,ANF_receptor; 2.59
422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polyp; Sm;; 2.59
428028; U52112; Hs.182018; interleukin-1 receptor-associated kinase; death,pkinase;TM=M;SS=N; 2.58
433573; AF234887; Hs.57552; cadherin, EGF LAG seven-pass G-type rece; 7tm_2,EGF,cadherin,laminin_EGF,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 2.58
422785; AI824114; Hs.289088; heat shock 90kD protein 1, alpha; zf-C2H2,none; 2.58
418685; U76376; Hs.87247; harakiri, BCL2-interacting protein (cont; none;TM=M;SS=M; 2.58
452329; N36626; Hs.29106; mitogen-activated protein kinase phospha; DSPc;TM=M;SS=N; 2.58
428405; Y00762; Hs.2266; cholinergic receptor, nicotinic, alpha p; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 2.58
421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;; 2.57
407245; X90568; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M;SS=N; 2.57
422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=M; 2.57
401751; ; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,ion_trans,PAC,PAS,none; 2.57
447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 2.57
422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB;TM=Y;SS=M; 2.57
439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; lipoxygenase,PLAT,lipoxygenase,PLAT; 2.57
425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 2.57
401218; ; ; eukaryotic translation elongation factor; ion_trans;TM=Y;SS=N; 2.57
412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc;TM=M;SS=N; 2.57
444743; AA045648; Hs.301957; nudix (nucleoside diphosphate linked moi; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 2.56
429782; NM_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain; rrm,NTF2;TM=M;SS=N; 2.56
442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 2.56
456602; AA411607; Hs.118964; ESTs, Weakly similar to KIAA1150 protein; none,pkinase; 2.56
422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 2.56
441699; AW511126; Hs.127572; ESTs; none,Aa_trans; 2.56
447912; AW576549; Hs.165728; ESTs, Weakly similar to I38022 hypotheti; none,GSHPx,ABC_tran; 2.56
442945; AI024849; Hs.131853; ESTs; pkinase,none; 2.56
453199; AI336266; Hs.32353; mitogen-activated protein kinase kinase ; pkinase;TM=M;SS=N; 2.56
451477; AI798425; Hs.42710; ESTs; SH3,none; 2.56
415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Coenzyme A sy; HMG_CoA_synt;; 2.55
413529; U11874; Hs.846; interleukin 8 receptor, beta; 7tm_1;TM=Y;SS=N; 2.55
425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-recept; Y_phosphatase,DSPc;TM=M;SS=M; 2.55
401321; ; ; receptor tyrosine kinase-like orphan rec; none;TM=M;SS=N; 2.55
446999; AA151520; Hs.351416; hypothetical protein MGC4485; none,none; 2.55
401057; ; ; eukaryotic translation elongation factor; ion_trans,IQ;TM=Y;SS=N; 2.55
414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 2.55
408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, m; Y_phosphatase;TM=M;SS=N; 2.54
424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK; pkinase,Activin_recp;TM=M;SS=M; 2.54
459060; H89244; Hs.303627; heterogeneous nuclear ribonucleoprotein ; rrm,pkinase;TM=M;SS=N; 2.54
450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2;TM=M;SS=N; 2.54

425966; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C;TM=M;SS=N; 2.54
446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 2.54
412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1,none; 2.54
457255; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (fr; none,none; 2.54
431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M;SS=N; 2.53
417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 2.53
414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; fn2,CIMR;TM=M;SS=M; 2.53
444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 2.53
422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 2.53
450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none,none; 2.53
400702; ; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor;TM=Y;SS=M; 2.53
432336; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase;TM=M;SS=N; 2.53
442643; U82756; Hs.374973; PRP4/STK/WD splicing factor; WD40;; 2.52
452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN2; ABC_tran,IRK,SWIB; 2.52
443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin,none; 2.52
428975; NM_004672; Hs.194694; mitogen-activated protein kinase kinase ; pkinase;; 2.52
407608; AI928218; Hs.380063; ATPase, Na? transporting, beta 3 polypep; none,none; 2.51
414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 2.51
410293; AK000047; Hs.61960; hypothetical protein; K_tetra;TM=M;SS=N; 2.51
429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, ; C2,PLA2_B;TM=M;SS=N; 2.51
425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;SS=N; 2.51
457013; AA037145; Hs.172865; cleavage stimulation factor, 3' pre-RNA,; WD40;TM=M;SS=N; 2.51
439221; AA737106; Hs.32250; ESTs, Moderately similar to I78885 serin; adh_short,Bcl-2,BH4,none; 2.51
405429; ; ; Target Exon; Y_phosphatase,none; 2.51
443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase,RIO1;TM=M;SS=N; 2.51
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 2.50
408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 2.50
414419; F06829; Hs.76090; tumor necrosis factor, alpha-induced pro; K_tetra;TM=M;SS=N; 2.50
405369; ; ; NM_005569*:Homo sapiens LIM domain kinas; pkinase,LIM,PDZ;; 2.50
418216; AA662240; Hs.283099; AF15q14 protein; Hemagglutinin,squash;TM=Y;SS=N; 2.50
404321; ; ; C7001741*:gi|2499629|sp|Q63932|MPK2_MOUS; none,none; 2.50
430900; U91939; Hs.248123; G protein-coupled receptor 25; 7tm_1;TM=Y;SS=M; 2.49
440861; BE244115; Hs.7482; KIAA0682 gene product; rrm,Guanylate_kin;TM=M;SS=N; 2.49
415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig;TM=Y;SS=N; 2.49
418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase,Activin_recp,pkinase,Activin_recp; 2.49
417034; NM_006183; Hs.80962; neurotensin; none;; 2.49
400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 2.49
408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;SS=N; 2.49
418255; AW135405; Hs.37251; ESTs; pkinase,none; 2.49
424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M;SS=N; 2.44
417791; AW965339; Hs.44269; ESTs; none,fer2,FAD_binding_5,Ald_Xan_dh_C,fer2_2,Ald_Xan_dh_C2,CO_deh_flav_C; 2.44
453941; U39817; Hs.36820; Bloom syndrome; DEAD,helicase_C,HRDC;TM=M;SS=N; 2.41
417849; AW291587; Hs.82733; nidogen 2; EGF,ldl_recept_b,thyroglobulin_1;TM=M;SS=M; 2.39
408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;; 2.32
428513; BE220806; Hs.184697; plexin C1; PSI,none; 2.31
426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 2.31
427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q,Collagen;; 2.28
412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M;SS=N; 2.28
452461; N78223; Hs.108106; transcription factor; zf-C3HC4,ubiquitin,PHD,YDG_SRA;TM=M;SS=N; 2.26
429547; AW009166; Hs.99376; FGENESH predicted novel secreted protein; none,none; 2.15
429486; AF155827; Hs.203963; hypothetical protein FLJ10339; SNF2_N,helicase_C;TM=M;SS=N; 2.15
401486; ; ; C4000647*:gi|4758508|ref|NP_004253.1| ai; none;TM=Y;SS=M; 2.15
416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA;TM=M;SS=N; 2.14
424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 BT095 Homo ; none;TM=M;SS=M; 2.14
423761; NM_006194; Hs.132576; paired box gene 9; PAX;TM=M;SS=N; 2.13
439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004858 3 U1 snr; none,none; 2.13
439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 2.03
445019; AI205540; Hs.281295; ESTs; none,none; 2.00
443211; AI128388; Hs.143655; ESTs; none,none; 1.98
449448; D60730; Hs.57471; ESTs; none,none; 1.92
435243; AW292886; Hs.348932; hypothetical protein dJ434O14.3; IRF,none; 1.85
406360; ; ; Target Exon; WD40;TM=M;SS=N; 1.84
411388; X72925; Hs.69752; desmocollin 1; cadherin;TM=Y;SS=N; 1.84
453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 1.79
419183; U60669; Hs.89663; cytochrome P450, subfamily XXIV (vitamin; p450;; 1.78
420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 1.77
432842; AW674093; Hs.334822; hypothetical protein MGC4485; Ribosomal_L4;TM=M;SS=N; 1.76
419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA sequence; none,none; 1.73
426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 1.62
437915; AI637993; Hs.202312; Homo sapiens clone N11 NTera2D1 teratoca; none,none; 1.58
433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR;; 1.50
434377; AW137148; Hs.306593; intron of periostin (OSF-2os); Fasciclin,none; 1.47
451592; AI805416; Hs.213897; ESTs; none,none; 1.47
404927; ; ; Target Exon; Galactosyl_T;TM=M;SS=Y; 1.28
421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;; 1.27
427335; AA448542; Hs.278444; G antigen 7B; none;; 1.25
431808; M30703; Hs.270833; amphiregulin (schwannoma-derived growth ; EGF;TM=Y;SS=M; 1.24
447993; AW139525; Hs.170362; ESTs; none,none; 1.21
428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_HUMAN G ANT; none;TM=M;SS=N; 1.18
453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); cadherin;TM=Y;SS=M; 1.14
438274; AI918906; Hs.55080; ESTs; PAX,none; 1.14
453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,ldl_recept_a,none; 1.10
413268; AL039079; Hs.75256; regulator of G-protein signalling 1; RGS;TM=M;SS=N; 1.07

429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;; 1.00
452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-FeII_Oxy;TM=M;SS=N; 1.00

TABLE 25B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
418869	12789_14	AA229762 AA230035
425802	8884_3	AA122298 AA360788
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
411133	1070995_1	AW819203 AW819204 AW819197 AW819202 AW819211 BE158469 AW819221 BE158473 AW819235 AW819207 AW819220 AW819208 AW819238 AW819198 AW819234

TABLE 25C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
405932	7767812	Minus	123525-123713
406467	9795551	Plus	182212-182958
402233	7690102	Plus	90281-91477
402558	9863760	Plus	19047-19145,21133-21293,33968-34069
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
403112	8980973	Minus	113051-113195
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
404891	7329392	Plus	84974-85125
406137	9166422	Minus	30487-31058
401752	9828651	Plus	144600-144794
405588	5002511	Plus	46180-46366
401812	7407975	Minus	55084-55391
405602	4753260	Plus	44647-44778
401751	9828651	Plus	139165-139322
401218	9929301	Minus	40793-41031
401321	9863631	Minus	104278-104748
401057	8117645	Plus	158309-159238
400702	8118856	Minus	11457-11585,26311-26536,27902-28067,3204
405429	7321905	Minus	51577-51723
405369	2078469	Minus	34183-34357,35686-35751
404321	9665209	Minus	76594-77805
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
406360	9256107	Minus	7513-7673
404927	7342002	Plus	68690-69563

TABLE 26A: 834 GENES UP-REGULATED IN EWING'S SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 26A lists about 834 genes up-regulated in Ewing's sarcoma compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 1.5. The "average" kidney cancer level was set to the 75th percentile amongst Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of Ewing sarcoma to normal tissue

Pkey	ExAccn	UniGeneID	UniGene Title	R1
101447	M21305		gb:Human alpha satellite and satellite 3	38.4
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	34.2
110278	AF061573	Hs.19492	protocadherin 8	32.2
121362	AF050147	Hs.97932	chondromodulin I precursor	30.3
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	26.3

	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	24.4
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	23.4
	104659	AW969769	Hs.105201	ESTs	20.2
	106533	AL134708	Hs.145998	ESTs	16.9
5	124006	AI147155	Hs.270016	ESTs	15.0
	110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	14.8
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	14.6
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	14.5
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	13.7
10	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	12.3
	129526	S69681	Hs.177582	surfactant, pulmonary-associated protein	12.1
	119791	AA554907	Hs.58291	ESTs	11.7
	116301	AW969706	Hs.293332	ESTs	11.2
	123308	C14187	Hs.103538	ESTs	10.9
15	127742	AW293496	Hs.180138	ESTs	10.8
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	10.7
	127489	AA650250	Hs.272076	ESTs	10.6
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.6
	101063	D54745	Hs.80247	cholecystokinin	10.6
20	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	10.5
	100299	D49493	Hs.2171	growth differentiation factor 10	10.1
	127987	AI022103	Hs.124511	ESTs	10.1
	131313	R96290	Hs.336629	ribosomal protein L44	9.2
	126799	AW753865	Hs.74376	olfactomedin related ER localized protei	8.5
25	125847	AW161885	Hs.249034	ESTs	7.0
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	6.9
	114837	BE244930	Hs.166895	ESTs	6.6
	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	6.6
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.5
30	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous r	6.5
	125186	AA610620	Hs.181244	major histocompatibility complex, class	6.4
	118644	AA443241	Hs.336629	ribosomal protein L44	6.3
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	6.3
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	6.1
35	113003	AW292315	Hs.7215	ESTs	5.8
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.7
	101050	AU077324	Hs.1832	neuropeptide Y	5.7
	116790	AW161357	Hs.101174	microtubule-associated protein tau	5.5
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	5.1
40	132315	AF091086	Hs.44563	hypothetical protein	5.0
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	4.9
	126077	M78772	Hs.210836	ESTs	4.7
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	4.6
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	4.5
45	123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	4.4
	128361	AW172570	Hs.130246	ESTs	4.3
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	4.3
	100020				4.2
	125556	AB033064	Hs.334806	KIAA1238 protein	4.2
50	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	4.0
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.0
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	3.9
	128132	AA225632		gb:nc08a07.r1 NCI_CGAP_Pr1 Homo sapiens	3.9
	129012	R81936	Hs.336629	ribosomal protein L44	3.9
55	125447	AI582222	Hs.128686	ESTs	3.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	3.6
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	3.6
	128391	AW188326	Hs.170652	ESTs	3.5
	123829	AF251237	Hs.112208	XAGE-1 protein	3.4
60	123949	AA621665	Hs.208957	EST	3.4
	126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	3.4
	101266	L36645	Hs.73964	EphA4	3.3
	121309	AA293834	Hs.97312	ESTs	3.3
	130637	AA356764	Hs.17109	integral membrane protein 2A	3.2
65	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	3.2
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	3.2
	107599	AW664072	Hs.60136	ESTs	3.2
	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.2
	131688	AI935413	Hs.30692	p21 (CDKN1A)-activated kinase 2	3.1
70	120147	AI917116	Hs.155376	hemoglobin, beta	3.1
	110343	AW136703	Hs.17268	ESTs	3.1
	127664	AA806164	Hs.116502	ESTs	3.0
	103076	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	3.0
	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.0
75	125558	R59305		gb:yh16c10.r1 Soares infant brain 1NIB H	3.0
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.9
	133421	AF134160	Hs.7327	claudin 1	2.8
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.8
	113577	AI300699	Hs.278937	PRO0470 protein	2.8
80	116397	BE139479	Hs.161492	ESTs	2.8
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530I15	2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2.8
	127262	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	2.8

106472	AI207162	Hs.3815	stathmin-like protein RB3	2.7
125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	2.7
127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	2.7
126600	AA699949	Hs.191385	ESTs	2.7
120325	AA195651	Hs.104106	ESTs	2.7
127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN	2.7
117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.7
126735	M69113	Hs.226795	glutathione S-transferase pi	2.7
102745	AW753865	Hs.74376	olfactomedin related ER localized protei	2.7
128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	2.6
129706	AA443241	Hs.336629	ribosomal protein L44	2.6
107731	AA016086	Hs.272106	ESTs, Weakly similar to I38022 hypotheti	2.6
128283	AI076570	Hs.134053	ESTs	2.6
125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	2.6
111148	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
105577	AW852257	Hs.171391	C-terminal binding protein 2	2.6
128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	2.6
130262	D63216	Hs.153684	frizzled-related protein	2.6
132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.6
102479	NM_001991	Hs.194669	enhancer of zeste (Drosophila) homolog 1	2.6
128531	H03721	Hs.2953	ribosomal protein S15a	2.6
126165	AI741816	Hs.125897	ESTs	2.6
126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	2.5
118967	AI668670	Hs.216756	ESTs	2.5
120830	AI568170	Hs.96886	ESTs	2.5
127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.5
129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	2.5
110151	H18835	Hs.31608	hypothetical protein FLJ20041	2.5
131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.5
133761	AF041430	Hs.75922	brain protein I3	2.5
125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.5
126693	C05723		gb:C05723 Human pancreatic islet Homo sa	2.5
126021	AA775894	Hs.187516	ESTs	2.5
125905	AI678636	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.5
102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	2.5
125743	H17151		gb:ym37a05.r1 Soares infant brain 1NIB H	2.5
130580	N32368	Hs.334370	uncharacterized hypothalamus protein HBE	2.5
113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	2.4
123110	AA486256	Hs.193510	EST	2.4
113283	T66813	Hs.12947	EST	2.4
107711	W96141	Hs.220687	ESTs	2.4
128992	H04150	Hs.107708	ESTs	2.4
106111	AW875398	Hs.6451	PRO0659 protein	2.4
129948	AI537162	Hs.263988	ESTs	2.4
125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	2.4
116726	F13687	Hs.227976	EST	2.4
103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	2.4
124971	T23800	Hs.151001	hypothetical protein FLJ14728	2.4
131019	W28614	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.4
128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory s	2.4
111795	AI435437	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.4
119127	AA708035	Hs.12248	ESTs	2.4
117602	N35020	Hs.44685	C3HC4-like zinc finger protein	2.4
111898	R38944	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
131916	AA025976	Hs.34569	ESTs	2.4
130850	AB040922	Hs.20237	DKFZP566C134 protein	2.4
100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	2.4
126722	N66148	Hs.11125	HSPC033 protein	2.4
123720	AA609734	Hs.112755	EST	2.4
113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovir	2.4
131136	AB033099	Hs.23413	KIAA1273 protein	2.4
129001	AA443323	Hs.107812	BPOZ protein	2.4
133529	W45623	Hs.74571	ADP-ribosylation factor 1	2.4
107593	AI093688	Hs.60051	ESTs	2.4
123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4
128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.4
103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	2.4
128367	AW611791	Hs.150742	ESTs	2.4
123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	2.4
112342	AW410273	Hs.92614	longevity assurance (LAG1, S. cerevisiae	2.3
114721	D61939	Hs.103822	ESTs	2.3
127768	AW085002	Hs.156187	ESTs	2.3
127706	AI174238	Hs.186982	ESTs	2.3
126029	AA704253	Hs.169359	ESTs	2.3
124250	AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.3
117265	AA451966	Hs.43005	RAB9-like protein	2.3
112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	2.3
129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.3
127252	AI049545	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	2.3
114092	H81213	Hs.14625	ESTs, Weakly similar to KIAA1503 protein	2.3
109252	BE440157	Hs.85944	ESTs	2.3
127889	AI147408	Hs.144941	ESTs	2.3

	121292	AA401807		gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_	2.3
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	2.3
	132985	AL045579	Hs.62113	KIAA0717 protein	2.3
	125174	W51835	Hs.231082	EST	2.3
5	125401	AI204637	Hs.337585	ESTs, Highly similar to KIAA0350 [H.sapi	2.3
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	2.3
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	2.3
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	2.3
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.3
10	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	2.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC	2.3
	101086	AA382524	Hs.250959	histatin 1	2.3
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	2.3
	126879	D90391	Hs.1265	branched chain keto acid dehydrogenase E	2.3
15	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	2.3
	124691	R05835	Hs.110153	ESTs	2.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	2.3
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	2.2
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	2.2
20	129248	W04606	Hs.171637	hypothetical protein MGC2628	2.2
	100780	BE561958	Hs.302063	immunoglobulin heavy constant mu	2.2
	135416	BE281018	Hs.99969	fusion, derived from t(12;16) malignant	2.2
	129928	AI338993	Hs.134535	ESTs	2.2
	103319	X83492	Hs.82359	tumor necrosis factor receptor superfami	2.2
25	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	2.2
	120734	AA299948		gb:EST12544 Uterus tumor I Homo sapiens	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128963	J03890	Hs.1074	surfactant, pulmonary-associated protein	2.2
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
30	134964	AI803516	Hs.272891	hippocalcin-like protein 4	2.2
	127248	AA364195		gb:EST75015 Pineal gland II Homo sapiens	2.2
	125761	R68351		gb:yh99b03.r1 Soares placenta Nb2HP Homo	2.2
	101358	M10058	Hs.12056	asialoglycoprotein receptor 1	2.2
	101613	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.2
35	107121	AB015427	Hs.250493	zinc finger protein 219	2.2
	118751	N74210	Hs.50454	ESTs	2.2
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	2.2
	126581	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 fis, clone MA	2.2
	127634	AA633469	Hs.193283	ESTs, Weakly similar to unnamed protein	2.2
40	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.2
	132867	AF226667	Hs.58553	CTP synthase II	2.2
	126323	N77584	Hs.68644	Homo sapiens microsomal signal peptidase	2.2
	111790	AW769683	Hs.6734	ESTs, Weakly similar to S26650 DNA-bindi	2.2
	125549	R20215		gb:yg18b09.r1 Soares infant brain 1NIB H	2.2
45	128059	AA972446	Hs.145096	ESTs	2.2
	132342	AW162758	Hs.45232	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.2
	125722	H29796	Hs.269622	ESTs	2.2
	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	2.2
	127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2.2
50	128179	AW293689	Hs.127116	ESTs	2.2
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	2.2
	126962	R12014	Hs.20976	ESTs	2.2
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	2.2
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.2
55	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypothet	2.2
	108743	AI580150	Hs.71074	ESTs	2.2
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	2.2
	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	2.2
	109929	AA773187	Hs.294027	ESTs	2.2
60	129059	AW069534	Hs.279583	CGI-81 protein	2.2
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	2.2
	116962	H79677		gb:yu76g10.s1 Soares fetal liver spleen	2.2
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	2.2
	106711	BE390125	Hs.143187	hypothetical protein	2.2
65	135191	X16866	Hs.301086	cytochrome P450, subfamily IID (debrisoq	2.2
	125822	H03162	Hs.268768	ESTs	2.2
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	2.2
	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.2
	126250	AL050391	Hs.321247	Homo sapiens mRNA; cDNA DKFZp586A181 (fr	2.2
70	103392	X94563		gb:H.sapiens dbl/acbp gene exon 1 & 2.	2.2
	129794	AF161399	Hs.23259	hypothetical protein FLJ13433	2.2
	100253	D38024	Hs.157425	double homeobox, 2	2.2
	130743	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.2
	125466	R08234	Hs.180461	ESTs	2.2
75	122682	AA984531	Hs.159293	ESTs	2.2
	133347	BE257758	Hs.71475	acid cluster protein 33	2.2
	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.2
	116332	AA491208	Hs.62620	chromosome 6 open reading frame 1	2.2
	131163	AA099524	Hs.23754	ESTs	2.2
80	109592	AI198059	Hs.26370	ESTs	2.2
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.1
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	2.1
	128434	AI190914	Hs.143880	ESTs	2.1

103163	AU077018	Hs.3235	keratin 4	2.1
112379	AK001713	Hs.17860	hypothetical protein FLJ10851	2.1
127507	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.1
133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
126153	H65692	Hs.40730	ESTs	2.1
122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	2.1
100554	M95923		gb:Human 12-lipoxygenase mRNA, partial c	2.1
104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	2.1
132664	AI740461	Hs.54542	ESTs	2.1
114620	AA642974		gb:nr60h01.s1 NCI_CGAP_Lym3 Homo sapiens	2.1
115348	AA281562	Hs.292100	ESTs	2.1
133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
133160	N54968	Hs.66309	hypothetical protein MGC11061	2.1
124656	AW297702	Hs.102915	ESTs	2.1
133576	M19650	Hs.150741	2',3'-cyclic nucleotide 3' phosphodieste	2.1
132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothet	2.1
126505	AA282881	Hs.190057	ESTs	2.1
118865	AA736405	Hs.54530	ESTs	2.1
134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.1
134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.1
133493	AW998046	Hs.194369	arginine-glutamic acid dipeptide (RE) re	2.1
112853	T02843		gb:FB11H5 Fetal brain, Stratagene Homo s	2.1
117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU	2.1
112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	2.1
134869	AL157518	Hs.90421	PRO2463 protein	2.1
128869	AA768242	Hs.80618	hypothetical protein	2.1
129179	AW969025	Hs.109154	ESTs	2.1
104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.1
101651	AL037111	Hs.75641	galactose-1-phosphate uridylyltransferas	2.1
129726	H15474	Hs.132898	fatty acid desaturase 1	2.1
117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
126271	AI250773	Hs.270012	ESTs	2.1
116925	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-ce	2.1
128468	T23625	Hs.150580	putative translation initiation factor	2.1
116031	AA452239	Hs.103329	KIAA0970 protein	2.1
130724	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	2.1
121897	AA427419	Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.1
123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	2.1
122333	AA625872	Hs.98977	ESTs, Moderately similar to T34561 hypot	2.1
127841	AW136558	Hs.125246	ESTs	2.1
100023				2.1
113002	BE243513	Hs.7212	hypothetical protein PP1044	2.1
111567	F12628	Hs.334786	hypothetical protein MGC16040	2.1
113697	T97183	Hs.17992	Homo sapiens mRNA; cDNA DKFZp434J1726 (f	2.1
128033	AI248705	Hs.149321	ESTs	2.1
105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.1
112370	AF052095	Hs.167344	Homo sapiens clone 23911 mRNA sequence	2.1
132786	BE083422	Hs.56851	hypothetical protein MGC2668	2.1
113226	AI821008	Hs.10697	ESTs	2.1
117997	N52090	Hs.47420	EST	2.1
116996	H83935	Hs.40535	ESTs	2.1
127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	2.1
122591	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.1
107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia	2.1
103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.1
110312	BE256986	Hs.11896	hypothetical protein FLJ12089	2.1
127447	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	2.1
128352	AW137413	Hs.169942	ESTs	2.1
113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.0
128275	AI218235	Hs.131240	ESTs	2.0
125976	AA436760		gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	2.0
120820	AA347417	Hs.96869	EST	2.0
134937	AI251449	Hs.171939	ESTs	2.0
129602	AI282193	Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	2.0
129535	AA397972	Hs.169965	chimerin (chimaerin) 1	2.0
106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.0
128538	R44214	Hs.101189	ESTs	2.0
105593	AA279341	Hs.174151	aldehyde oxidase 1	2.0
105788	AB009698	Hs.23965	solute carrier family 22 (organic anion	2.0
128148	AA918175	Hs.126637	ESTs	2.0
125982	R98091		gb:yr30e11.r1 Soares fetal liver spleen	2.0
125746	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
127835	AA748762	Hs.163113	ESTs, Weakly similar to I38022 hypotheti	2.0
100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	2.0
124282	AA018408	Hs.110287	ESTs	2.0
126926	AA179472	Hs.832	ESTs, Highly similar to A41029 integrin	2.0
100221	D28383		gb:Human mRNA for ATP synthase B chain,	2.0
126053	H64450		gb:yu62d01.r1 Weizmann Olfactory Epithel	2.0
100944	L07518	Hs.159593	mucin 6, gastric	2.0
125581	AI272848	Hs.75309	eukaryotic translation elongation factor	2.0
128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.0
114612	AI124557	Hs.95456	ESTs	2.0
130453	U80735	Hs.173854	PAX transcription activation domain inte	2.0

	135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.0
	114419	AI248013	Hs.106532	ESTs, Weakly similar to I38588 reverse t	2.0
	126283	N40359	Hs.271896	ESTs	2.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.0
5	127391	AW380893	Hs.11039	hypothetical protein MGC2722	2.0
	127717	F12209	Hs.173380	CK2 interacting protein 1; HQ0024c prote	2.0
	126893	AJ252060	Hs.26320	TRABID protein	2.0
	106798	BE252749	Hs.20558	hypothetical protein FLJ20345	2.0
	103760	AA642973	Hs.183842	ubiquitin B	2.0
10	118922	AW206193	Hs.91065	hypothetical protein DKFZp761B2423	2.0
	133195	AI434760	Hs.279949	KIAA1007 protein	2.0
	133424	AA350994	Hs.20281	KIAA1700	2.0
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.0
	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypotheti	2.0
15	125599	H13295	Hs.106135	ESTs	2.0
	114459	AW445217	Hs.103362	ESTs	2.0
	128478	AA708205	Hs.100343	ESTs	2.0
	127271	H96820		gb:yv99b03.r1 Soares melanocyte 2NbHM Ho	2.0
	111122	N63753	Hs.16492	DKFZP564G2022 protein	2.0
20	130695	T97205	Hs.17998	ESTs, Weakly similar to 2109260A B cell	2.0
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	2.0
	119244	AW407564	Hs.275865	ribosomal protein S18	2.0
	127603	AI016798	Hs.9925	hypothetical protein FLJ20772	2.0
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
25	128115	AI435590	Hs.130168	ESTs	2.0
	117639	AA377165	Hs.44833	ESTs	2.0
	127033	AF169301	Hs.9098	sulfate transporter 1	2.0
	112411	R43090	Hs.271510	ESTs, Moderately similar to ALU1_HUMAN A	2.0
	114601	AA075566		gb:zm88f06.s1 Stratagene ovarian cancer	2.0
30	127573	AA594196	Hs.269464	ESTs, Weakly similar to S65657 alpha-1C-	2.0
	125500	AW952654	Hs.244624	ESTs	2.0
	119416	T97186		gb:ye50h09.s1 Soares fetal liver spleen	2.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	2.0
	128902	AA036637	Hs.107052	ESTs	2.0
35	127684	AA668631	Hs.32556	KIAA0379 protein	2.0
	126288	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	2.0
	122059	AA431737	Hs.98749	EST, Moderately similar to T42671 hypoth	2.0
	125486	AI023895	Hs.190587	ESTs	2.0
	128895	AW467000	Hs.106985	ESTs	2.0
40	105301	AW352357	Hs.7457	MAGE1 protein	2.0
	125536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	121387	AA405854		gb:zu66g06.s1 Soares_testis_NHT Homo sap	2.0
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	2.0
	126860	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.0
45	102907	BE409861	Hs.202833	heme oxygenase (decycling) 1	2.0
	127804	AA740634	Hs.292084	ESTs	2.0
	130566	R85474	Hs.16073	ESTs	1.9
	113782	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.9
	124119	AA040123	Hs.248953	solute carrier family 27 (fatty acid tra	1.9
50	132490	NM_001290	Hs.4980	LIM domain binding 2	1.9
	125494	AU077029	Hs.177543	antigen identified by monoclonal antibod	1.9
	100237	D30715	Hs.306333	Human PAP (pancreatitis-associated prot	1.9
	127687	AW772383	Hs.300635	ESTs	1.9
	103136	AF087917	Hs.247936	olfactory receptor, family 1, subfamily	1.9
55	125704	R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	126208	N22588	Hs.288548	Homo sapiens cDNA FLJ12368 fis, clone MA	1.9
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	1.9
	126660	AA011597	Hs.177398	ESTs	1.9
	116049	N53145		gb:yv55f09.s1 Soares fetal liver spleen	1.9
60	134624	AF035119	Hs.8700	deleted in liver cancer 1	1.9
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.9
	126414	AI363157	Hs.24756	hepatocyte growth factor-regulated tyros	1.9
	120861	AA350394	Hs.96952	ESTs	1.9
	124669	AI571594	Hs.102943	hypothetical protein MGC12916	1.9
65	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	1.9
	103891	NM_007212	Hs.124186	ring finger protein 2	1.9
	128727	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.9
	126831	AI929107	Hs.79933	cyclin I	1.9
	125360	AW898892	Hs.189741	ESTs	1.9
70	124276	H83465		gb:ys91a11.s1 Soares retina N2b5HR Homo	1.9
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
	126647	AK000283	Hs.270502	hypothetical protein FLJ20276	1.9
	125957	H41694		gb:yo06b06.r1 Soares adult brain N2b5HB5	1.9
	121782	AW452957	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	1.9
75	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetl	1.9
	130945	U20582	Hs.2149	actin like protein	1.9
	126348	T16243	Hs.6473	Homo sapiens cDNA FLJ13992 fis, clone Y7	1.9
	103558	BE616547	Hs.2785	keratin 17	1.9
	126982	AA211419		gb:zn55g05.s1 Stratagene muscle 937209 H	1.9
80	125613	AA765957	Hs.21077	KIAA0532 protein	1.9
	129601	AB032964	Hs.115726	KIAA1138 protein	1.9
	126007	H51097	Hs.143261	ESTs	1.9
	123627	AA909619	Hs.112668	ESTs	1.9

	111587	AI125867	Hs.20734	ESTs	1.9
	135231	BE613615	Hs.74280	hypothetical protein FLJ22237	1.9
	128897	AW979134	Hs.10700	hypothetical protein	1.9
	109891	H04757	Hs.323176	ESTs	1.9
5	127704	AA679609		gb:ag72c02.s1 Gessler Wilms tumor Homo s	1.9
	129340	H75334	Hs.11050	F-box only protein 9	1.9
	126502	T10077	Hs.13453	hypothetical protein FLJ14753	1.9
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	1.9
	127136	R36277	Hs.7773	Homo sapiens ubiquitin conjugating enzym	1.9
10	110636	H72868	Hs.19110	ESTs	1.9
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	1.9
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.9
	130829	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	1.9
	125768	AI557486	Hs.119122	ribosomal protein L13a	1.9
15	123613	AA609158	Hs.291166	EST	1.9
	127506	T61039	Hs.252574	ribosomal protein L10a	1.9
	123546	AA608817	Hs.112597	EST	1.9
	126516	R95872	Hs.117572	chemokine binding protein 2	1.9
	103973	AA305729	Hs.18272	amino acid transporter system A1	1.9
20	127426	AA854756	Hs.124076	ESTs	1.9
	112339	R56570	Hs.50547	ESTs	1.9
	129101	NM_013403	Hs.108665	zinedin	1.9
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	1.9
	118103	AA401733	Hs.184134	ESTs	1.9
25	125752	AW136622	Hs.206673	ESTs	1.9
	102926	W28363	Hs.239752	nuclear receptor subfamily 2, group F, m	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
	127329	AW160551	Hs.124021	soggy-1 gene	1.8
30	126659	T16245		gb:NIB1005R Normalized infant brain, Ben	1.8
	127297	AW629485	Hs.140720	GSK-3 binding protein FRAT2	1.8
	127640	AI557486	Hs.119122	ribosomal protein L13a	1.8
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	1.8
	127964	F06298		gb:HSC13F081 normalized infant brain cDN	1.8
35	122365	AA813546	Hs.99034	GTP-binding protein Rho7	1.8
	128193	AJ224442	Hs.155020	putative methyltransferase	1.8
	115173	BE612940	Hs.88252	ESTs	1.8
	125532	AI734146	Hs.271800	ESTs, Weakly similar to alternatively sp	1.8
	126541	AJ271671	Hs.7854	zinc/iron regulated transporter-like	1.8
40	127309	AI669765	Hs.133184	ESTs	1.8
	129062	AA452970	Hs.155218	E1B-55kDa-associated protein 5	1.8
	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	1.8
	127775	AA128808	Hs.179902	transporter-like protein	1.8
	126994	AA455265	Hs.86686	ESTs, Moderately similar to I54374 gene	1.8
45	130734	AW137091	Hs.18624	KIAA1052 protein	1.8
	114461	AA531187	Hs.126705	ESTs	1.8
	100842	U05597		gb:Human anion exchanger 3 cardiac isofo	1.8
	127389	T65126	Hs.12743	carnitine O-octanoyltransferase	1.8
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	1.8
50	107736	AA016239	Hs.60715	ESTs	1.8
	125669	R51308	Hs.333256	ESTs, Weakly similar to ALU8_HUMAN ALU	1.8
	100370	D79989	Hs.184884	KIAA0167 gene product	1.8
	113479	AI023133	Hs.10739	ESTs	1.8
	105165	BE280787	Hs.16079	hypothetical protein FLJ10233	1.8
55	120602	AA808018	Hs.109302	ESTs	1.8
	112399	R60920	Hs.296770	KIAA1719 protein	1.8
	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	1.8
	134212	AA654353	Hs.17719	EBP50-PDZ interactor of 64 kD	1.8
	104204	AK001691	Hs.57655	hypothetical protein FLJ10829	1.8
60	127464	AW971875	Hs.292071	ESTs	1.8
	116715	AL117440	Hs.170263	tumor protein p53-binding protein, 1	1.8
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.8
	132380	AW373665	Hs.46853	ESTs	1.8
	120087	AF186780	Hs.79219	RalGDS-like gene; KIAA0959 protein	1.8
65	116356	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	1.8
	125499	H10543		gb:ym04c06.r1 Soares infant brain 1NIB H	1.8
	128846	AA730767	Hs.285753	SCG10-like-protein	1.8
	123669	AA620924	Hs.112923	EST	1.8
	108889	AA135722	Hs.61481	ESTs	1.8
70	126528	Z24895		gb:HSB67F122 STRATAGENE Human skeletal m	1.8
	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	130004	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	1.8
	130847	AI672483	Hs.20220	lipase protein	1.8
	111620	R14853	Hs.307478	EST, Weakly similar to I39058 hypotheti	1.8
75	131971	BE567100	Hs.154938	hypothetical protein MDS025	1.8
	121360	AA405635	Hs.96854	ESTs, Weakly similar to DYLX_HUMAN CYTOP	1.8
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	1.8
	124687	AA833902	Hs.270745	ESTs	1.8
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	1.8
80	126730	AA442429		gb:zv70g02.r1 Soares_total_fetus_Nb2HF8_	1.8
	127916	AI239950	Hs.294111	ESTs, Moderately similar to B34087 hypo	1.8
	128408	AI183407	Hs.143704	EST	1.8
	128440	AW090340	Hs.14337	Homo sapiens cDNA FLJ14407 fis, clone HE	1.8

123783	AA610112		gb:af19g05.s1 Soares_total_fetus_Nb2HF8_	1.8
109152	AW380723	Hs.73451	ESTs, Weakly similar to S55024 nebulin,	1.8
107242	AB020672	Hs.175411	KIAA0865 protein	1.8
132804	AI805943	Hs.326067	hypothetical protein MGC5178	1.8
125387	AJ243669	Hs.8127	KIAA0144 gene product	1.8
121578	AA398791	Hs.178185	ESTs	1.8
132944	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	1.8
126295	AI281459	Hs.270114	ESTs	1.8
133335	BE251012	Hs.263812	nuclear distribution gene C (A.nidulans)	1.8
129879	AK001696	Hs.13109	Ran binding protein 11	1.7
125175	W52355	Hs.303030	EST	1.7
126919	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	1.7
127773	AA725863	Hs.120508	ESTs	1.7
126495	AB029021	Hs.137732	KIAA1098 protein	1.7
126948	AW968535	Hs.14328	hypothetical protein FLJ20071	1.7
126671	C03105	Hs.285847	CGI-19 protein	1.7
115428	AA284112	Hs.94680	ESTs, Weakly similar to I78885 serine/t	1.7
128232	AI830319	Hs.334641	hypothetical protein DKFZp434I1916	1.7
126082	H61168	Hs.269571	ESTs	1.7
120467	AW292562	Hs.187628	ESTs	1.7
124041	AW590171	Hs.101413	ESTs	1.7
105012	AF096158	Hs.9329	chromosome 20 open reading frame 1	1.7
123951	AB012922	Hs.173043	metastasis-associated 1-like 1	1.7
126449	AF223944	Hs.325443	breast cell glutaminase	1.7
124554	N65961		gb:za27d03.s1 Soares fetal liver spleen	1.7
133651	AI301740	Hs.173381	dihydropyrimidinase-like 2	1.7
126780	R12421	Hs.5811	chromosome 21 open reading frame 59	1.7
125661	AA491630	Hs.25689	ESTs	1.7
125888	H18298		gb:yn48b09.r1 Soares adult brain N2b5HB5	1.7
127245	AA323958		gb:EST26810 Cerebellum II Homo sapiens c	1.7
111223	AA852773	Hs.334838	KIAA1866 protein	1.7
115611	R44789	Hs.33191	Homo sapiens, Similar to transmembrane r	1.7
124846	R59977	Hs.158196	transcriptional adaptor 3 (ADA3, yeast	1.7
100397	D84424	Hs.57697	hyaluronan synthase 1	1.7
127180	T27097	Hs.22790	ESTs	1.7
102598	BE250742	Hs.106673	eukaryotic translation initiation factor	1.7
134076	AF086215		gb:Homo sapiens full length insert cDNA	1.7
115659	W99382	Hs.283709	lipopolysaccharide specific response-7 p	1.7
125555	R19382	Hs.117869	ESTs	1.7
128382	AI138886	Hs.143243	ESTs	1.7
127710	AA682867	Hs.191901	ESTs	1.7
125445	AI452722	Hs.7709	WW domain binding protein 1	1.7
129951	AL110282	Hs.268024	Homo sapiens, clone IMAGE:3873720, mRNA	1.7
119898	R93325	Hs.58690	ESTs	1.7
129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	1.7
133531	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.7
119726	AF086289	Hs.234766	skin-specific protein	1.7
125198	W69474	Hs.323140	ESTs	1.7
121414	AW291477	Hs.188763	testis expressed sequence 13A	1.7
112542	AI458867	Hs.24276	ESTs	1.7
101368	M13058	Hs.73952	proline-rich protein HaeIII subfamily 2	1.7
125820	AA730136	Hs.75561	teratocarcinoma-derived growth factor 1	1.7
129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	1.7
132609	U20165	Hs.53250	bone morphogenetic protein receptor, typ	1.7
119447	W31714	Hs.122656	ESTs, Highly similar to formin 2-like pr	1.7
113675	T81034	Hs.14841	ESTs	1.7
113701	T97301	Hs.18026	ESTs	1.7
116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7
127133	AA280740	Hs.292072	ESTs, Moderately similar to A46010 X-lin	1.7
113316	T70318	Hs.268581	ESTs	1.7
123316	AI290561	Hs.155361	ESTs	1.7
122638	AL137476	Hs.123609	Homo sapiens mRNA; cDNA DKFZp434I0623 (f	1.7
105053	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.7
103305	X62279		gb:H.sapiens Fas, Apo-1 gene (promoter a	1.7
110384	H45282	Hs.268798	ESTs	1.7
115626	AW630870	Hs.86674	ESTs, Weakly similar to hypothetical pro	1.7
126905	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	1.7
130820	AL353934	Hs.288798	hypothetical protein FLJ21012	1.7
112394	AK000373	Hs.8358	hypothetical protein FLJ20366	1.7
129589	AW504292	Hs.11517	ESTs	1.7
126446	NM_015670	Hs.118926	sentrin/SUMO-specific protease 3	1.7
126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	1.7
120287	AF219946	Hs.102237	tubby super-family protein	1.7
129991	R26386	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7
123912	AA621283	Hs.332855	EST	1.7
102071	AL120051	Hs.144700	ephrin-B1	1.7
121046	AB033083	Hs.97377	KIAA1257 protein	1.7
128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.7
104268	AL043864	Hs.70604	ATPase, Class II, type 9A	1.7
111598	R11505	Hs.268912	ESTs	1.7
128109	AW269421	Hs.128093	ESTs	1.7
125435	R08480	Hs.272138	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.7
133104	AI091195	Hs.65029	growth arrest-specific 1	1.7

	126826	AA099764		gb:zn61f12.r1 Stratagene muscle 937209 H	1.7
	106483	NM_006548	Hs.30299	IGF-II mRNA-binding protein 2	1.7
	129765	M86933	Hs.1238	amelogenin (Y chromosome)	1.7
	115904	AI167560	Hs.61297	ESTs	1.7
5	125514	AB040912	Hs.191098	hypothetical protein FLJ11598	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	133179	U81599	Hs.66731	homeo box B13	1.7
	115167	AA749209	Hs.43728	hypothetical protein	1.7
	118036	AI471862	Hs.196006	Homo sapiens cDNA FLJ11723 fis, clone HE	1.7
10	124540	N63232		gb:yz39a12.s1 Morton Fetal Cochlea Homo	1.7
	126183	BE018708	Hs.81972	SHC (Src homology 2 domain-containing) t	1.7
	127897	AA773681		gb:af77b12.r1 Soares_NhHMPu_S1 Homo sapi	1.7
	126680	F07097	Hs.133865	transmembrane 6 superfamily member 1	1.7
	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.7
15	130605	BE514362	Hs.306024	FK506-binding protein 3 (25kD)	1.7
	127541	AA573449	Hs.171515	ESTs	1.7
	127392	AI816736	Hs.14896	DHHC1 protein	1.7
	106879	AI190765	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	1.7
	128303	AI096444	Hs.7187	hypothetical protein FLJ10707	1.7
20	126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.7
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	1.7
	132332	AW978906	Hs.45005	hypothetical protein FLJ12960	1.6
	127142	AW452942	Hs.130393	ESTs	1.6
	128416	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.6
25	103790	AL122044	Hs.331633	hypothetical protein DKFZp566N034	1.6
	134578	AL110193	Hs.224137	hypothetical protein	1.6
	110023	AW294701	Hs.31040	ESTs	1.6
	125511	AJ271379	Hs.76194	ribosomal protein S5	1.6
	111483	R06569	Hs.269534	ESTs	1.6
30	127363	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	1.6
	126231	AA991766	Hs.300793	ESTs	1.6
	106181	AI803651	Hs.191608	ESTs	1.6
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	1.6
	119929	W86464	Hs.304825	ESTs	1.6
35	132542	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.6
	127155	AA284993		gb:zt23e10.r1 Soares ovary tumor NbHOT H	1.6
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.6
	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.6
	131330	D13969	Hs.184669	zinc finger protein 144 (Mel-18)	1.6
40	129445	W52452	Hs.29797	ribosomal protein L10	1.6
	113427	T85105	Hs.15471	ESTs	1.6
	106124	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	1.6
	128135	AA954381	Hs.269721	ESTs, Moderately similar to ALU1_HUMAN	1.6
	111460	R02728	Hs.117331	ESTs	1.6
45	125636	H12382	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	1.6
	134118	BE336680	Hs.182877	KIAA0116 protein	1.6
	111570	AF059203	Hs.20580	sterol O-acyltransferase 2	1.6
	113511	T89578	Hs.189740	ESTs	1.6
	113296	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	1.6
50	109875	H03260	Hs.30385	ESTs	1.6
	105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.6
	105564	BE616694	Hs.288042	hypothetical protein FLJ14299	1.6
	128063	AI377750	Hs.167177	ESTs	1.6
	109779	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	1.6
55	125334	T86569	Hs.182118	ESTs	1.6
	127206	AW816490	Hs.337508	ESTs	1.6
	108845	AW362901	Hs.58864	ESTs, Weakly similar to phosphatidylseri	1.6
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.6
	114062	AI560984	Hs.27283	ESTs	1.6
60	122550	AA451859	Hs.99253	ESTs	1.6
	113413	R08872	Hs.186512	ESTs	1.6
	127019	AI929355	Hs.286128	hypothetical protein FLJ23329	1.6
	106251	R12607	Hs.35101	proline-rich Gla (G-carboxyglutamic acid	1.6
	112670	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	1.6
65	114913	AI435199	Hs.58940	ESTs, Weakly similar to I38022 hypotheti	1.6
	126604	AI023299	Hs.269806	ESTs	1.6
	125324	R07785		gb:yf15c06.r1 Soares fetal liver spleen	1.6
	121438	AW445024	Hs.139389	ESTs	1.6
	127269	AI041014	Hs.220752	ESTs, Weakly similar to unnamed protein	1.6
70	126935	AI198535	Hs.89463	potassium large conductance calcium-acti	1.6
	132430	AW973652	Hs.283105	ESTs	1.6
	133541	H75334	Hs.11050	F-box only protein 9	1.6
	102612	U65402	Hs.248124	G protein-coupled receptor 31	1.6
	120228	AI192528	Hs.164537	ESTs	1.6
75	122652	AA454641		gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	103456	AA496425	Hs.9629	papillary renal cell carcinoma (transloc	1.6
	105355	AL031447	Hs.26938	Homo sapiens, clone IMAGE:4053044, mRNA,	1.6
	108043	AA042873	Hs.160412	ESTs	1.6
	128695	NM_003478	Hs.101299	cullin 5	1.6
80	127984	AA846377	Hs.193706	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.6
	124405	AA226137	Hs.25005	hypothetical protein MGC3329	1.6
	103934	BE278111	Hs.134200	DKFZP564C186 protein	1.6
	124195	H83034		gb:yq48e07.r1 Soares fetal liver spleen	1.6

	110938	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT	1.6
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.6
	121226	AA364109	Hs.177990	ESTs	1.6
	120415	AA235810		gb:zs41a03.s1 Soares_NhHMPu_S1 Homo sapi	1.6
5	123864	AA620882		gb:af95g01.s1 Soares_testis_NHT Homo sap	1.6
	125045	AI114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H	1.6
	133425	AA444390	Hs.155482	hydroxyacyl glutathione hydrolase	1.6
	126578	AF151861	Hs.107528	androgen induced protein	1.6
	102406	U43177		(NONE)	1.6
10	114126	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	1.6
	125233	W85713	Hs.110092	ESTs	1.6
	109635	F04296	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.6
	125675	BE294972	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	1.6
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	1.6
15	127569	AI765107	Hs.274422	hypothetical protein FLJ20550	1.6
	113302	T66919	Hs.268575	ESTs	1.6
	119705	AI984203	Hs.57874	ESTs	1.6
	127226	AL036559	Hs.3463	ribosomal protein S23	1.6
	123489	AA599708		gb:ag11a10.s1 Gessler Wilms tumor Homo s	1.6
20	107468	AA740979	Hs.91389	ESTs	1.6
	115916	AI052731	Hs.91910	ESTs	1.6
	127815	AA743490	Hs.255015	ESTs	1.6
	100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.6
	125568	AW615396	Hs.105613	ESTs	1.6
25	105260	N81201	Hs.31755	ESTs	1.6
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	1.6
	111275	N70970	Hs.35006	ESTs	1.6
	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.6
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.6
30	124770	AA984414	Hs.120429	ESTs	1.6
	117936	AI382904	Hs.47213	ESTs	1.6
	134385	M14660	Hs.169274	ESTs, Highly similar to IFT2_HUMAN INTER	1.6
	108367	AW410478	Hs.104019	transforming, acidic coiled-coil contain	1.6
	131143	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	1.6
35	105441	N28522	Hs.8935	quinolinate phosphoribosyltransferase (n	1.6
	128215	AA973310		gb:op91e06.s1 Soares_NFL_T_GBC_S1 Homo s	1.6
	127344	AI003929	Hs.80624	hypothetical protein MGC2560	1.6
	126478	BE541249	Hs.109697	ESTs	1.6
	122053	AI637498	Hs.98745	ESTs	1.5
40	111760	BE551929	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	1.5
	112401	R61279	Hs.237536	ESTs, Weakly similar to AF151067 1 HSPC2	1.5
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.5
	125575	H14983		gb:ym19h09.r1 Soares infant brain 1NIB H	1.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	1.5
45	108935	AA147648	Hs.67991	hypothetical protein DKFZp434G0522	1.5
	121221	AI140708	Hs.97461	ESTs	1.5
	120091	AW024672	Hs.59558	EST	1.5
	107375	BE011845	Hs.251064	high-mobility group (nonhistone chromoso	1.5
	125803	AW876115	Hs.29852	ESTs	1.5
50	115132	AA811762	Hs.71433	ESTs	1.5
	113346	AF143876	Hs.14318	Homo sapiens clone IMAGE:113399 mRNA seq	1.5
	107357	U63973	Hs.103501	rhodopsin kinase	1.5
	125443	BE251057	Hs.177592	ribosomal protein, large, P1	1.5
	133803	M24461	Hs.76305	surfactant, pulmonary-associated protein	1.5
55	113378	T80738	Hs.14757	ESTs	1.5
	105540	BE391690	Hs.9265	hypothetical protein FLJ20917	1.5
	127446	F13008		gb:HSC3HE011 normalized infant brain cDN	1.5
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	1.5
	127585	AA604144	Hs.190632	ESTs	1.5
60	125824	Z45258	Hs.286013	short coiled-coil protein	1.5
	127606	AA621135	Hs.136552	ESTs	1.5
	125585	AW298113	Hs.92909	SON DNA binding protein	1.5
	107757	BE621721	Hs.280792	hypothetical protein FLJ12387 similar to	1.5
	109978	H09356	Hs.22528	ESTs	1.5
65	132297	BE272446	Hs.265317	hypothetical protein MGC2562	1.5
	115784	AW402151	Hs.54673	tumor necrosis factor (ligand) superfami	1.5
	127880	W39735	Hs.73818	ubiquinol-cytochrome c reductase hinge p	1.5
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.5
	102868	X02419	Hs.77274	plasminogen activator, urokinase	1.5
70	133457	J04948	Hs.333509	alkaline phosphatase, placental-like 2	1.5
	130339	AA435746		gb:zt79e03.s1 Soares_testis_NHT Homo sap	1.5
	125444	N28476	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	1.5
	123470	AW303285	Hs.303632	Human DNA sequence from clone RP11-110H4	1.5
	100025				1.5
75	127063	AI276526	Hs.331564	Homo sapiens mRNA; cDNA DKFZp434H1215 (f	1.5
	127945	AA815031	Hs.123598	ESTs	1.5
	111557	R09510	Hs.20373	EST	1.5
	116009	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	1.5
	119858	W01370	Hs.46824	ESTs	1.5
80	106509	AI042309	Hs.64552	hypothetical protein MGC15563	1.5
	124124	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HE	1.5
	126713	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	1.5
	126475	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	1.5

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	126851	R40611	Hs.137565	ESTs	1.5
	104820	AW162768	Hs.22620	ESTs	1.5
	127235	AI817309	Hs.225583	ESTs, Weakly similar to 2004399A chromos	1.5
	126552	AF168711	Hs.159397	x 010 protein	1.5
5	127523	AA617637		gb:np34h12.s1 NCI_CGAP_Lu1 Homo sapiens	1.5
	131692	BE559681	Hs.30736	KIAA0124 protein	1.5
	112974	AL353965	Hs.101174	microtubule-associated protein tau	1.5
	118921	N91914	Hs.54751	ESTs	1.5
	100676	X02761	Hs.287820	fibronectin 1	1.5
10	127721	T59578	Hs.188440	ESTs, Weakly similar to ALUF_HUMAN !!!!	1.5
	115254	AA279024	Hs.269316	ESTs, Weakly similar to S65657 alpha-1C	1.5
	128173	AI457242	Hs.127024	ESTs	1.5
	126846	AA663527	Hs.116910	ESTs	1.5
	125294	R40025	Hs.106551	ESTs	1.5
15	127494	AW978730	Hs.291956	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.5
	134191	W26632	Hs.7979	KIAA0736 gene product	1.5
	107394	AA864798	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	1.5
	131562	NM_003512	Hs.28777	H2A histone family, member L	1.5
	127310	AW450671	Hs.189284	ESTs	1.5
20	122359	AA523486		gb:ni67f11.s1 NCI_CGAP_Pr12 Homo sapiens	1.5
	100524	M80902	Hs.183704	ubiquitin C	1.5
	128422	T77794		gb:yd20d09.r1 Soares fetal liver spleen	1.5
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.5
	126784	T81887	Hs.108854	HSPC163 protein	1.5
25	123343	AI761902	Hs.99597	ESTs	1.5
	105456	AW954377	Hs.26412	ring finger protein 26	1.5
	112266	AI652534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.5
	127622	AA628222	Hs.97883	ESTs	1.5
	113659	R06545	Hs.189781	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.5
30	116892	AI573283	Hs.38458	ESTs	1.5
	126995	NM_014351	Hs.189810	sulfortranferase family 4A, member 1	1.5
	111657	R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	100243	AB028125	Hs.77854	regucalcin (senescence marker protein-30	1.5
	116153	AF107203	Hs.57937	ataxin 2-binding protein 1	1.5
35	108892	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	1.5
	113294	AI037922	Hs.11000	leptin receptor overlapping transcript-l	1.5
	126691	W03046	Hs.283664	aspartate beta-hydroxylase	1.5
	106979	AW015227	Hs.289053	hypothetical protein FLJ14733	1.5
	125546	H09950		gb:ym01d12.r1 Soares infant brain 1NIB H	1.5
40	113990	AI497945	Hs.83097	hypothetical protein FLJ22955	1.5
	129295	U63127	Hs.110121	SEC7 homolog	1.5
	125431	AW851639	Hs.75584	polymyositis/scleroderma autoantigen 2 (	1.5
	112558	AK001621	Hs.15921	hypothetical protein FLJ10759	1.5
	122046	AI560456	Hs.107319	ESTs	1.5
45	122472	AA448509	Hs.128652	ESTs	1.5
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	1.5
	131714	AA642831	Hs.31016	putative DNA binding protein	1.5
	101233	AL135173	Hs.878	sorbitol dehydrogenase	1.5
	109501	AF047437	Hs.90436	sperm associated antigen 7	1.5
50	126984	AA213820	Hs.256533	ESTs, Weakly similar to S11998 finger pr	1.5
	125765	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly	1.5
	127693	AA676727		gb:zj68b11.s1 Soares_fetal_liver_spleen_	1.5
	128453	X02761	Hs.287820	fibronectin 1	1.5
	119418	T97590	Hs.221711	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
55	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr	1.5
	116708	F10528	Hs.70001	ESTs, Moderately similar to JC6169 nucl	1.5
	122420	AA446971		gb:zw65f11.s1 Soares_total_fetus_Nb2HF8_	1.5
	100238	L24959	Hs.348	calcium/calmodulin-dependent protein kin	1.5
	109710	D20044	Hs.12929	hypothetical protein FLJ20721	1.5
60	105704	AI282341	Hs.75431	fibrinogen, gamma polypeptide	1.5
	112712	R91060	Hs.330761	ESTs	1.5
	100098	AF003743		gb:Homo sapiens delayed rectifier potass	1.5
	114122	R46128	Hs.12751	ESTs	1.5
	132397	AA021160	Hs.4750	hypothetical protein DKFZp564K0822	1.5
65	107881	AI568350	Hs.61273	hypothetical protein MGC2650	1.5
	106302	AA398859	Hs.18397	hypothetical protein FLJ23221	1.5
	125898	AK001823	Hs.92287	Homo sapiens mRNA; cDNA DKFZp564C2478 (f	1.5
	104957	AI359009	Hs.10026	mitochondrial ribosomal protein L17	1.5
	102909	NM_005269	Hs.2693	glioma-associated oncogene homolog (zinc	1.5
70	125559	BE297488	Hs.279877	cell division protein FtsJ	1.5
	109634	H17063	Hs.183646	ESTs	1.5
	116607	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.5
	127175	R11937		gb:yf54b08.r1 Soares infant brain 1NIB H	1.5
	110617	W93231	Hs.285901	Homo sapiens, clone IMAGE:3948563, mRNA,	1.5
75	125988	W27648		gb:37e10 Human retina cDNA randomly prim	1.5
	115093	AI241932	Hs.3542	hypothetical protein FLJ11273	1.5
	121207	AA705799	Hs.183714	ESTs	1.5
	112652	BE269699	Hs.235782	solute carrier family 21 (organic anion	1.5
	125213	AB014554	Hs.109299	protein tyrosine phosphatase, receptor t	1.5
80	125912	AW867467	Hs.278712	eukaryotic translation initiation factor	1.5
	133046	R96881	Hs.63609	Hpall tiny fragments locus 9C	1.5
	122791	AL122055	Hs.129836	KIAA1028 protein	1.5

Table 26B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
108451	13766_27	AA079195 AA084955 AA126308 AA084956
124195	2606_3	H83034 H52379
123619	371681_1	AA602964 AA609200
125165	1852047_1	W45350 W45406
125324	1692163_1	R07785 T85948 T86972
126053	1601236_1	H64450 H64464
126086	1606216_1	H75681 H70975
126098	1629789_1	M79088 N88221
125464	168460_1	N71807 AA203399
125499	1562851_1	H10543 R11878
126127	1205826_1	N95428 W24040 AW751366 H81987
125546	356478_1	H09950 R18413 AA570553 AW973425
125549	1702179_1	R20215 R18767
125558	1703083_1	R59305 R19748
125575	1566885_1	H14983 R21554
125743	5025_5	H17151 H11956
125761	1744008_1	R68351 R68364
126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
127155	200358_1	AA284993 AA478122 AA477923
127175	1695805_1	R11937 Z45532
126528	1276201_1	Z24895 AW891336 R01294
125957	1583542_1	H41694 H45213
125976	296453_1	AA436760 AW237453 BE327496 N47347 N56967
125982	1766315_1	R98091 W92898
125988	1365728_1	W27648 R99193 BE090398
127245	226662_1	AA323958 AA370268
127248	227560_1	AA364195 AA325029 AW962050
127262	231725_1	AA828125 AA834883 AA330555
126659	1541209_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
126693	87363_1	C05723 AA018342
127315	37938_1	AF116622 AI114507 AA640834 AA377999
126730	297653_1	AA442429 T19477
103898	187213_-3	AA248884
127446	16001_2	F13008 T75435
126826	127356_1	AA099764 AA112950
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073, BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
128132	177108_1	AA225632 AI820970 AI820952 AA226472 AI732140 AI732059 AA226307 AA225500
127523	351071_1	AA617637 AA554963
126982	171753_1	AA211419 AA211566
128215	530345_-1	AA973310
127704	405690_1	AA679609 AA694592
127705	966283_2	AJ003322 AJ003324
128422	1811283_1	T77794 T85681
127897	446527_1	AA773681 AA773857
120734	208882_1	AA299948 AA299949
100098	25117_-13	AF003743
114620	32062_8	AA642974 AA084223
122652		26401_-30 AA454641
100842		tigr_HT4398 U05597
123783		genbank_AA610112
125032		genbank_T74884
123808		genbank_AA620552
123864		genbank_AA620882
118049		genbank_N53145
102406		entrez_U43177
116962		genbank_H79677
134076	40321_1	AF086215 W02702 AA284288 W25655
125888	266863_1	H18298 H46830
127271	321389_1	H96820 H79463
113119		genbank_T47910 T47910
104799		genbank_AA029703 AA029703
127693	790317_1	AA676727 AA704704
120415		genbank_AA235810 AA235810
127964	135151_1	F06298 R18057
122359		681003_1 AA523486 AW026780 AI821660 AA443898
122420		genbank_AA446971
124276		genbank_H83465
101447		entrez_M21305
124540		genbank_N63232
124554		genbank_N65961
117357		genbank_N24829
103305		entrez_X82279

103392	entrez_X94563
119416	genbank_T97186
105225	genbank_AA211777
121292	genbank_AA401807
112853	genbank_T02843
121387	genbank_AA405854
114601	genbank_AA075566
100221	entrez_D28383
130339	genbank_AA435746
100554	tigr_HT2241
123423	genbank_AA598484
123474	genbank_AA599209
123489	genbank_AA599708

TABLE 27A: ABOUT 895 GENES UP-REGULATED IN COMBINED LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 27A lists about 895 genes that are upregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with the normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of fibrosis to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	56.0
424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone L	26.5
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	25.5
457200	U33749	Hs.197764	thyroid transcription factor 1	22.2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	21.1
429272	W25140	Hs.110667	ESTs	19.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	19.1
442006	AW975183	Hs.292663	ESTs	18.8
445885	AI734009	Hs.127699	KIAA1603 protein	18.0
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	17.8
422426	W79117	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	17.4
444929	AI685841	Hs.161354	ESTs	16.5
440807	AW269421	Hs.128093	ESTs	16.3
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	14.2
446967	AI699629	Hs.156781	ESTs	13.3
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	12.3
437119	AI379921	Hs.177043	ESTs	12.3
451103	R52804	Hs.25956	DKFZP564D206 protein	11.5
443450	N66045	Hs.133529	ESTs	11.4
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	11.3
432519	AI221311	Hs.130704	ESTs	11.3
414142	AW368397	Hs.150042	ESTs	11.0
433283	BE041135	Hs.175622	ESTs	10.1
441082	AW444804	Hs.202655	ESTs	10.1
452039	AI922988	Hs.172510	ESTs	10.0
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	9.9
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	9.8
412372	R65998	Hs.118615	ESTs	9.8
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	9.7
431007	AF039564	Hs.248211	retinoblastoma-binding protein 9	9.4
443709	AI082692	Hs.134662	ESTs	9.3
446232	AI281848	Hs.165547	ESTs	9.2
448253	H25899	Hs.201591	ESTs	9.2
432133	AB033088	Hs.272567	KIAA1262 protein	9.1
409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	9.0
431353	AA828032	Hs.189076	ESTs	8.8
450050	AI681268	Hs.257883	ESTs	8.8
458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	8.8
414968	C16096	Hs.297777	ESTs	8.7
425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.7
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	8.6
453672	U73531	Hs.34526	G protein-coupled receptor	8.5
429420	AK001679	Hs.202289	hypothetical protein FLJ10376	8.5
421478	AI683243	Hs.97258	ESTs	8.4
404916				8.4
444396	T65213	Hs.4257	ESTs	8.3
442275	AW449467	Hs.54795	ESTs	8.3
437479	R61866	Hs.101277	ESTs	8.2
432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.2
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	7.9
406747	AI925153	Hs.217493	annexin A2	7.8

445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	7.7
450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	7.6
421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	7.5
421155	H87879	Hs.102267	lysyl oxidase	7.5
446917	AI347863	Hs.156672	ESTs	7.5
422798	R92347	Hs.34574	ESTs	7.4
426830	AA385751	Hs.160392	ESTs	7.4
437157	BE048860	Hs.120655	ESTs	7.4
433231	AB040926	Hs.143552	KIAA1493 protein	7.3
451561	N52812	Hs.177403	ESTs	7.1
430656	AA482900	Hs.162080	ESTs	7.1
448206	BE622585	Hs.3731	ESTs	7.1
420209	AA256444	Hs.32295	Homo sapiens cDNA FLJ12604 fis, clone NT	7.0
426803	AA362568	Hs.179747	ecotropic viral integration site 5	6.9
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.9
409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.8
443324	R44013	Hs.164225	ESTs	6.8
431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	6.8
427356	AW023482	Hs.97849	ESTs	6.7
418735	N48769	Hs.44609	ESTs	6.7
429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	6.6
407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.6
430099	AW194988	Hs.20537	Homo sapiens cDNA FLJ13942 fis, clone Y7	6.6
441835	AB036432	Hs.184	advanced glycosylation end product-speci	6.5
428508	BE252383	Hs.184668	SBBI31 protein	6.5
438202	AW169287	Hs.22588	ESTs	6.5
441233	AA972965	Hs.135568	ESTs	6.4
433384	AI021992	Hs.124244	ESTs	6.3
427043	AA397679	Hs.298460	ESTs	6.3
425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	6.3
438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
433365	AF026944	Hs.293797	ESTs	6.3
456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.2
445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.2
431337	N48107	Hs.292593	ESTs	6.1
434819	AA650099	Hs.291541	ESTs	6.0
458219	H22195	Hs.31874	ESTs	6.0
434377	AW137148	Hs.136348	osteoblast specific factor 2 (fasciclin	5.9
435933	AA805520	Hs.192075	ESTs	5.9
436954	AA740151	Hs.130425	ESTs	5.9
445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	5.8
449108	AI140683	Hs.98328	ESTs	5.8
410334	AW979261	Hs.291993	ESTs	5.7
447112	H17800	Hs.7154	ESTs	5.7
447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serin	5.7
449208	AW263635	Hs.48643	ESTs	5.7
445657	AW612141	Hs.279575	ESTs	5.7
421554	AW137676	Hs.97775	ESTs, Weakly similar to Testis-specific	5.7
435299	AI745458	Hs.122614	ESTs, Weakly similar to apoptotic protea	5.6
416769	AI339257	Hs.115436	ESTs	5.6
433527	AW235613	Hs.133020	ESTs	5.6
452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat	5.6
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.5
411514	AW850178	Hs.18995	KIAA1304 protein	5.5
424084	AI940675	Hs.20914	Homo sapiens cDNA: FLJ23056 fis, clone L	5.5
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.4
429710	AI337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fis, clone L	5.4
432113	AA935065	Hs.152385	ESTs	5.4
447997	H00656	Hs.29792	ESTs	5.4
449328	AI962493	Hs.197647	ESTs	5.3
416575	W02414	Hs.38383	ESTs	5.3
432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	5.3
434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.3
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	5.2
414299	AA142989	Hs.71730	ESTs	5.2
431041	AA490967	Hs.105276	ESTs	5.2
448104	AI674818	Hs.178391	ribosomal protein L44	5.2
445279	R41900	Hs.22245	ESTs	5.1
408978	AL133617	Hs.49421	Homo sapiens mRNA; cDNA DKFZp434M0728 (f	5.1
415094	D59513		gb:HUM042H10B Clontech human fetal brain	5.1
428244	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.1
452784	BE463857	Hs.151258	Homo sapiens cDNA: FLJ21062 fis, clone C	5.1
455431	AW938484	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	5.1
449416	AI651016	Hs.246311	ESTs	5.1
421659	NM_014459	Hs.106511	protocadherin 17	5.1
407638	AJ404672	Hs.288693	Homo sapiens cDNA FLJ11667 fis, clone HE	5.0
446164	AW273539	Hs.199329	Homo sapiens cDNA: FLJ23577 fis, clone L	5.0
413048	M93221	Hs.75182	mannose receptor, C type 1	5.0
446608	N75217	Hs.257846	ESTs	4.9
419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	4.9
447164	AF026941	Hs.17518	Homo sapiens clg5 mRNA, partial sequence	4.9
442652	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	4.9
429496	AA453800	Hs.192793	ESTs	4.8

	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	4.8
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	4.8
	425509	AF079363	Hs.158213	sperm associated antigen 6	4.8
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.8
5	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	4.8
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.7
	453382	AA709285	Hs.5997	Homo sapiens cDNA FLJ13078 fis, clone NT	4.7
	447033	AI357412	Hs.157601	ESTs	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
10	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	4.7
	427652	AI673025	Hs.43874	ESTs	4.7
	431255	AA497043	Hs.115685	ESTs	4.7
	441143	AI027604	Hs.159650	ESTs	4.7
	452293	AI871833		gb:wm51h09.x1 NCI_CGAP_Ut2 Homo sapiens	4.7
15	443903	AI220547	Hs.135223	ESTs	4.7
	422352	AA766296	Hs.99200	ESTs	4.7
	424105	AI142336	Hs.43977	ESTs	4.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	4.6
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.6
20	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.6
	425804	BE501698	Hs.258189	ESTs	4.6
	435347	AW014873	Hs.116963	ESTs	4.6
	446002	AI346468	Hs.145789	ESTs	4.6
	452883	X80031	Hs.150318	ESTs	4.6
25	442176	AA983764	Hs.128910	ESTs	4.6
	443253	AI041212	Hs.132117	ESTs	4.5
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.5
	439920	H05430	Hs.144455	ESTs	4.5
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	4.5
30	434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone L	4.4
	408625	AW243323	Hs.266785	ESTs	4.4
	449299	AA299919		gb:EST12592 Uterus tumor I Homo sapiens	4.4
	450656	AA010539	Hs.18912	ESTs	4.4
	433815	AI696602	Hs.112757	ESTs	4.4
35	416879	H98899	Hs.42599	ESTs	4.3
	432182	AW607789	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.3
	445386	AI422005	Hs.160380	ESTs	4.3
	450478	AW451709	Hs.271200	ESTs	4.3
	453080	AI423056	Hs.23921	Homo sapiens cDNA FLJ12482 fis, clone NT	4.3
40	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	4.3
	443257	AI334040	Hs.11614	Homo sapiens cDNA: FLJ23555 fis, clone L	4.3
	453921	AI824009	Hs.44577	ESTs	4.3
	419721	NM_001650	Hs.288650	aquaporin 4	4.2
	432316	AW973235	Hs.293697	ESTs	4.2
45	435202	AI971313	Hs.170204	KIAA0551 protein	4.2
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	4.2
	438796	W67821	Hs.109590	genethonin 1	4.2
	400269				4.2
	447724	AW298375	Hs.24477	ESTs	4.1
50	446509	AF169693	Hs.132892	protocadherin 20	4.1
	451620	AW449888	Hs.257224	ESTs	4.1
	451963	AI825440	Hs.224952	ESTs	4.1
	456408	AI288348	Hs.23450	mRNA for FLJ00023 protein	4.1
	425895	AI269484	Hs.161427	zinc finger protein 215	4.1
55	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	4.1
	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	4.0
	415929	AA724373	Hs.295306	ESTs, Highly similar to unnamed protein	4.0
	426625	T78300	Hs.171409	serologically defined colon cancer antig	4.0
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	4.0
60	437138	AI935622	Hs.271245	ESTs	4.0
	455024	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo	4.0
	436246	AW450963	Hs.119991	ESTs	4.0
	416030	H15261	Hs.21948	ESTs	4.0
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	3.9
65	445122	AW241632	Hs.147377	Homo sapiens cDNA: FLJ23598 fis, clone L	3.9
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.9
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	3.9
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.9
	429208	AA447990	Hs.190478	ESTs	3.9
70	442957	AI949952	Hs.49397	ESTs	3.9
	444050	AW138295	Hs.135024	ESTs	3.9
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.9
	451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_	3.9
	442832	AW206560	Hs.253569	ESTs	3.9
75	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	3.9
	451895	T93573	Hs.16970	ESTs	3.9
	442353	BE379594	Hs.49136	ESTs	3.8
	421464	AA291553	Hs.190086	ESTs	3.8
	404043				3.8
80	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	3.8
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	3.8
	410247	AF181721	Hs.61345	RU2S	3.8
	417461	R38403	Hs.13305	ESTs	3.8

	423609	AA328348	Hs.218289	ESTs	3.8
	440444	AA885221	Hs.156984	ESTs	3.8
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT	3.8
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	3.8
5	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	3.8
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	3.8
	444271	AW452569	Hs.149804	ESTs	3.8
	434217	AW014795	Hs.23349	ESTs	3.8
	452571	W31518	Hs.34665	ESTs	3.7
10	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	3.7
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.7
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	3.7
	445034	AW293376	Hs.160323	ESTs	3.7
	438842	AA827176	Hs.124316	ESTs	3.7
15	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	415025	AW207091	Hs.72307	ESTs	3.7
	420313	AB023230	Hs.96427	KIAA1013 protein	3.7
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.7
	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.7
20	434636	AA083764	Hs.241334	ESTs	3.7
	435747	AI079519	Hs.134398	ESTs	3.7
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.sa	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	410060	NM_001448	Hs.58367	glypican 4	3.7
25	426116	AA868729	Hs.144694	ESTs	3.7
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	3.7
	414259	W44633	Hs.25044	Homo sapiens cDNA: FLJ23131 fis, clone L	3.7
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.6
	431889	AA521277	Hs.124946	ESTs	3.6
30	430414	AW365665	Hs.120388	ESTs	3.6
	433426	H69125	Hs.133525	ESTs	3.6
	421764	AI681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN CALCI	3.6
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	3.6
	455235	AW875951		gb:CM1-PT0013-131299-067-f09 PT0013 Homo	3.6
35	408399	NM_005426	Hs.44585	tumor protein p53-binding protein, 2	3.6
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	3.6
	432837	AA310693	Hs.279512	HSPC072 protein	3.6
40	452166	AI948607	Hs.264680	ESTs	3.5
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234 Homo	3.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	3.5
	424202	BE350295	Hs.15032	ESTs, Weakly similar to RAN binding prot	3.5
	410658	AW105231	Hs.192035	ESTs	3.5
45	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	419503	AA243642	Hs.137422	ESTs	3.5
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.5
	424268	AA397653	Hs.144339	Human DNA sequence from clone 495O10 on	3.5
50	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.5
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.5
	428927	AA441837	Hs.90250	ESTs	3.5
	422544	AB018259	Hs.118140	KIAA0716 gene product	3.4
	431207	AA495925	Hs.9394	ESTs	3.4
55	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	3.4
	441484	AA935481	Hs.58972	ESTs	3.4
	425916	NM_006786	Hs.162200	urotensin 2	3.4
	401793				3.4
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.4
60	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	3.4
	439619	AW975998	Hs.58595	ESTs	3.4
	446577	AB040933	Hs.15420	KIAA1500 protein	3.4
	450445	AW974636	Hs.194563	ESTs	3.4
	459482	AA625339	Hs.237052	EST, Weakly similar to ALU1_HUMAN ALU SU	3.4
65	445495	BE622641	Hs.38489	ESTs	3.4
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.4
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.4
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	3.3
	419235	AW470411	Hs.288433	neurotrimin	3.3
70	429703	T93154	Hs.28705	ESTs	3.3
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.3
	406182				3.3
	417307	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	3.3
	430140	AW296771	Hs.221999	ESTs	3.3
75	436111	AI803082	Hs.157212	ESTs	3.3
	449729	R72032	Hs.29235	ESTs	3.3
	457620	AA602711		gb:np03h06.s1 NCI_CGAP_Pr2 Homo sapiens	3.3
	428434	AW363590	Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	3.3
	406554				3.3
80	451381	BE241831		gb:TCAAP2E0011 Pediatric acute myelogeno	3.3
	443113	AI040686	Hs.132908	ESTs	3.3
	421470	R27496	Hs.1378	annexin A3	3.3
	446428	AW082270	Hs.210617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3

	435031	AI632091	Hs.116877	ESTs	3.3
	413136	BE066941		gb:PM0-BT0340-091299-002-a11 BT0340 Homo	3.2
	429228	AI553633	Hs.104985	ESTs	3.2
	420252	AW270404	Hs.193161	ESTs	3.2
5	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.2
	444339	T96555	Hs.31562	ESTs	3.2
	434164	AW207019	Hs.148135	ESTs	3.2
	404599				3.2
	426920	AA393351	Hs.132121	ESTs	3.2
10	453736	AL118674	Hs.34871	KIAA0569 gene product	3.2
	408923	H73881	Hs.255436	ESTs	3.2
	430919	AA489041	Hs.295448	ESTs	3.2
	431622	AW979271	Hs.293184	ESTs	3.2
	433584	AW295399		gb:UI-H-BI2-ahv-h-03-0-UI.s1 NCI_CGAP_Su	3.2
15	437073	AI885608	Hs.94122	ESTs	3.2
	438394	BE379623	Hs.27693	CGI-124 protein	3.2
	446242	N66336	Hs.7360	ESTs	3.2
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	3.2
	454009	AW015927	Hs.233071	ESTs	3.2
20	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN AL	3.2
	415652	T79213	Hs.272073	ESTs	3.2
	453931	AL121278	Hs.25144	ESTs	3.2
	439382	BE247684	Hs.103070	ESTs	3.2
	420077	AW512260	Hs.87767	ESTs	3.2
25	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.2
	446745	AW118189	Hs.156400	ESTs	3.1
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	3.1
	450320	AW291775	Hs.213793	ESTs	3.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.1
30	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
	451110	AI955040	Hs.301584	ESTs	3.1
	431745	AW972448	Hs.163425	ESTs	3.1
	410781	AI375672	Hs.165028	ESTs	3.1
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
35	444330	AI597655	Hs.49265	ESTs	3.1
	408761	AA057264	Hs.238936	ESTs	3.1
	409026	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	3.1
	432055	AW972359	Hs.293334	ESTs	3.1
	432441	AW292425	Hs.163484	ESTs	3.1
40	408045	AW138959	Hs.245123	ESTs	3.1
	427191	BE221825	Hs.97691	ESTs	3.1
	416965	N26223	Hs.160436	ESTs	3.1
	441594	AL041080	Hs.208765	ESTs	3.1
	406992	S82472		gb:beta -pol=DNA polymerase beta {exon a	3.0
45	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.0
	438323	AI985394	Hs.123369	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	424296	AI631874	Hs.169391	ESTs	3.0
	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.0
50	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.0
	417991	AA731452	Hs.190008	ESTs	3.0
	422589	AA312735	Hs.179725	ESTs	3.0
	437583	AA761190	Hs.244627	ESTs	3.0
	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.0
55	449494	AW237014	Hs.288650	aquaporin 4	3.0
	444188	AI393165	Hs.19175	ESTs	3.0
	400297	AI127076	Hs.288381	hypothetical protein DKFZp564O1278	3.0
	410811	AW805687	Hs.300648	ESTs	3.0
	450584	AA040403	Hs.60371	ESTs	3.0
60	428043	T92248	Hs.2240	uteroglobin	3.0
	436120	AI248193	Hs.119860	ESTs	3.0
	442324	R63578	Hs.28426	ESTs	2.9
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	2.9
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.9
65	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	2.9
	408427	AW194270	Hs.177236	ESTs	2.9
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to U4/U6 small nucl	2.9
	408938	AA059013	Hs.22607	ESTs	2.9
70	419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	2.9
	422022	AA302420	Hs.200442	ESTs	2.9
	426890	AA393167	Hs.41294	ESTs	2.9
	427374	AI150033	Hs.143686	ESTs	2.9
	434208	T92641	Hs.127648	hypothetical protein PRO2176	2.9
75	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	2.9
	451229	AW967707	Hs.48473	ESTs	2.9
	415511	AI732617	Hs.182362	ESTs	2.9
	408776	AA057365	Hs.63356	ESTs	2.9
	421110	AJ250717	Hs.1355	cathepsin E	2.9
80	453636	R67837	Hs.169872	ESTs	2.9
	436578	AI091435	Hs.134859	ESTs	2.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to dJ202I21.4 [H.sa	2.8

	408171	AA301228	Hs.43299	Homo sapiens cDNA FLJ12890 fis, clone NT	2.8
	445189	AI936450	Hs.147462	ESTs	2.8
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.8
	427457	AW779105	Hs.164682	ESTs, Weakly similar to ORF2 consensus s	2.8
5	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	2.8
	446932	AA961459	Hs.125644	ESTs	2.8
	439140	W85737	Hs.290830	ESTs	2.8
	405041				2.8
	421306	AA806207	Hs.125889	ESTs	2.8
10	427514	AA640773	Hs.209224	ESTs	2.8
	427939	T92459	Hs.16886	ESTs	2.8
	429127	AA749382	Hs.107233	ESTs	2.8
	429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	2.8
	433163	R40468	Hs.163582	ESTs	2.8
15	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone H	2.8
	448015	AI458065	Hs.23196	ESTs	2.8
	456761	D59899	Hs.127842	CGI-142	2.8
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	2.8
20	447020	T27308	Hs.16986	hypothetical protein FLJ11046	2.8
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.8
	433515	AA595800	Hs.190246	ESTs	2.8
	424450	AL137526	Hs.147472	dynein intermediate chain 2	2.8
	438122	AI620270	Hs.129837	ESTs	2.8
25	424086	AI351010	Hs.102267	lysyl oxidase	2.8
	438885	AI886558	Hs.184987	ESTs	2.8
	412903	BE007967	Hs.155795	ESTs	2.8
	454111	AW081681	Hs.269064	ESTs	2.8
	439398	AA284267	Hs.221504	ESTs	2.8
30	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	2.8
	434812	AA649860	Hs.189496	ESTs	2.8
	432583	AW023624	Hs.162282	ESTs	2.8
	428104	AA421350	Hs.191604	ESTs	2.8
	408217	AI433201	Hs.279860	hypothetical protein FLJ20030	2.8
35	438016	AI949638	Hs.109150	SH3-domain binding protein 5 (BTK-associ	2.8
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	2.7
	430887	N66801	Hs.260287	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	416185	AW975861	Hs.291995	ESTs	2.7
40	408613	AW242086	Hs.253967	ESTs	2.7
	442510	AF150179	Hs.249890	ESTs	2.7
	433293	AF007835	Hs.32417	ESTs	2.7
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.7
	404488				2.7
45	408936	AL138043	Hs.293549	ESTs	2.7
	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, clone C	2.7
	436738	AW102613	Hs.152913	ESTs	2.7
	451797	AW663858	Hs.56120	ESTs	2.7
	452163	AI863140		gb:tz43h12.x1 NCI_CGAP_Brn52 Homo sapien	2.7
50	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.7
	459366	AA129703		gb:zn92b05.r1 Stratagene lung carcinoma	2.7
	431448	AL137517	Hs.288381	hypothetical protein DKFZp564O1278	2.7
	430733	AW975920	Hs.283361	ESTs	2.7
	453652	AW009640	Hs.28368	ESTs	2.7
55	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	2.7
	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	2.7
	408729	AA195764	Hs.72639	ESTs	2.7
	450726	AW204600	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.7
	447720	AL038765	Hs.161304	ESTs	2.7
60	451497	H83294	Hs.284122	Wnt inhibitory factor-1	2.7
	442074	C17511	Hs.128430	ESTs	2.7
	424115	AA335497	Hs.293965	ESTs	2.7
	417728	AW138437	Hs.24790	KIAA1573 protein	2.7
	433803	AI823593	Hs.27688	ESTs	2.7
65	419247	S65791	Hs.89764	fragile X mental retardation 1	2.7
	424310	AA338648	Hs.50334	ESTs	2.6
	438504	AW665281	Hs.224625	ESTs	2.6
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	2.6
	430417	AA461045	Hs.50701	ESTs	2.6
70	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	422505	AL120862	Hs.124165	ESTs	2.6
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-typ	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
75	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.6
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.6
	403903				2.6
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.6
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	2.6
80	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.6
	436645	AW023424	Hs.156520	ESTs	2.6
	408380	AF123050	Hs.44532	diubiquitin	2.6
	402629				2.6

	406594				2.6
	415122	D60708	Hs.22245	ESTs	2.6
	416747	AW876523	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT	2.6
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
5	444361	W76027	Hs.23920	Homo sapiens cDNA FLJ13124 fis, clone NT	2.6
	446609	BE395090	Hs.15535	Human gene from PAC 886K2, chromosome 1	2.6
	449260	AA741180	Hs.29879	ESTs	2.6
	452311	AW304029	Hs.252744	ESTs	2.6
	413802	AW964490	Hs.32241	ESTs	2.6
10	417318	AW953937	Hs.12891	ESTs	2.6
	440028	AW473675	Hs.125843	ESTs	2.6
	437960	AI669586	Hs.222194	ESTs	2.6
	433687	AA743991		gb:ny57g01.s1 NCI_CGAP_Pr18 Homo sapiens	2.6
	430573	AA744550	Hs.136345	ESTs	2.6
15	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.6
	453204	R10799	Hs.191990	ESTs	2.6
	436751	AA732217	Hs.294054	ESTs	2.6
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	2.6
	431120	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens	2.5
20	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	2.5
	438458	AW975186	Hs.162875	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	446063	AI720140	Hs.151079	ESTs	2.5
	430499	AW969408	Hs.231991	ESTs	2.5
	450496	AW449251	Hs.257131	ESTs	2.5
25	441330	AI692984	Hs.129354	ESTs	2.5
	424433	H04607	Hs.9218	ESTs	2.5
	434677	AW444575	Hs.130834	ESTs	2.5
	445779	AI253104	Hs.189267	ESTs	2.5
	444649	AW207523	Hs.197628	ESTs	2.5
30	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	2.5
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.5
	404288				2.5
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	2.5
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
35	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	2.5
	410095	AW589638	Hs.258947	ESTs	2.5
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	2.5
	418343	AA216372	Hs.159501	ESTs	2.5
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.5
40	428637	AW979268		gb:EST391378 MAGE resequences, MAGP Homo	2.5
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	2.5
	432507	BE391093		gb:601286042F1 NIH_MGC_44 Homo sapiens c	2.5
	433858	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT	2.5
	438651	H64500	Hs.123646	ESTs	2.5
45	443830	AI142095	Hs.143273	ESTs	2.5
	446800	AI341635	Hs.156486	ESTs	2.5
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN A	2.5
	451343	AW975057	Hs.293353	ESTs	2.5
	451539	AA059467	Hs.218933	ESTs	2.5
50	452412	AA029608	Hs.61373	ESTs	2.5
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	2.5
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.5
	424943	AU077260	Hs.153924	death-associated protein kinase 1	2.5
	440106	AA864968	Hs.127699	KIAA1603 protein	2.5
55	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	2.5
	415261	T40928	Hs.8346	ESTs	2.5
	420026	AI831190	Hs.166676	ESTs	2.5
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	2.5
	458722	AA741545	Hs.282832	ESTs	2.5
60	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	2.5
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.5
	433644	AW342028	Hs.256112	ESTs	2.5
	419172	AW338625	Hs.22120	ESTs	2.5
	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	2.5
65	443348	AW873596	Hs.57572	ESTs	2.5
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.5
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.5
	448030	N30714	Hs.20161	HDCME31P protein	2.5
	417203	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	2.5
70	449275	AW450848	Hs.205457	KIAA1620 protein	2.4
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.4
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	2.4
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.4
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
75	453142	AA033648	Hs.7473	ESTs	2.4
	425657	T89839	Hs.119471	ESTs	2.4
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone H	2.4
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	2.4
	458332	AI000341	Hs.220491	ESTs	2.4
80	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.4
	459644				2.4
	429125	AA446854	Hs.271004	ESTs	2.4
	448337	AW205453	Hs.3782	ESTs	2.4

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	427778	AA412323	Hs.105323	ESTs	2.4
	425371	D49441	Hs.155981	mesothelin	2.4
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.4
	447610	AW296286	Hs.255534	ESTs	2.4
5	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.4
	440817	AI341423	Hs.270165	ESTs	2.4
	420020	BE295866	Hs.94382	adenosine kinase	2.4
	435395	AA729235	Hs.117907	ESTs	2.4
10	424144	AA454033	Hs.41644	Homo sapiens cDNA: FLJ23003 fis, clone L	2.4
	405494				2.4
	458145	AI239457	Hs.130794	ESTs	2.4
	408547	AA574291	Hs.57837	ESTs	2.4
	408941	AI452469	Hs.165221	ESTs	2.4
15	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276 Homo	2.4
	417137	U46265	Hs.81281	hypothetical protein	2.4
	418950	T78517	Hs.13941	ESTs	2.4
	420756	AA411800	Hs.189900	ESTs	2.4
	428316	AI860775	Hs.98506	ESTs	2.4
20	432896	NM_014097	Hs.279778	PRO1693 protein	2.4
	436148	BE005252		gb:CM1-BN0116-030400-171-g02 BN0116 Homo	2.4
	436284	AA708016	Hs.190389	ESTs	2.4
	437327	AL353942		gb:Homo sapiens mRNA; cDNA DKFZp761L2312	2.4
	442611	BE077155	Hs.177537	ESTs	2.4
25	456062	AI866286	Hs.71962	ESTs	2.4
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.4
	401335				2.4
	428771	AB028992	Hs.193143	KIAA1069 protein	2.4
	419140	AI982647	Hs.215725	ESTs	2.4
30	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	2.4
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.4
	407339	AA777542	Hs.132670	ESTs	2.4
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	2.4
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	2.4
35	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.4
	452561	AI692181	Hs.49169	KIAA1634 protein	2.4
	427878	C05766	Hs.181022	CGI-07 protein	2.4
	419752	AA249573	Hs.152618	ESTs	2.4
	430073	U86136	Hs.232070	telomerase-associated protein 1	2.4
40	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	2.4
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.3
	407905	AW103655	Hs.252905	ESTs	2.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.3
	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3 (G	2.3
45	453049	BE537217	Hs.30343	ESTs	2.3
	438568	R98865	Hs.11135	major histocompatibility complex, class	2.3
	453445	AL036532	Hs.91453	ESTs	2.3
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.3
	446346	AI290205		gb:qi79g06.x1 Soares_NhHMPu_S1 Homo sapi	2.3
50	441974	AI683782	Hs.128245	ESTs	2.3
	444805	AB007899	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	2.3
	424027	AW337575	Hs.201591	ESTs	2.3
	419606	AW294795	Hs.198529	ESTs, Weakly similar to similar to acyl-	2.3
	428613	AB037749	Hs.186928	KIAA1328 protein	2.3
55	434340	AI193043	Hs.128685	ESTs	2.3
	450297	AW901347	Hs.38592	Homo sapiens cDNA: FLJ23342 fis, clone H	2.3
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.3
	433650	AA603472	Hs.28456	ESTs	2.3
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	2.3
60	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PL	2.3
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo	2.3
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.3
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	2.3
	400610				2.3
65	402222				2.3
	407162	N63855	Hs.142634	zinc finger protein	2.3
	415250	F02614	Hs.27319	ESTs	2.3
	421751	AW813731	Hs.159153	ESTs	2.3
	428552	AW274560	Hs.129520	ESTs	2.3
70	432658	AW973769	Hs.162319	ESTs	2.3
	434742	AA648302	Hs.291695	ESTs	2.3
	436586	AI308862	Hs.167028	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicu	2.3
75	443160	AI467915	Hs.36053	ESTs	2.3
	448764	AI568607	Hs.182112	ESTs	2.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	2.3
	439810	AL109710	Hs.85568	EST	2.3
	413714	AI560944	Hs.71428	ESTs	2.3
80	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	2.3
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	2.3
	438670	AI275803	Hs.123428	ESTs	2.3
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.3

	459702				2.3
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	2.3
	438474	AW865818	Hs.6232	KIAA0764 gene product	2.3
	453037	AA045175	Hs.177552	ESTs	2.3
5	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	2.3
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	2.3
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	2.3
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.3
10	406506				2.3
	448330	AL036449	Hs.207163	ESTs	2.3
	409719	AI769160	Hs.108681	ESTs	2.3
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.3
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.3
15	427961	AW293165	Hs.143134	ESTs	2.3
	447357	AI375922	Hs.159367	ESTs	2.3
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	2.3
	453715	AA037675	Hs.152675	ESTs	2.3
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
20	407949	W21874	Hs.247057	ESTs	2.2
	427972	AA864870	Hs.181304	putative gene product	2.2
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, clone H	2.2
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	2.2
	424238	AA337401	Hs.137635	ESTs	2.2
25	452930	AW195285	Hs.194097	ESTs	2.2
	424527	AW138558	Hs.267158	ESTs	2.2
	453095	AW295660	Hs.252756	ESTs	2.2
	449161	N53431	Hs.47647	ESTs, Weakly similar to KIAA0423 [H.sapi	2.2
	429586	T73510	Hs.209153	angiopoietin-like 3	2.2
30	423782	AI472209	Hs.288369	ESTs	2.2
	458124	AW005548	Hs.124590	ESTs	2.2
	450109	AI539295	Hs.17967	ESTs	2.2
	421461	AW291023	Hs.97255	ESTs	2.2
	412222	AA528283	Hs.292737	ESTs	2.2
35	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	441736	AW292779	Hs.169799	ESTs	2.2
	401049				2.2
	440727	AI073991	Hs.134268	ESTs	2.2
	419751	AW195581	Hs.93121	KIAA0761 protein	2.2
40	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.2
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.2
	410292	AA843087	Hs.124194	ESTs	2.2
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	2.2
45	449695	AA164569	Hs.34550	ESTs	2.2
	429399	AA452244	Hs.16727	ESTs	2.2
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.2
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.2
	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	2.2
50	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.2
	445268	AI218358	Hs.175048	ESTs	2.2
	402481				2.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.2
	416521	H60929	Hs.44197	hypothetical protein DKFZp564D0462	2.2
55	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
	421211	AA284966	Hs.266308	ESTs, Weakly similar to AF216312 1 type	2.2
	427541	AI798983	Hs.97961	ESTs	2.2
	432013	AI796879	Hs.162102	ESTs	2.2
60	436461	AW511956	Hs.293261	ESTs	2.2
	438002	AI560246	Hs.201648	ESTs, Weakly similar to ZN42_HUMAN ZINC	2.2
	440312	AW614597	Hs.72475	ESTs	2.2
	440479	AA886461	Hs.208161	ESTs	2.2
	441178	W90789	Hs.153976	ESTs	2.2
65	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.2
	443314	AW771701	Hs.54646	ESTs	2.2
	422165	AL041199	Hs.1481	histidine decarboxylase	2.2
	450696	AI654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	2.2
	432974	BE348793		gb:ht70g02.x1 NCI_CGAP_Lu24 Homo sapiens	2.2
70	404200				2.2
	435990	AI015862	Hs.131793	ESTs	2.2
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.2
	416642	T96118	Hs.226313	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
75	406672	M26041	Hs.198253	major histocompatibility complex, class	2.2
	417819	AI253112	Hs.133540	ESTs	2.2
	417355	D13168	Hs.82002	endothelin receptor type B	2.2
	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.2
	404274				2.2
80	415086	AI597963	Hs.118726	ESTs	2.2
	418210	R54575	Hs.13337	ESTs, Weakly similar to unnamed protein	2.2
	419220	AA811938	Hs.291759	ESTs	2.2
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.2

	451050	AW937420	Hs.69662	ESTs	2.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	2.2
	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.2
	412925	AI089319	Hs.179243	ESTs	2.2
5	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.2
	410976	R36207	Hs.25092	ESTs	2.2
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.2
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.2
	449321	AA001150	Hs.132937	ESTs	2.2
10	418557	BE140602	Hs.246645	ESTs	2.2
	416320	H47867	Hs.34024	ESTs	2.2
	426384	AI472078		gb:tj85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.2
	414140	AA281279	Hs.23317	ESTs	2.2
	419520	AB009303	Hs.297790	Human clone 23734 mRNA sequence	2.2
15	446999	AA151520	Hs.279525	hypothetical protein PRO2605	2.2
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	2.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.1
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	2.1
	410048	W76467	Hs.274550	proline oxidase homolog	2.1
20	400880				2.1
	418092	R45154	Hs.106604	ESTs	2.1
	428780	AI478578	Hs.50636	ESTs	2.1
	431067	AW574823	Hs.200413	ESTs	2.1
	432803	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	2.1
25	412104	AW205197	Hs.240951	ESTs	2.1
	422819	AL122084	Hs.121073	hypothetical protein FLJ10466	2.1
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	2.1
	424806	AA382523	Hs.105689	ESTs	2.1
	434445	AI349306	Hs.11782	ESTs	2.1
30	442994	AI026718	Hs.16954	ESTs	2.1
	410371	AA084482	Hs.115850	ESTs	2.1
	450232	BE300815	Hs.201326	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	2.1
	430899	BE018217	Hs.183528	ESTs, Weakly similar to Bem46-like prote	2.1
35	431814	BE256242	Hs.270847	delta-tubulin	2.1
	417543	AA203620	Hs.110153	ESTs, Weakly similar to BCGF_HUMAN B-CEL	2.1
	444542	AI161293	Hs.146862	ESTs, Weakly similar to KIAA0525 protein	2.1
	404593				2.1
	434803	AW974640		gb:EST386744 MAGE resequences, MAGM Homo	2.1
40	451623	H77818	Hs.268991	ESTs	2.1
	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on	2.1
	402046				2.1
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.1
	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	2.1
45	401987				2.1
	423119	AA322201	Hs.131976	EST	2.1
	427112	Z32887	Hs.290951	ESTs	2.1
	414464	AI870175	Hs.13957	ESTs	2.1
	447829	AI433029	Hs.164104	ESTs	2.1
50	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	2.1
	405472				2.1
	413621	AI808648	Hs.184156	ESTs	2.1
	432212	AW137742	Hs.293451	ESTs	2.1
	404289				2.1
55	415362	F06735		gb:HSC1JB091 normalized infant brain cDN	2.1
	427739	AW196755	Hs.98105	ESTs	2.1
	427772	AA412289	Hs.98123	ESTs	2.1
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.1
	434335	AA630107	Hs.213220	ESTs	2.1
60	436052	AI021983	Hs.271432	ESTs	2.1
	442773	AB037722	Hs.8707	Homo sapiens mRNA; cDNA DKFZp434N1131 (f	2.1
	446799	AW976373	Hs.49221	ESTs, Weakly similar to zinc finger prot	2.1
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.1
	455673	BE065939		gb:RC3-BT0319-100100-012-c11 BT0319 Homo	2.1
65	458624	AI362790	Hs.181801	ESTs	2.1
	405095				2.1
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	2.1
	433589	AA886530	Hs.188912	ESTs	2.1
	438398	AA806526	Hs.130277	ESTs	2.1
70	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 fis, clone H	2.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.1
	431087	H12723	Hs.290791	ESTs	2.1
	409064	AA062954	Hs.141883	ESTs	2.1
	427558	D49493	Hs.2171	growth differentiation factor 10	2.1
75	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	2.1
	438118	AW753311	Hs.259415	ESTs	2.1
	427621	BE621182	Hs.179882	Homo sapiens cDNA FLJ12437 fis, clone NT	2.1
	452114	N22687	Hs.8236	ESTs	2.1
	448782	AL050295	Hs.301550	KIAA0758 protein	2.1
80	403937				2.1
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	2.1
	452416	AA026115	Hs.114777	ESTs	2.1
	451609	AL046019	Hs.209276	ESTs	2.1

	435934	R19382	Hs.117869	ESTs	2.1
	445158	AI992108	Hs.127206	ESTs	2.1
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.1
	439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen	2.1
5	443949	AW827419	Hs.235070	ESTs	2.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.1
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.1
	438676	AA813745	Hs.123446	ESTs	2.1
	405848				2.1
10	416940	N75620	Hs.43157	ESTs	2.1
	442381	AI185136	Hs.48650	ESTs	2.1
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	2.1
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	2.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.1
15	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.1
	439425	AF086244	Hs.114659	ESTs	2.1
	421168	AF182277	Hs.1360	cytochrome P450, subfamily IIB (phenobar	2.1
	449611	AI970394	Hs.197075	ESTs	2.1
	404548				2.1
20	416734	H81213	Hs.14825	ESTs	2.1
	435865	AA883552	Hs.16810	ESTs	2.1
	439072	AF085930	Hs.269123	ESTs	2.1
	447482	AB033059	Hs.18705	KIAA1233 protein	2.1
	457292	AI921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	2.1
25	444974	AI203500	Hs.151612	ESTs	2.1
	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.1
	430634	AI860651	Hs.26685	ESTs	2.1
	426782	R14614	Hs.191254	ESTs	2.0
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.0
30	445326	AI220072	Hs.165893	ESTs	2.0
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.0
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.0
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.0
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.0
35	417321	N68722	Hs.191368	ESTs	2.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.0
	404323				2.0
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
	421047	AW514772	Hs.104473	ESTs	2.0
40	425497	AA524596	Hs.188844	ESTs	2.0
	444623	AI183829	Hs.202111	ESTs	2.0
	412303	AW936336		gb:QV4-DT0021-2B1299-070-g11 DT0021 Homo	2.0
	433563	AI732637	Hs.277901	ESTs	2.0
	406485				2.0
45	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.0
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.0
	425465	L18964	Hs.1904	protein kinase C, iota	2.0
	449424	AW448937	Hs.197030	ESTs	2.0
	427940	AA417812	Hs.38775	ESTs	2.0
50	411502	AW946605	Hs.250154	Homo sapiens cDNA FLJ12973 fis, clone NT	2.0
	411365	M76477	Hs.278242	tubulin, alpha, ubiquitous	2.0
	412369	H80456	Hs.285243	Homo sapiens cDNA: FLJ22029 fis, clone H	2.0
	452959	AI933416	Hs.189674	ESTs	2.0
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.0
55	428775	AA434579	Hs.143691	ESTs	2.0
	420000	AB036063	Hs.180726	Homo sapiens cDNA FLJ13543 fis, clone PL	2.0
	408321	AW405882	Hs.44205	cortistatin	2.0
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.0
	411050	AW814902		gb:MR1-ST0206-120400-022-f08 ST0206 Homo	2.0
60	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.0
	428978	AA442784	Hs.125445	ESTs	2.0
	458562	N34128	Hs.145268	ESTs	2.0
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.0
	403760				2.0
65	424368	AB037766	Hs.146085	KIAA1345 protein	2.0
	421229	AI056590	Hs.7086	Homo sapiens cDNA: FLJ23000 fis, clone L	2.0
	436304	AA339622	Hs.108887	ESTs	2.0
	453498	BE181412	Hs.23245	Homo sapiens cDNA FLJ11767 fis, clone HE	2.0
	439018	AW300887	Hs.26638	ESTs, Weakly similar to unnamed protein	2.0
70	453280	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (fr	2.0
	420193	AI460080	Hs.202869	ESTs	2.0
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.0
	401575				2.0
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.0
75	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.0
	410763	AF279145	Hs.8966	tumor endothelial marker 8	2.0
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	2.0
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.0
	405963				2.0
80	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.0
	420831	AA280824	Hs.190035	ESTs	2.0
	424152	AL133591	Hs.301405	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.0
	424641	AB001106	Hs.151413	glia maturation factor, beta	2.0

	427616	AI698684	Hs.98028	ESTs	2.0
	435115	AI821726	Hs.116603	ESTs	2.0
	437636	AA764781	Hs.291844	ESTs	2.0
	438295	AI394151	Hs.37932	ESTs	2.0
5	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	2.0
	445388	AI925280	Hs.236842	EST	2.0
	447101	N72185	Hs.44189	ESTs	2.0
	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.0
	449623	C00719	Hs.120440	ESTs	2.0
10	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN CALPA	2.0
	456613	R19992	Hs.106620	Homo sapiens clone 23950 mRNA sequence	2.0
	457233	AI355009	Hs.221698	ESTs	2.0
	457384	AA501760	Hs.18075	chromosome 9 open reading frame 3	2.0
	457471	AW971364		gb:EST383453 MAGE resequences, MAGL Homo	2.0
15					

TABLE 27B

20	Pkey: Unique Eos probeset identifier number
	CAT number: Gene cluster number
	Accession: Genbank accession numbers

Pkey	CAT number	Accession
409457	1132521_1	AW818081 AW392887 AW514700 AW392881
409519	113722_1	AA075368 AA075369
410008	116812_1	AA079552 BE142525 BE142527
410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
411050	1230330_1	AW814902 BE156656 BE156667 BE156590 BE156441 BE156447
411880	1263110_1	AW872477 BE088101 T05990
411905	1265181_1	BE265067 BE264978 AW875420
412303	1288130_1	AW936336 AW936339
413136	1350379_1	BE066941 BE066911 BE066979 BE066929 BE066925
413499	1373910_1	BE144884 H97942
413875	1396765_1	BE176776 H85072
415094	1522103_1	D59513 D59515 D80174 D59514
415362	1534980_1	F06735 R55896 R12110 H08697
416624	1604694_1	H69044 T47567 H75691 T50292
418378	174656_1	AW962081 AA218925 AA354237
419546	185766_1	AA244199 AA244272 H57440
419807	188252_1	R77402 AA262462 AA250988 R06794
420637	195241_1	AW976153 AA278945 AA747691
422429	216469_1	AA310527 AW962295 Z44865 H06641
423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235
426384	266211_1	AI472078 AA377209 AA865807
428637	293660_1	AW979268 AA878419 AA431342 AA431628
430153	313709_1	AW968128 AA468102 AA468165
430844	324570_1	T94960 AA487679 T95013
431120	328264_1	AA492588 AA492498 AA492571
431169	328799_1	AW971240 AA493843 AA493723
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
432009	34025_1	AL137424 BE007148 T52277
432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
432507	348711_1	BE391093 AA551334 BE389643
432779	354024_1	AW979241 AA565006 AA847102
432803	354267_1	AA565398 AW894072 H97930
432869	355475_1	AW974094 AA569074 AA602574
432974	356950_1	BE348793 AA573118 N79366
433492	367934_1	AW605849 AW262898 N41060 AA594852
433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
433687	373061_1	AA743991 AA604852 AW272737
434803	393471_1	AW974640 AA649516 N75626
436148	41500_1	BE005252 AK000786
437327	43610_1	AL353942 AW994305
438909	46684_1	AF085839 R69137 AW188788 R69254
440320	491930_1	AA879294 N67538 AI474541
444314	600667_1	AI140497 AW749625 AW749626 AW749644
444610	612257_1	AI174783 R83569 R12271
446346	673545_1	AI290205 AW235762 AI651268
447197	711623_1	R36075 AI366546 R36167
448404	761515_1	BE089973 AI498612 AW805032
449299	80436_1	AA299919 AW957012 AA001107 T83631 BE156389
449540	80945_2	AA001713 H53836
449677	81270_1	AA002071 AA002232 T99209
450522	837264_1	AI698839 AI909260 AI909259
451024	85565_1	AA442176 AA259181
451381	867770_1	BE241831 AW249135 BE548847 AW250245
452163	902067_1	AI863140 W80703 R43474
452293	909195_-1	AI871833
452453	918300_1	AI902519 AI902518 AI902516
452542	921410_1	AW812256 AW812257 AI906423 AI906422
452771	930983_1	T05477 T07855 AI917711
454359	1130674_1	N71277 AW390764

454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424	
455024	1249196_1	AW851309 AW850888 AW851419 AW851412 AW851299	
455226	1262534_1	AW902103 AW869012 AW869139	
455235	1265634_1	AW875951 AW875950 AW875936 AW875948 AW875939 AW875957	
455673	1349656_1	BE065939 BE066079 BE065956	
455807	1370914_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108	
456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363	
457471	340916_1	AW971364 AA525021 AA570759	
457620	371514_1	AA602711 BE078290	
458154	491768_1	AW816379 AA888282 AA879046 AA879195	
459267	966605_1	AJ003631 AJ003650 AJ003651	

TABLE 27C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source: 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400610	9887671	Minus	117606-117928,124040-124147
400880	9931121	Plus	29235-29336,36363-36580
401049	7232177	Plus	149157-150692
401335	9884881	Plus	15736-16352
401575	7229804	Minus	76253-76364
401793	7263888	Minus	102945-103083
401987	4406829	Minus	72893-73021,76938-77049
402046	8072415	Plus	166394-166556,168167-168395
402222	9958106	Plus	3261-3834,3939-4269
402481	9797406	Plus	87891-88991
402629	9931216	Plus	33641-33775,34182-34372,36003-36084,40343-40612
403760	7712202	Minus	45910-46260,47563-47824
403903	7710671	Minus	101165-102597
403937	7711761	Minus	12609-12773
404043	9558573	Plus	29042-29135,46597-46699
404200	6010176	Minus	7066-7210
404274	9885189	Plus	104127-104318
404288	2769644	Plus	3512-3691
404289	2769644	Plus	15049-15286,30267-30457
404323	9719753	Minus	31913-32219
404488	8113286	Minus	64835-64994
404548	8570305	Minus	83896-84162
404593	9944086	Minus	74922-75788
404599	8705107	Plus	110443-110733
404916	7341826	Plus	91057-91188
405041	7547195	Plus	121230-121714
405095	8072599	Plus	138877-139066
405472	8439781	Plus	106297-106447,108462-108596
405494	8050952	Minus	70284-70518
405848	7651809	Minus	28135-28244
405963	8247786	Plus	4056-4699
406182	5923650	Minus	28256-28935
406485	7711305	Plus	125036-125422
406506	7711374	Minus	6843-8077
406554	7711566	Plus	106956-107121
406594	8248611	Minus	35543-35845

TABLE 28A: ABOUT 796 GENES DOWN-REGULATED IN LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 28A lists of about 796 genes that are downregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues sample expression was less than or equal to 0.1. The "average" normal lung tissue level was set to the 75th percentile amongst normal lung tissues. The "average" fibrosis expression level was set to the 95th percentile amongst fibrosis samples. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of normal lung to fibrosis

Pkey	ExAccn	Unigene ID	Unigene Title	R1
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	18.18
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	9.39
404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	8.30
404795				5.56

	403211				5.46
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	5.43
	400489				5.19
	425571	AJ007292	Hs.158306	ephrin-A2	5.19
5	406357				5.08
	407979	AA046306	Hs.62927	ESTs	5.08
	452378	AA025855	Hs.19597	ESTs	4.78
	408053	AW139474	Hs.246862	ESTs	4.62
	421770	AA374192	Hs.108124	ribosomal protein L41	4.52
10	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	4.49
	402386				4.39
	402448				4.37
	448245	AI923551	Hs.170843	ESTs	4.31
	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	4.29
15	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.24
	447768	X86400	Hs.19520	FXYD domain-containing ion transport reg	4.21
	405163				4.19
	437120	AI356125	Hs.157767	ESTs, Weakly similar to human HOXA2 [H.s	4.19
	409020	AA062549	Hs.21162	ESTs	4.09
20	431073	BE254470	Hs.249186	cone-rod homeobox	4.07
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	4.05
	403716				3.99
	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.94
	404348				3.90
25	407070	Y10209		gb:H.sapiens mRNA for CD30L protein	3.82
	412919	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.81
	402409				3.80
	456150	Z42308		gb:HSC0FB121 normalized infant brain cDN	3.79
	427030	AA397600	Hs.97531	ESTs	3.76
30	426328	AW631296		gb:hh83c09.y1 NCI_CGAP_GU1 Homo sapiens	3.74
	429307	AU076592	Hs.198951	jun B proto-oncogene	3.71
	400172				3.70
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	3.68
	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-r	3.68
35	446850	R71245	Hs.174303	ESTs	3.67
	405147				3.64
	406821	AA977896	Hs.128873	ESTs, Highly similar to ALFA_HUMAN FRUCT	3.57
	402762				3.55
	401496				3.50
40	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	3.50
	402911				3.49
	425330	D25216	Hs.155650	KIAA0014 gene product	3.49
	438004	AA774984	Hs.220649	ESTs, Weakly similar to FCE2 MOUSE LOW A	3.46
	448185	AI633040	Hs.172730	ESTs	3.46
45	433367	AA584930	Hs.269451	ESTs, Weakly similar to XAP-5-like prote	3.43
	416596	H67669	Hs.38564	ESTs	3.41
	400545				3.39
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB5	3.37
	426507	AA380285		gb:EST93491 Supt cells Homo sapiens cDNA	3.35
50	403479				3.34
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (iso	3.34
	401919				3.33
	449031	AI867502	Hs.271462	ESTs	3.33
	400116				3.31
55	401590				3.29
	401007				3.28
	404610	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.25
	408641	AW245207	Hs.5555	Homo sapiens cDNA FLJ13170 fis, clone NT	3.25
	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	3.23
60	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bi	3.23
	433232	AI658621	Hs.127769	ESTs	3.23
	457937	AW976930	Hs.128760	ESTs	3.23
	406101				3.18
	407080	Z38133	Hs.113973	myosin, heavy polypeptide 8, skeletal mu	3.18
65	419947	AW298744	Hs.118894	ESTs	3.16
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	3.16
	454019	D31846	Hs.37025	aquaporin 2 (collecting duct)	3.16
	428674	AA431734	Hs.104915	ESTs	3.14
	402056				3.06
70	425182	AF041259	Hs.155040	zinc finger protein 217	3.06
	425393	NM_000218	Hs.156115	potassium voltage-gated channel, KQT-lik	3.06
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.05
	402158				3.03
	404938				3.02
75	403376				3.01
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-typ	3.00
	402423				2.99
	416253	BE250659	Hs.15463	ESTs	2.99
	435265	AA779958	Hs.185932	ESTs	2.99
80	425655	BE614551	Hs.158675	ribosomal protein L14	2.98
	428704	AA432007	Hs.249484	ESTs	2.98
	425439	D38024	Hs.157425	double homeobox, 2	2.97
	445613	BE550889	Hs.158491	ESTs	2.97

	402714				2.96
	403526				2.96
	403605				2.95
	441852	AB028968	Hs.7989	KIAA1045 protein	2.95
5	417629	T76945	Hs.64211	ESTs, Weakly similar to similar to acyl-	2.94
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgra	2.91
	419821	AW967486	Hs.189119	ESTs	2.90
	446993	AI570964	Hs.164257	ESTs	2.89
	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	2.88
10	423379	AI985349	Hs.157492	Homo sapiens cDNA FLJ14079 fis, clone HE	2.88
	440206	AI762232	Hs.46794	ESTs	2.88
	402212	AW502761	Hs.30909	KIAA0430 gene product	2.87
	406059				2.86
	423548	AF007194	Hs.129782	mucin 3A, intestinal	2.86
15	402051				2.85
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	2.85
	455446	AW947749		gb:RC0-MT0005-130300-031-b01 MT0005 Homo	2.85
	442428	BE464988	Hs.298302	ESTs	2.84
	403247				2.83
20	404825				2.83
	459184	L35001	Hs.95669	ESTs	2.83
	402968				2.82
	417575	R00382	Hs.191199	ESTs	2.82
	404668				2.81
25	420619	AF130255	Hs.99430	testis zinc finger protein	2.81
	447241	BE382838	Hs.19322	ESTs	2.80
	448793	AI864581	Hs.215477	ESTs	2.79
	453014	AI937242	Hs.176590	ESTs	2.79
	446775	AI792836	Hs.232273	ESTs	2.78
30	455075	AW854850		gb:QV2-CT0261-201099-011-h03 CT0261 Homo	2.78
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	2.75
	457546	AA568484	Hs.153632	ESTs	2.75
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.74
	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN A	2.74
35	405703				2.73
	408840	AW277132	Hs.254880	ESTs	2.73
	413958	BE277913	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	2.73
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein,	2.73
	406702	Z20556	Hs.278432	myosin, heavy polypeptide 6, cardiac mus	2.72
40	408664	R56362		gb:yg93c07.r1 Soares infant brain 1NIB H	2.72
	402457				2.71
	403612				2.71
	407049	X72632		(NONE)	2.71
	415423	AA164743	Hs.187617	Homo sapiens cDNA FLJ13941 fis, clone Y7	2.70
45	402862				2.69
	403540				2.69
	431465	AW293178	Hs.180086	ESTs	2.69
	406563				2.68
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.68
50	426220	AI383475	Hs.171697	ESTs, Weakly similar to immunoglobulin s	2.68
	446707	AI591214	Hs.156336	ESTs	2.68
	447557	AW028809	Hs.229570	ESTs	2.68
	413529	U11874	Hs.846	interleukin 8 receptor, beta	2.67
	403997				2.66
55	408704	AA056635	Hs.5366	Homo sapiens cDNA: FLJ21522 fis, clone C	2.66
	407005	U20230		gb:Human guanyl cyclase C gene, partial	2.65
	405075				2.64
	430728	AW968522		gb:EST380598 MAGE resequences, MAGJ Homo	2.64
	405327				2.63
60	409419	BE207219	Hs.20474	ESTs, Highly similar to S17112 interfero	2.63
	434300	AA740944	Hs.116295	ESTs	2.63
	405895				2.62
	431929	AW294163	Hs.146127	ESTs	2.61
	405217				2.60
65	437569	AA760849	Hs.294052	ESTs	2.60
	419822	AW966864	Hs.255780	ESTs	2.59
	445918	AW014139	Hs.145656	ESTs	2.59
	446149	BE242960	Hs.203181	ESTs	2.59
	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.sa	2.58
70	404282				2.53
	409778	AW499705		gb:UI-HF-BR0p-ajk-b-05-0-UI.r1 NIH_MGC_5	2.53
	445353	BE551465	Hs.175211	ESTs	2.53
	458764	BE619386		gb:601473204F1 NIH_MGC_68 Homo sapiens c	2.53
	402195				2.52
75	404247				2.52
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.52
	402588				2.50
	432301	U34249	Hs.167075	ring finger protein 9	2.50
	424958	AA984420	Hs.283659	ESTs	2.49
80	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo	2.49
	415003	M11437	Hs.77741	kininogen	2.48
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	2.48
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	2.47

	440424	AI991125	Hs.189109	Homo sapiens cDNA: FLJ21458 fis, clone C	2.47
	402153				2.46
	432152	AK000245	Hs.272790	Homo sapiens cDNA FLJ20238 fis, clone CO	2.46
	454414	R55574	Hs.164675	ESTs	2.45
5	401603				2.44
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.44
	408513	AW206468	Hs.103118	ESTs	2.43
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	2.42
	400672				2.41
10	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.41
	449748	H23963	Hs.32043	ESTs	2.41
	453756	AW139415	Hs.61906	ESTs	2.41
	400624				2.40
	403125				2.40
15	406118				2.39
	402165				2.38
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.38
	425515	W26609		gb:35f12 Human retina cDNA randomly prim	2.38
	402951				2.37
20	427886	AA417083	Hs.104789	ESTs	2.37
	447173	AW449385	Hs.157294	ESTs	2.37
	448703	BE613942	Hs.170890	Homo sapiens cDNA: FLJ21129 fis, clone C	2.37
	426344	H41821	Hs.169393	transcriptional activator of the c-fos p	2.36
	401840				2.35
25	403731				2.34
	405378				2.34
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	2.34
	416559	AI039195	Hs.128060	ESTs, Weakly similar to cDNA EST yk481g5	2.34
	438216	Z83952	Hs.252815	ESTs	2.34
30	448427	BE395260		gb:601311130F1 NIH_MGC_44 Homo sapiens c	2.34
	451588	AW072057		gb:ws58g05.x1 NCI_CGAP_Brn25 Homo sapien	2.34
	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA	2.33
	451172	AW206465	Hs.207423	ESTs	2.33
	401015				2.32
35	414705	BE464157	Hs.281455	ESTs	2.32
	439894	AA853077		gb:NHTBCae03a05f1 Normal Human Trabecula	2.31
	446305	AW270149	Hs.254515	ESTs, Moderately similar to AF248953 1 g	2.31
	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker pr	2.29
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo s	2.28
40	457197	AB016092	Hs.197114	RNA binding protein; AT-rich element bin	2.28
	457275	AA463422	Hs.209431	ESTs	2.28
	458766	AW183618	Hs.188417	ESTs, Weakly similar to ZnT-3 [H.sapiens	2.28
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	2.27
	430210	AL157426	Hs.235390	Homo sapiens mRNA; cDNA DKFZp761B101 (fr	2.27
45	442614	AI269030		gb:qj73c12.x1 NCI_CGAP_Kid3 Homo sapiens	2.27
	402538				2.26
	439891	AL389940	Hs.109968	ESTs	2.26
	440056	BE294828	Hs.13323	hypothetical protein FLJ22059	2.26
	406150				2.25
50	426880	AA453482		gb:zx47a11.r1 Soares_testis_NHT Homo sap	2.25
	447129	AW014123	Hs.161402	ESTs	2.25
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.25
	456778	AI458309	Hs.117406	ESTs	2.24
	401728				2.23
55	404139				2.23
	414095	BE293546		gb:601186671F1 NIH_MGC_15 Homo sapiens c	2.23
	432037	AW450592	Hs.300459	ESTs	2.23
	451965	AA021163	Hs.22287	ESTs	2.23
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.22
60	427586	AA609661	Hs.190592	ESTs	2.22
	454108	AA161071	Hs.71465	squalene epoxidase	2.22
	429749	AI685174	Hs.22293	ESTs	2.21
	434507	AW511138	Hs.256581	ESTs	2.21
	436652	AA724543	Hs.168824	ESTs	2.21
65	437433	R74016	Hs.121581	ESTs	2.21
	401688				2.20
	441748	R14439	Hs.209194	ESTs	2.19
	453072	BE251845	Hs.221516	ESTs, Weakly similar to tetraspan TM4SF	2.19
	400635				2.18
70	417176	AW974475	Hs.143467	ESTs	2.18
	427858	NM_001971	Hs.21	elastase 1, pancreatic	2.18
	454886	AW837063		gb:QV1-LT0037-150200-069-g08 LT0037 Homo	2.18
	458232	BE217872	Hs.279537	ESTs	2.18
	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB5	2.17
75	423668	Y10148	Hs.131138	neurotensin receptor 2	2.17
	440338	R62431	Hs.12758	ESTs	2.17
	403115				2.16
	409125	R17268	Hs.301560	ESTs	2.16
	426887	AI971975	Hs.212892	ESTs	2.16
80	413811	BE168828		gb:QV1-HT0517-020400-145-f04 HT0517 Homo	2.15
	442962	AI025315	Hs.131615	ESTs	2.15
	403921				2.14
	413140	T06607	Hs.6846	hypothetical protein FLJ13055	2.14

	421996	AW583807	Hs.1460	glucagon	2.14
	436130	AA341497	Hs.31408	ESTs	2.14
	407243	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	2.13
	407708	AF019968	Hs.37936	suppressor of variegation 3-9 (Drosophil	2.13
5	442792	AI352340	Hs.131194	ESTs	2.12
	454406	AA213605	Hs.267861	ESTs	2.12
	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	2.11
	433963	AI218808	Hs.187778	ESTs	2.11
	400736				2.10
10	406343				2.10
	409702	AI752244	Hs.285749	Human DNA from chromosome 19-specific co	2.10
	432092	AF135026		gb:Homo sapiens kallikrein-like protein	2.10
	441915	AI566116	Hs.207066	ESTs, Weakly similar to FOG [M.musculus]	2.10
	453147	AA733098	Hs.279909	CGI-05 protein	2.10
15	415604	Z44177	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.08
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.08
	401211	AJ004832	Hs.5038	neuropathy target esterase	2.07
	413808	J00287	Hs.182183	caldesmon 1	2.07
	414433	BE407755	Hs.169100	Homo sapiens cDNA FLJ12529 fis, clone NT	2.07
20	421978	AJ243662	Hs.110196	NICE-1 protein	2.07
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	2.07
	433605	AI378012	Hs.147953	ESTs	2.06
	449383	AW444712	Hs.196573	ESTs	2.06
	455652	BE064675		gb:RC1-BT0313-301299-012-h11 BT0313 Homo	2.05
25	402382				2.04
	407282	AI345597	Hs.254727	ESTs	2.04
	457273	AI167145	Hs.165538	ESTs	2.04
	459073	AW968616	Hs.296234	ESTs, Highly similar to mitogen-activate	2.04
	402394				2.03
30	428875	AW451624	Hs.178202	ESTs	2.03
	456634	AA609911	Hs.109012	ESTs	2.03
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.02
	439281	AA100768	Hs.48485	ESTs	2.02
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.02
35	401122				2.01
	444340	AI143198	Hs.143561	ESTs	2.01
	455104	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.01
	415011	AW963085		gb:EST375158 MAGE resequences, MAGH Homo	2.00
	440144	AW082297	Hs.88523	ESTs	2.00
40	403183				1.99
	409802	AW500732		gb:UI-HF-BN0-akm-h-07-0-UI.r1 NIH_MGC_50	1.98
	430144	AI732722	Hs.187694	ESTs	1.98
	444580	AI168365	Hs.268663	ESTs	1.98
	401704				1.97
45	401810				1.97
	424473	AK001405	Hs.148584	Homo sapiens cDNA FLJ10543 fis, clone NT	1.97
	438573	AW135084	Hs.299865	ESTs	1.97
	412921	BE009345	Hs.128942	ESTs	1.96
	422233	AB002058	Hs.113275	purinergic receptor P2X-like 1, orphan r	1.96
50	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	1.96
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	1.95
	414323	NM_014759	Hs.239500	KIAA0273 gene product	1.94
	428119	AW298211	Hs.255737	ESTs	1.94
	424510	AK001841	Hs.149797	hypothetical protein FLJ10979	1.92
55	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	1.92
	429785	H82114	Hs.301769	ESTs	1.92
	437344	R90921	Hs.6846	hypothetical protein FLJ13055	1.92
	451819	AI819096	Hs.249260	ESTs	1.92
	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein	1.92
60	422664	AA315933	Hs.120879	ESTs	1.91
	432247	AA531287	Hs.105805	ESTs	1.91
	453820	R77494	Hs.75416	DAZ associated protein 2	1.91
	400675				1.90
	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	1.90
65	407099	M94891	Hs.278423	pregnancy specific beta-1-glycoprotein 4	1.90
	440297	BE560553	Hs.205450	Homo sapiens cDNA: FLJ22570 fis, clone H	1.90
	443104	AA088470	Hs.83135	p53-responsive gene 6	1.90
	444329	W73753	Hs.58330	ESTs	1.90
	402690				1.89
70	432354	AW137262	Hs.192713	ESTs	1.89
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.88
	443322	AI825817	Hs.143272	ESTs	1.88
	458185	AI762757	Hs.129869	ESTs, Weakly similar to AF113685 1 PRO09	1.88
	459072	AI815978	Hs.160427	ESTs	1.88
75	402534				1.87
	409689	AA078492		gb:7P04D11 Chromosome 7 Placental cDNA L	1.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	1.87
	430176	AL161995	Hs.234775	neurturin	1.87
	430631	AJ003147	Hs.278464	olfactory receptor, family 1, subfamily	1.87
80	433114	AA121579		gb:zn77f02.r1 Stratagene NT2 neuronal pr	1.87
	439254	U57352	Hs.6517	amiloride-sensitive cation channel 1, ne	1.87
	448461	AW166358	Hs.124979	ESTs	1.87
	450675	AA010662	Hs.188639	ESTs	1.87

	401767				1.86
	449891	N64867	Hs.37848	ESTs	1.85
	400527				1.84
	428581	AA430570	Hs.104881	ESTs	1.84
5	443647	AV653846	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.84
	444785	AV651441	Hs.282475	ESTs	1.84
	449566	AA001778	Hs.288156	Homo sapiens cDNA: FLJ21819 fis, clone H	1.84
	436752	AW298529	Hs.255774	ESTs	1.83
	437405	AA338837	Hs.42547	Homo sapiens cDNA FLJ13975 fis, clone Y7	1.83
10	449174	T66136	Hs.12880	ESTs	1.83
	449887	AW080843	Hs.200275	ESTs	1.83
	453261	AA034116	Hs.118494	ESTs	1.83
	454243	AW241901	Hs.250683	ESTs	1.83
	459188	AA216382	Hs.30002	SH3-containing protein SH3GLB2	1.83
15	424334	AA393460		gb:zt71e05.r1 Soares_testis_NHT Homo sap	1.82
	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	1.82
	408123	AW163377		gb:au94e02.y1 Schneider fetal brain 0000	1.81
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	1.80
	442196	AI902646	Hs.31844	Homo sapiens cDNA FLJ12586 fis, clone NT	1.80
20	421419	M99587	Hs.104134	homeo box (H6 family) 1	1.79
	405420				1.78
	405737				1.78
	414016	AA134594	Hs.71528	ESTs	1.78
	415744	AW964850	Hs.279307	ESTs	1.78
25	420375	AF182077	Hs.97244	glioma tumor suppressor candidate region	1.78
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	1.78
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1	1.77
	401743				1.75
	405187				1.75
30	442763	AI017037	Hs.131121	ESTs	1.75
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	1.75
	413248	T64858	Hs.21433	ESTs	1.74
	423913	NM_016436	Hs.301055	hepatocellular carcinoma-associated anti	1.74
	439999	AA115811	Hs.6838	ras homolog gene family, member E	1.74
35	440185	AW104546	Hs.270929	ESTs	1.74
	450482	AI697844	Hs.221720	ESTs	1.74
	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYD	1.73
	420476	AW575863	Hs.136232	ESTs	1.73
	428748	AW593206	Hs.98785	ESTs	1.73
40	431148	AA502653	Hs.28621	ESTs	1.73
	447205	BE617015	Hs.11006	ESTs	1.73
	455994	BE179190		gb:RC0-HT0613-210300-032-f07 HT0613 Homo	1.73
	401039				1.72
	403251				1.72
45	409762	AW498884	Hs.257970	ESTs	1.72
	440914	AA909552	Hs.143884	ESTs	1.72
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	1.72
	409605	AW444477	Hs.258507	ESTs	1.71
	441212	AW242447	Hs.146182	ESTs, Weakly similar to lactase phlorizi	1.71
50	445624	AW140103	Hs.78880	ilvB (bacterial acetolactate synthase)-l	1.71
	458619	AA872064	Hs.301218	ESTs, Weakly similar to Unknown gene pro	1.71
	401969				1.70
	403327				1.70
	407245	X90568	Hs.172004	titin	1.70
55	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil	1.70
	436034	AF282693	Hs.150185	inflammation-related G protein-coupled r	1.70
	442682	AI014545	Hs.231027	EST	1.70
	458494	AI380906	Hs.158436	ESTs	1.70
	404682				1.69
60	407402	AF035303		gb:Homo sapiens clone 23943 mRNA sequenc	1.69
	409368	AA071059		gb:zm66a10.r1 Stratagene neurocepithelium	1.69
	440362	AA883812	Hs.125508	ESTs	1.69
	448866	BE297743	Hs.284203	myogenic factor 3	1.69
	402201				1.68
65	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.68
	403186				1.67
	409543	AW410200		gb:fh05b12.x1 NIH_MGC_17 Homo sapiens cD	1.67
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.67
	450391	AI694522	Hs.202280	ESTs	1.67
70	408919	AW295352	Hs.251836	ESTs	1.66
	416136	H45027	Hs.181770	ESTs	1.66
	416865	H97863	Hs.42456	ESTs	1.66
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	1.66
	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo sapiens c	1.66
75	429134	AA446953	Hs.99004	ESTs	1.65
	445041	T64183	Hs.11398	ESTs	1.65
	453240	AI969564	Hs.284249	Homo sapiens cDNA: FLJ22334 fis, clone H	1.65
	405243				1.64
	426039	BE265133	Hs.217493	annexin A2	1.64
80	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	1.64
	435942	R06285	Hs.191215	ESTs	1.64
	448106	AI800470	Hs.171941	ESTs	1.64
	408591	AF015224	Hs.46452	mammaglobin 1	1.63

	410881	AW809157		gb:RC0-ST0118-041099-031-c07_1 ST0118 Ho	1.63
	417743	R14738	Hs.8312	ESTs, Weakly similar to AF170723 1 prote	1.62
	430632	AC004597	Hs.248088	olfactory receptor, family 10, subfamily	1.62
	448651	BE246440	Hs.93728	pre-B-cell leukemia transcription factor	1.62
5	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, c	1.62
	459499	AW402653	Hs.28355	Homo sapiens cDNA: FLJ22402 fis, clone H	1.62
	412374	X01388	Hs.73849	apolipoprotein C-III	1.61
	419113	AI446586	Hs.21835	ESTs	1.61
	426795	AI810474	Hs.196945	ESTs	1.61
10	426998	BE274360		gb:601121068F1 NIH_MGC_20 Homo sapiens c	1.61
	428407	NM_003963	Hs.184194	transmembrane 4 superfamily member 5	1.61
	444475	C75571		gb:C75571 Human pancreatic islet Homo sa	1.61
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	1.61
	456275	AW976183	Hs.88414	ESTs, Weakly similar to dJ512E2.1 [H.sap	1.61
15	414060	BE246327		gb:TCBAP1E1967 Pediatric pre-B cell acut	1.60
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.60
	428651	AF196478	Hs.188401	annexin A10	1.60
	443853	AI089064	Hs.250644	ESTs	1.60
	407007	U22961		gb:Human mRNA clone with similarity to L	1.59
20	412067	N45697		gb:yy78d01.r1 Soares_multiple_sclerosis_	1.59
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.59
	448619	AI867182	Hs.202255	ESTs	1.59
	403665				1.58
	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory	1.58
25	424286	AA338285	Hs.90744	proteasome (prosome, macropain) 26S subu	1.58
	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	1.57
	430218	AW998865	Hs.186703	ESTs	1.57
	431882	NM_001426	Hs.271977	engrailed homolog 1	1.57
	450797	AI761930	Hs.205127	ESTs	1.57
30	455366	AW947563		gb:RC0-MT0004-140300-031-g11 MT0004 Homo	1.57
	408421	AW193734	Hs.253067	ESTs	1.56
	421907	BE018556	Hs.109358	ATPase, Class V, type 10B	1.56
	432742	AA564453	Hs.162339	ESTs	1.56
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	1.56
35	439543	W75935	Hs.146083	ESTs	1.56
	443317	AI051601	Hs.200191	ESTs	1.56
	449097	BE271708	Hs.95110	ESTs, Weakly similar to PIP6_HUMAN 1-PHO	1.56
	457127	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	1.56
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1,	1.55
40	418837	U48263	Hs.89040	prepronociceptin	1.55
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.55
	458475	AI650322	Hs.143249	ESTs	1.55
	402561				1.54
	411187	AW821291		gb:PM3-ST0307-241299-002-f03 ST0307 Homo	1.54
45	419224	NM_012189	Hs.252716	fibrousheathin II	1.54
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	1.53
	415426	Z41991	Hs.23197	ESTs	1.53
	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.53
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.53
50	428489	AI807459	Hs.98582	ESTs	1.53
	437728	AA766719		gb:oa39c09.s1 NCI_CGAP_GCB1 Homo sapiens	1.53
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.52
	414932	C14577	Hs.194517	ESTs	1.52
	433500	AF064255	Hs.111401	very long-chain acyl-CoA synthetase homo	1.52
55	439688	AW445181	Hs.209637	Homo sapiens cDNA FLJ12921 fis, clone NT	1.52
	453391	AW600302	Hs.232655	ESTs	1.52
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	1.51
	436895	AF037335	Hs.5336	carbonic anhydrase XII	1.51
	443012	AI566813	Hs.132278	ESTs	1.51
60	415824	D42039	Hs.78871	mesoderm development candidate 2	1.50
	445152	AI214667	Hs.283597	ESTs	1.50
	455941	BE160011	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1.50
	457889	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.50
	458503	AL133933	Hs.64310	interleukin 11 receptor, alpha	1.50
65	400694				1.49
	420937	AW966719	Hs.1340	colipase, pancreatic	1.49
	426752	X69490	Hs.172004	titin	1.49
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.49
	428874	W32133	Hs.194366	transthyretin (prealbumin, amyloidosis t	1.49
70	444287	AI033077	Hs.10755	dihydropyrimidinase	1.49
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.49
	425747	AI457620	Hs.205360	ESTs	1.48
	432378	AI493046	Hs.146133	ESTs	1.48
	447999	AW138840	Hs.201778	ESTs	1.48
75	453888	AW450670	Hs.252819	ESTs	1.48
	406667	M12523	Hs.75442	albumin	1.47
	418129	X52997	Hs.1144	glycoprotein IX (platelet)	1.47
	426309	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	1.47
	426755	BE253469		gb:601108143F1 NIH_MGC_16 Homo sapiens c	1.47
80	414258	AA203285	Hs.294141	ESTs, Weakly similar to dJ733D15.1 [H.sa	1.46
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	1.46
	420562	AI345569	Hs.190046	ESTs	1.46
	425011	T51986	Hs.283108	hemoglobin, gamma G	1.46

	443050	AI612788	Hs.132348	ESTs, Weakly similar to diaphanous 1 [H.	1.46
	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.45
	434680	T11738	Hs.127574	ESTs	1.45
	454771	AW819939	Hs.273629	ESTs	1.45
5	415672	N53097	Hs.193579	ESTs	1.44
	418141	AW845738	Hs.171118	Homo sapiens mRNA for FLJ00026 protein,	1.44
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.43
	418197	AA214253		gb:zn58g02.r1 Stratagene muscle 937209 H	1.43
	431821	AW452256	Hs.271221	hypothetical protein FLJ20064	1.43
10	455433	AW939463		gb:QV1-DT0072-310100-056-g02 DT0072 Homo	1.43
	407743	AW814118		gb:MR3-ST0203-151199-011-d09 ST0203 Homo	1.42
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	1.42
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	1.42
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.42
15	452456	BE080763		gb:QV1-BT0631-150200-071-f09 BT0631 Homo	1.42
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.42
	408349	BE546947	Hs.44276	homeo box C10	1.41
	420391	AA456891	Hs.79123	KIAA0084 protein	1.41
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	1.41
20	449329	AW752783		gb:IL3-CT0219-221199-029-F03 CT0219 Homo	1.41
	453615	AA195712	Hs.132696	ESTs	1.41
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	1.40
	420287	AA740907	Hs.88297	ESTs	1.40
	427583	M82962	Hs.179704	meprin A, alpha (PABA peptide hydrolase)	1.40
25	418787	AW296134	Hs.86999	ESTs	1.39
	422072	AB018255	Hs.111138	KIAA0712 gene product	1.39
	425988	BE045897	Hs.274454	ESTs	1.39
	428087	AA100573	Hs.182421	troponin C2, fast	1.39
	438136	NM_002390	Hs.6088	a disintegrin and metalloproteinase doma	1.39
30	455579	BE011320		gb:PM3-BN0218-090500-002-d09 BN0218 Homo	1.39
	402316				1.38
	417084	H08370	Hs.33067	ESTs	1.38
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.38
	433787	AI472951	Hs.173688	ESTs	1.38
35	413830	BE263439	Hs.13144	HSPC160 protein	1.37
	423576	NM_000383	Hs.129829	autoimmune regulator (autoimmune polyen	1.37
	401886				1.36
	412688	AW583062	Hs.74502	chymotrypsinogen B1	1.36
	401238				1.34
40	421511	AA488940	Hs.105216	hypothetical protein FLJ11125	1.34
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11	1.34
	425450	U14755	Hs.157449	LIM homeobox protein 1	1.34
	427333	AF067797	Hs.176658	aquaporin 8	1.34
	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	1.34
45	445204	AW135523	Hs.245853	ESTs	1.34
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	1.34
	456379	W22206		gb:63E10 Human retina cDNA Tsp509I-cleav	1.34
	457416	BE142052		gb:CM3-HT0137-150999-011-b05 HT0137 Homo	1.34
	415741	AI902761	Hs.272087	ESTs	1.33
50	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITHO	1.33
	429188	AB011171	Hs.198037	KIAA0599 protein	1.33
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	1.33
	454748	AW862014		gb:RC3-CT0347-160200-013-d09 CT0347 Homo	1.33
	437744	AW290905	Hs.300288	ESTs, Weakly similar to CGHU2E collagen	1.32
55	451997	AA021351	Hs.158497	KIAA0724 gene product	1.32
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.32
	411879	BE145354	Hs.273758	Homo sapiens cDNA: FLJ23112 fis, clone L	1.31
	424304	NM_001395	Hs.144879	dual specificity phosphatase 9	1.31
	401442				1.30
60	403942				1.30
	443687	F13040	Hs.182937	peptidylprolyl isomerase A (cyclophilin	1.30
	401624				1.29
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	1.29
	418575	AA225313	Hs.222886	ESTs	1.29
65	419818	AI657122	Hs.301931	ESTs	1.29
	429845	AB020337	Hs.225943	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	1.29
	447586	AI081980	Hs.285829	solute carrier family 25 (mitochondrial	1.29
	407013	U35637		gb:Human nebulin mRNA, partial cds	1.28
	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	1.28
70	429780	AL137518	Hs.300388	ESTs	1.28
	453539	AW731886	Hs.95196	ESTs, Weakly similar to T20B12.3 [C.eleg	1.28
	400846				1.27
	420257	AA257035	Hs.190042	ESTs	1.27
	429184	AF095735	Hs.198003	sarcosine dehydrogenase	1.27
75	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	1.27
	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	1.27
	451139	AW293316	Hs.205558	ESTs	1.27
	431284	AA570148	Hs.126783	Homo sapiens cDNA: FLJ22610 fis, clone H	1.26
	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	1.26
80	406158				1.25
	419548	T73661	Hs.91877	ESTs, Highly similar to THIH_HUMAN THYRO	1.25
	430681	AW969675	Hs.291232	ESTs	1.25
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.25

436217	T53925	Hs.107	fibrinogen-like 1	1.25
440089	AA864468	Hs.135646	ESTs	1.25
446787	U67167	Hs.315	mucin 2, intestinal/tracheal	1.25
448207	AI475490	Hs.170577	ESTs	1.25
454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	1.25
413271	AA127873	Hs.114949	ESTs	1.24
422619	AA313322		gb:EST185218 Colon carcinoma (HCC) cell	1.24
422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo	1.24
427530	AA405093	Hs.126519	ESTs	1.24
437727	AA766707	Hs.153039	ESTs	1.24
426435	AI827946	Hs.189118	ESTs	1.23
426429	X73114	Hs.169849	myosin-binding protein C, slow-type	1.22
407964	AW130334	Hs.281111	ESTs	1.21
430628	AI763257	Hs.86327	Homo sapiens cDNA: FLJ22431 fis, clone H	1.21
432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	1.21
457843	AW138211	Hs.128746	ESTs	1.21
413242	BE074165		gb:PM3-BT0564-030300-002-e12 BT0564 Homo	1.20
446057	AI420227	Hs.149358	ESTs	1.20
447198	D61523	Hs.283435	ESTs	1.20
449513	AI653232	Hs.195059	EST	1.20
415566	F12119		gb:HSC35H091 normalized infant brain cDN	1.19
423315	R54109	Hs.26096	ESTs	1.19
455817	BE142384		gb:CM2-HT0144-210999-011-d04 HT0144 Homo	1.19
459354	BE514778		gb:601317094F1 NIH_MGC_9 Homo sapiens cD	1.19
408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	1.18
414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.18
419251	NM_001486	Hs.89771	glucokinase (hexokinase 4) regulatory pr	1.18
456702	AI684534		gb:wa72f10.x1 Soares_NFL_T_GBC_S1 Homo s	1.18
458009	AI221409	Hs.144983	ESTs	1.18
410193	AJ132592	Hs.59757	zinc finger protein 281	1.17
417779	AA829526	Hs.124977	ESTs	1.17
435101	AI743156	Hs.131064	ESTs	1.17
445360	AI798776	Hs.156029	ESTs	1.17
414160	BE257021		gb:601117426F1 NIH_MGC_16 Homo sapiens c	1.15
418078	AA521268	Hs.86508	ESTs	1.15
425133	NM_002613	Hs.154729	3-phosphoinositide dependent protein kin	1.15
437935	AW939591	Hs.5940	hypothetical protein FLJ20063	1.15
446377	AW014022	Hs.170953	ESTs	1.15
420097	AA700127	Hs.190504	ESTs	1.13
446591	H44186	Hs.15456	PDZ domain containing 1	1.13
451477	AI798425	Hs.42710	ESTs	1.13
459197	BE244587		gb:TCBAP2E0851 Pediatric pre-B cell acut	1.13
428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	1.12
431191	AW972118	Hs.100002	HSPC162 protein	1.12
424403	F05183	Hs.1799	CD1D antigen, d polypeptide	1.11
433546	AI075877	Hs.125461	Homo sapiens cDNA FLJ11539 fis, clone HE	1.11
451179	W05469	Hs.31818	ESTs	1.11
400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	1.10
420774	AA280209	Hs.165270	ESTs	1.10
428887	AA437009	Hs.98984	ESTs	1.10
430582	AI215509	Hs.143964	ESTs	1.10
453642	AI370936	Hs.34074	dipeptidylpeptidase VI	1.10
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.09
417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo	1.09
456387	W28876		gb:52h7 Human retina cDNA randomly prime	1.09
427965	D00306	Hs.183864	elastase 3B	1.08
447388	AW630534	Hs.76277	ESTs, Weakly similar to TB2 [H.sapiens]	1.08
413841	M34276	Hs.75576	plasminogen	1.07
429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.07
433313	W20128	Hs.296039	ESTs	1.07
439450	R51613	Hs.125304	ESTs	1.07
458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat homolog)	1.07
405161				1.06
406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	1.06
424294	BE299311		gb:601119256F1 NIH_MGC_17 Homo sapiens c	1.06
424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.06
444687	AW972109	Hs.135107	ESTs	1.06
444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1.06
421243	AW873803	Hs.102876	pancreatic lipase	1.05
444290	AA262496	Hs.29280	ESTs	1.05
407984	AW134708	Hs.243569	ESTs	1.04
439706	AW872527	Hs.59761	ESTs	1.04
402194				1.03
427506	AK000134	Hs.179100	hypothetical protein FLJ20127	1.03
428819	AL135623	Hs.193914	KIAA0575 gene product	1.03
434590	T47232		gb:yb64b08.s1 Stratagene ovary (937217)	1.03
416378	AW044467	Hs.73708	ESTs, Weakly similar to A57291 cytokine	1.02
431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	1.02
443316	AI478463	Hs.18443	ESTs	1.02
428585	AB007863	Hs.185140	KIAA0403 protein	1.01
400440	X83957	Hs.83870	nebulin	1.00
404619	BE514535	Hs.77171	minichromosome maintenance deficient (S.	1.00
407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB H	1.00

	408052	AW501117	Hs.283585	ESTs	1.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.00
	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	1.00
5	410319	R23413	Hs.71935	putative zinc finger protein from EUROIM	1.00
	411000	N40449	Hs.201619	ESTs, Weakly similar to SEB4B [H.sapiens	1.00
	412098	AI493054	Hs.158968	ESTs	1.00
	412446	AI768015	Hs.92127	ESTs	1.00
	412637	AA115097	Hs.261313	ESTs	1.00
10	413147	BE067271		gb:PM2-BT0349-161299-001-b05 BT0349 Homo	1.00
	413597	AW302885	Hs.117183	ESTs	1.00
	414117	W88559	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	1.00
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	1.00
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.00
15	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	1.00
	419768	T72104	Hs.93194	apolipoprotein A-I	1.00
	420182	Z44245	Hs.22999	ESTs	1.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	1.00
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.00
20	421204	AW081587	Hs.165051	ESTs	1.00
	422189	AF252292	Hs.112933	Tax interaction protein 40	1.00
	422792	AI951548	Hs.135163	ESTs	1.00
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	1.00
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.00
25	424922	BE386547	Hs.217112	ESTs, Weakly similar to Similarity to Ye	1.00
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.00
	425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	1.00
	425983	AK000226	Hs.165619	mucin and cadherin-like	1.00
	426004	AW600300	Hs.124123	ESTs, Weakly similar to syncollin [R.nor	1.00
30	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	1.00
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	1.00
	429027	AL022314	Hs.194750	Human DNA sequence from clone 1170K4 on	1.00
	429231	AA813214		gb:aj32e09.s1 Soares_testis_NHT Homo sap	1.00
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	1.00
35	429930	AI580809	Hs.99569	ESTs	1.00
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1.00
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	1.00
	431845	AA516469	Hs.270554	ESTs	1.00
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	1.00
40	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00
	434452	AA634333	Hs.116822	ESTs	1.00
	435499	R89344	Hs.14148	ESTs	1.00
	438433	AB018274	Hs.6214	KIAA0731 protein	1.00
	442403	AW207724	Hs.129516	ESTs	1.00
45	442803	AI675298	Hs.199917	ESTs	1.00
	443266	AI277101	Hs.25890	ESTs, Weakly similar to transducin [H.sa	1.00
	444656	AI277924	Hs.145199	ESTs	1.00
	445573	AI439646	Hs.157494	ESTs, Weakly similar to KIAA0676 protein	1.00
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00
50	447359	NM_012093	Hs.18268	adenylate kinase 5	1.00
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac mus	1.00
	448657	BE147857	Hs.293841	ESTs, Weakly similar to KIAA0672 protein	1.00
	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	1.00
	450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 fis, clone C	1.00
55	450390	N93227	Hs.98403	ESTs	1.00
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	1.00
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	1.00
	452528	AA742457	Hs.291479	ESTs	1.00
	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	1.00
60	453754	AW972580	Hs.172753	ESTs	1.00
	453991	AW014915	Hs.273741	ESTs	1.00
	454517	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	1.00
	459367	BE146877		gb:CM4-HT0244-111199-040-h12 HT0244 Homo	1.00
	408021	AW137133	Hs.245867	ESTs	0.99
65	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	0.99
	437206	AW975934	Hs.283382	ESTs, Weakly similar to Protein sequence	0.99
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	0.98
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	0.98
	441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.98
70	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.97
	453534	NM_014796	Hs.33187	KIAA0748 gene product	0.97
	457787	AA683268		gb:ae92b04.s1 Stratagene schizo brain S1	0.97
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	0.96
	422069	AJ010063	Hs.111110	titin-cap (telethonin)	0.96
75	425260	L47726	Hs.1870	phenylalanine hydroxylase	0.96
	418406	X73501	Hs.84905	cytokeratin 20	0.95
	425670	AW968536	Hs.190146	ESTs	0.95
	416373	AA195845	Hs.73680	ESTs, Weakly similar to AF198455 1 epith	0.94
	452243	AL355715	Hs.28555	programmed cell death 9	0.94
80	411908	L27943	Hs.72924	cytidine deaminase	0.93
	415067	AI264969	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.93
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	0.93
	450685	L15533	Hs.423	pancreatitis-associated protein	0.92

	427450	AB014526	Hs.178121	KIAA0626 gene product	0.91
	432440	X63597	Hs.2996	sucrase-isomaltase	0.91
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.90
	414910	X12662	Hs.29679	cofactor required for Sp1 transcriptiona	0.89
5	423317	AJ272204	Hs.64616	chromosome 12 open reading frame 3	0.89
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	0.89
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDN	0.89
	452689	F33868	Hs.284176	transferrin	0.89
	446240	AI535736	Hs.170165	ESTs	0.88
10	449110	H56112	Hs.277053	ESTs	0.88
	453817	AW755253	Hs.61920	ESTs	0.88
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.87
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	0.87
	446525	AW967069	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone H	0.87
15	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	0.87
	403740				0.86
	420156	AW449258	Hs.6187	ESTs	0.86
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.86
	421142	AW503944	Hs.130822	ESTs	0.85
20	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.85
	419415	AW451692	Hs.192036	ESTs	0.84
	423321	AB013885	Hs.126926	beta-ureidopropionase	0.84
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	0.84
	433447	U29195	Hs.3281	neuronal pentraxin II	0.84
25	403047				0.83
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.81
	407782	AA608956	Hs.112619	ESTs, Weakly similar to PQ0109 Purkinje	0.81
	405232				0.80
	437776	AA768037	Hs.291671	ESTs	0.80
30	415505	R39870	Hs.12548	ESTs	0.79
	444436	N25871	Hs.177337	ESTs	0.78
	409096	AA194412	Hs.50550	sarcomeric muscle protein	0.77
	432134	AI816782	Hs.122583	Homo sapiens cDNA: FLJ21934 fis, clone H	0.76
	437066	AA743570	Hs.200935	ESTs	0.76
35	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	0.75
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.73
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	0.71
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	0.71
	447145	AA761073	Hs.192943	ESTs	0.71
40	452103	R42764	Hs.3248	mutS (E. coli) homolog 6	0.71
	410929	H47233	Hs.30643	ESTs	0.70
	400301	X03635	Hs.1657	estrogen receptor 1	0.69
	415702	F28877		gb:HSPD18414 HM3 Homo sapiens cDNA clone	0.67
	411396	C04646	Hs.85428	ESTs	0.65
45	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.65

50 TABLE 28B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
407743	1012151_1	AW814118 AW814257 AW072376
408123	1040435_1	AW163377 AW160398
408432	1058667_1	AW195262 R27868 AW811262
408664	1073340_1	R56362 AW248096 R07152 R07285
408922	109017_1	R87388 R84328 AA058916
409368	112377_1	AA071059 AA085201 AA085020
409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309
409689	114833_1	AA078492 AA078333 AA077450 AA077746 AA076896
409778	1154206_1	AW499705 AW502537 AW503016
409802	1155179_1	AW500732 AW504061
410285	119128_1	AA083609 AA083790 AA112048
410881	1225682_1	AW809157 AW812181 AW812175 AW812172 AW812161 AW812165
411187	1235092_1	AW821291 AW821264 AW821287 AW821290 AW821285 AW821280 AW821259
412067	1275641_1	N45697 N45540 AW890595
413147	1350637_1	BE067271 BE067266 BE067286 BE067278 BE067299 BE067285
413242	1355323_1	BE074165 BE075001 BE075009
413811	1391117_1	BE168828 BE168830 BE168823 BE168928 BE168820 BE168826
414060	1413697_1	BE246327 BE244704
414095	1416521_1	BE293546 BE249848
414160	1422273_1	BE257021 BE258316 BE257099
414580	1463848_1	BE386918 BE408833 BE385437
415011	151328_1	AW963085 AA159005 AW963073
415566	1539861_1	F12119 Z45475 T64832
415702	1547874_1	F28877 F35687
417998	171375_1	AW967420 AA210915 AA236991 AA210916
418197	172864_1	AA214253 AA214259 Z28472 Z28881 Z17828
418464	1759038_-2	R87580
418556	1767866_-1	T02850

422619	218670_1	AA313322 BE408282 AA465612 BE073362
422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361 T06241 AA326794 AL138130 AW407975 AW999277
424294	237907_1	BE299311 AA338954 AA338468 AW960907
424334	238221_1	AA393460 AA338940 AW966277 AA419006
424648	241947_1	AA344576 AA732430 AA344601
425515	252721_1	W26609 W27360 AA358818
426328	264901_1	AW631296 AA375484
426507	268382_1	AA380285 AW934727 AW934914
426755	271382_1	BE253469 BE176417 BE176415 AA384133
426880	273277_2	AA453482 AF012388
426998	274259_-1	BE274360
429231	301463_1	AA813214 AI936567 AI743529 AA448279 AA994476 AI807452 AI218180 AA972858
430728	322706_1	AW968522 AA485112 AA485162 AW968698
432092	34124_1	AF135026 AA583908
433114	35904_1	AA121579 AB005217
434590	38931_1	T47232 AF147365 T47231
437237	43506_-2	BE513073
437728	441520_1	AA766719 AA767041 AW977440
439894	478738_1	AA853077 AA852175
442197	535550_1	AW837912 AW837934 AA984475 AW997490
442614	547073_1	AI269030 AI204085 AI004047
444475	607874_1	C75571 AI150469 T10778
448427	762970_1	BE395260 AW291036 AI500420
449329	80484_1	AW752783 H38266 AA001166
451588	87667_1	AW072057 AI225096 AA018702
452456	918391_1	BE080763 T96699 BE081135 AI902630 H49182 AI904021 AI902697
454517	1221063_1	AW803340 AW803280 AW803275 AW803415 AW803343 AW803422
454748	1233013_1	AW862014 AW858740 AW858735 AW818542 AW858765 AW862027 AW858775 AW858771 AW858763
454869	1238137_1	AW836004 AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836082 AW836086 AW836088 AW836166 AW836164 AW836002 AW836078 AW836161 AW862135 AW836165 AW836003
454886	1238987_1	AW837063 AW935882 AW935957
455075	1252389_1	AW854850 AW854848
455104	1253737_1	BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665 BE064650 BE064691
455366	1284685_1	AW947563 AW947543 AW947553 AW947549 AW947717 AW902859 AW902927 BE011032
455433	1290311_1	AW939463 AW939484 AW939480 AW939459 AW939546 AW939593 AW939548 AW939595 AW939106
455446	1291969_1	AW947749 AW947746 AW947754 AW946636 AW946674
455579	1333944_1	BE011320 BE006381 BE006361 BE011180 BE011328 BE011325 BE011157 BE006384 BE006387 BE006385 BE011160 BE011319 BE011346 BE006370 BE006386 BE011173 BE006389 BE006376 BE006375 BE006364 BE011321 BE006379
455652	1348736_1	BE064675 BE064761 BE064809 BE064673 BE064672 BE064674
455817	1371986_1	BE142384 BE142387
455994	1398737_1	BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
456150	1574395_1	Z42308 H23514
456379	1839113_2	W22206 W22498 W26922
456387	1842730_1	W28876 W26158
456702	219191_1	AI684534 BE262411 AA314031 AW752724
457416	334503_1	BE142052 AW265588 AA506741
457787	407235_1	AA683268 BE002903 BE002672
458764	73207_1	BE619386 AA300687
459197	924229_1	BE244587 AW938684 AW176490 AI940102 AW844995 AW938670 AI909850 AI909885 AI940079 AI909873

TABLE 28C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400489	8954013	Plus	131475-131652
400527	9796886	Plus	160750-161007
400545	9800107	Minus	124618-124881
400624	7228177	Minus	94097-94756
400635	8567750	Minus	102800-102932,107482-107689
400672	8118724	Minus	148067-148503
400675	8118750	Plus	11223-11816
400694	8118802	Plus	94288-94442
400736	8118985	Plus	143447-143851
400846	9188605	Plus	39310-39474
401007	8117333	Minus	140821-141050
401015	8117441	Plus	72260-72369
401039	7232177	Plus	6588-6884
401122	8570296	Plus	68256-68444
401238	9954455	Minus	49473-49644
401442	8346725	Minus	85674-85910
401496	7381769	Minus	82790-83002
401590	9956320	Minus	33547-33649
401603	7689963	Minus	116659-116780
401624	8575907	Plus	168318-168444,172964-173647

401688	2347081	Plus	22016-22624
401704	3097841	Plus	24712-25374
401728	8134856	Minus	82117-82920
401743	2865207	Plus	115475-115640
401767	9958312	Plus	156823-156921,157364-157554
401810	7342191	Plus	129063-129476
401840	7684597	Plus	56283-56439
401886	7229913	Minus	79215-79393
401919	9502466	Plus	67536-67666
401969	3126777	Plus	44863-45366
402051	8082020	Minus	19346-19480,20041-20119
402056	8084234	Plus	207002-207288
402153	8247879	Minus	122580-122987
402158	8516165	Minus	148298-148429,148566-148677
402165	8569830	Minus	65064-65979
402194	8576113	Plus	70917-71191
402195	7689778	Minus	147901-148884
402201	8576119	Plus	655-951
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
402382	9690314	Minus	155331-155528
402386	9799769	Plus	22069-22303
402394	9929690	Plus	33308-33482
402409	9796255	Minus	8571-10061
402423	9796344	Minus	62487-62664
402448	9796640	Plus	112942-113069,114303-114521
402457	9796782	Minus	16513-16577,16838-16926
402534	9801061	Plus	58989-59457
402538	9801137	Minus	96314-96539
402561	9864675	Plus	72967-73163
402588	9908948	Minus	33027-33183,59060-59198
402690	8348058	Plus	13368-13998
402714	8969253	Minus	18811-18886,19105-19328,19525-19764
402762	9230904	Minus	123298-124035
402862	2956660	Minus	18518-18656
402911	7263904	Plus	142689-142979
402951	9408717	Plus	73252-73329,73718-73877,76217-76299,78195-78401
402968	9581763	Minus	58658-58924
403047	3540153	Minus	59793-59968
403115	7331404	Minus	142952-143094,145474-145653,146269-146445,152816-152998
403125	9180936	Minus	197548-197712
403183	9838273	Plus	109930-110074
403186	9838287	Minus	117513-117856
403211	7630841	Minus	159211-159369
403247	7656833	Minus	76626-77140
403251	7677983	Plus	100391-100652
403327	8440025	Minus	174311-174451,174587-174705,175523-175592
403376	9369545	Minus	108698-108830
403479	7329292	Minus	148369-148533,150678-150809
403526	8017144	Plus	55367-55483
403540	8077057	Minus	56315-56450
403605	6862654	Plus	91614-91718
403612	8469060	Minus	94723-94859
403665	7249278	Plus	69027-69375
403716	7239669	Plus	86899-87122
403731	7543752	Minus	144000-144618
403740	7630882	Plus	86504-87227
403921	7711590	Minus	3297-3536
403942	7711825	Minus	99606-99757
403997	7708819	Plus	134427-134593
404139	9838113	Plus	76707-76891
404247	7406725	Minus	83949-84214,84312-84415,84499-84677,84878-85114
404282	2276311	Plus	61503-62205
404348	7630858	Minus	28895-29062
404668	9797204	Minus	11332-11546,12584-12718
404682	9797231	Minus	40977-41150
404795	4826439	Plus	147501-147780
404825	6478944	Plus	210382-210494
404938	7381808	Minus	165838-165950
405075	7770506	Minus	124680-125321
405147	9438278	Minus	158996-159557
405161	9966260	Plus	157607-157785
405163	9966267	Minus	161171-161299
405187	7229826	Plus	117025-117170,118567-118736
405217	7239551	Plus	32646-33138
405232	7249042	Plus	125904-126063
405243	7249201	Minus	22312-23197
405327	6094661	Minus	120550-120750
405378	6491714	Plus	91139-91440
405420	7211837	Minus	13428-13582
405703	4240388	Minus	15850-16061
405737	9943984	Minus	104275-104508,104755-104877
405895	7677903	Minus	66990-67484
406059	9103984	Minus	13856-14004

406101	9124019	Plus	125325-125831
406118	9143818	Plus	53997-54629
406150	9886026	Minus	59331-59701
406158	7144874	Plus	62393-63016,65012-65578
406343	9255974	Plus	17284-17440,18489-18646,18917-19004,19384-19538
406357	9256093	Minus	77181-77415
406563	7711604	Plus	34401-34538

TABLE 29A: 2286 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO NORMAL BODY

Table 29A lists about 2286 genes that are up regulated in idiopathic pulmonary fibrosis samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis expression level to "average" normal adult tissues sample expression was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of IPF to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	211.8
442275	AW449467	Hs.54795	ESTs	189.7
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	134.1
441835	AB036432	Hs.184	advanced glycosylation end product-speci	130.4
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	116.8
421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	92.1
406964	M21305		gb:Human alpha satellite and satellite 3	80.7
443709	AI082692	Hs.134662	ESTs	67.1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	61.4
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	57.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	54.6
457200	U33749	Hs.197764	thyroid transcription factor 1	44.9
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	42.7
443324	R44013	Hs.164225	ESTs	39.8
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	27.3
442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	27.1
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	27.1
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	26.9
424084	AI940675	Hs.20914	hypothetical protein FLJ23056	22.2
421659	NM_014459	Hs.106511	protocadherin 17	21.0
450478	AW451709	Hs.271200	ESTs	20.2
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	19.7
447033	AI357412	Hs.157601	ESTs	19.4
445885	AI734009	Hs.127699	KIAA1603 protein	18.9
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	17.9
432437	W07088	Hs.293685	ESTs	17.8
424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	17.3
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	17.2
440807	AW269421	Hs.128093	ESTs	16.7
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	16.4
433365	AF026944	Hs.293797	ESTs	16.4
445279	R41900	Hs.22245	ESTs	16.4
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	16.4
405654				16.1
449328	AI962493	Hs.197647	ESTs	16.1
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	15.7
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	15.5
417728	AW138437	Hs.24790	KIAA1573 protein	15.0
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	14.8
452039	AI922988	Hs.172510	ESTs	14.4
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	14.3
421464	AA291553	Hs.190086	ESTs	14.1
421554	AW137676	Hs.97775	ESTs	13.8
431889	AA521277	Hs.124946	ESTs, Weakly similar to A46010 X-linked	13.2
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	13.2
431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	12.9
459702				12.7
421110	AJ250717	Hs.1355	cathepsin E	12.6
407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	12.6
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	12.5
423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	12.2
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	12.1
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	12.1
451561	N52812	Hs.177403	ESTs	12.0
424086	AI351010	Hs.102267	lysyl oxidase	12.0
435299	AI745458	Hs.122614	ESTs, Weakly similar to T20593 hypotheti	12.0
429496	AA453800	Hs.192793	ESTs	11.9

	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	403637				11.2
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	11.2
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	10.9
5	421470	R27496	Hs.1378	annexin A3	10.8
	440209	H05049	Hs.22269	neurexin 3	10.8
	428927	AA441837	Hs.90250	ESTs	10.7
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	10.5
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.4
10	416402	NM_000715	Hs.1012	complement component 4-binding protein,	10.4
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.4
	442176	AA983764	Hs.128910	ESTs	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
	452883	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	10.3
15	417015	M83772	Hs.80876	flavin containing monooxygenase 3	10.3
	422022	AA302420	Hs.200442	ESTs	10.3
	447724	AW298375	Hs.24477	ESTs	10.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	10.0
	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	9.9
20	446232	AI281848	Hs.194691	retinoic acid induced 3	9.9
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	9.9
	453382	AA709285	Hs.5997	hypothetical protein FLJ13078	9.8
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	9.8
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	9.8
25	407568	AA740964	Hs.62699	ESTs	9.8
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	9.6
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	9.5
	441484	AA935481	Hs.58972	ESTs	9.5
	422426	W79117	Hs.58559	ESTs	9.4
30	406747	AI925153	Hs.217493	annexin A2	9.4
	450050	AI681268	Hs.257883	ESTs	9.4
	431337	N48107	Hs.292593	ESTs	9.3
	408427	AW194270	Hs.177236	ESTs	9.3
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	9.3
35	453636	R67837	Hs.169872	ESTs	9.3
	443450	N66045	Hs.133529	ESTs	9.2
	418735	N48769	Hs.44609	ESTs	9.2
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	9.1
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	9.1
40	441233	AA972965	Hs.135568	ESTs	9.1
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	9.0
	436246	AW450963	Hs.119991	ESTs	9.0
	445189	AI936450	Hs.147482	ESTs	8.9
	410781	AI375672	Hs.165028	ESTs	8.9
45	446868	AV660737	Hs.135100	ESTs	8.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.8
	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	8.8
	410334	AW979261	Hs.291993	ESTs	8.8
50	442510	AF150179	Hs.249890	ESTs	8.8
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	8.7
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	8.7
	444929	AI685841	Hs.161354	ESTs	8.7
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	8.6
55	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	8.6
	412719	AW016610	Hs.129911	ESTs	8.6
	453445	AL036532	Hs.91453	ESTs	8.5
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	8.5
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	8.5
60	433815	AI696602	Hs.112757	ESTs	8.3
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.3
	451103	R52804	Hs.25956	DKFZP564D206 protein	8.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.3
	424989	AA985520	Hs.23575	ESTs	8.3
65	433231	AB040926	Hs.143552	KIAA1493 protein	8.2
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	8.1
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	8.1
	436751	AA732217	Hs.294054	ESTs	8.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	8.0
70	413048	M93221	Hs.75182	mannose receptor, C type 1	8.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	7.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	7.8
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.7
75	421013	M62397	Hs.1345	mutated in colorectal cancers	7.7
	437479	R61866	Hs.101277	ESTs	7.6
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	7.6
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	7.6
	444396	T65213	Hs.4257	ESTs	7.6
80	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	7.6
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.6
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	7.6
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	7.6

	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.5
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.5
	416030	H15261	Hs.21948	ESTs	7.5
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	7.4
5	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	7.4
	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	7.3
	432133	AB033088	Hs.272567	KIAA1262 protein	7.3
	447112	H17800	Hs.7154	ESTs	7.3
	446917	AI347863	Hs.156672	ESTs	7.3
10	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.3
	431761	AW002846	Hs.105468	hypothetical protein FLJ22690	7.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	7.2
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	7.2
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	7.2
15	438122	AI620270	Hs.129837	ESTs, Weakly similar to Z263_HUMAN ZINC	7.2
	449611	AI970394	Hs.197075	ESTs	7.2
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	7.2
	410060	NM_001448	Hs.58367	glypican 4	7.2
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
20	452571	W31518	Hs.34665	ESTs	7.2
	453736	AL118674	Hs.34871	zinc finger homeobox 1B	7.2
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	7.2
	405494				7.2
	442832	AW206560	Hs.253569	ESTs	7.1
25	420193	AI460080	Hs.202869	ESTs	7.1
	434217	AW014795	Hs.23349	ESTs	7.0
	427356	AW023482	Hs.97849	ESTs	7.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.9
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.9
30	442377	AA993807	Hs.167367	ESTs	6.9
	441143	AI027604	Hs.159650	ESTs	6.9
	445122	AW241632	Hs.147377	hypothetical protein FLJ23598	6.9
	431353	AA828032	Hs.189076	ESTs	6.9
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.8
35	426753	T89832	Hs.170278	ESTs	6.8
	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.8
	451963	AI825440	Hs.224952	ESTs	6.8
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.8
	433426	H69125	Hs.133525	ESTs	6.8
40	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	6.8
	415236	R41400		gb:yf94b12.s1 Soares infant brain 1NIB H	6.8
	409031	AA376836	Hs.76728	ESTs	6.7
	427558	D49493	Hs.2171	growth differentiation factor 10	6.7
	437259	AI377755	Hs.120695	ESTs	6.7
45	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	6.7
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	6.7
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	6.7
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	6.7
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.7
50	424750	D29956	Hs.152818	ubiquitin specific protease 8	6.6
	403574				6.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	6.6
	415025	AW207091	Hs.72307	ESTs	6.5
	448104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	6.5
55	444271	AW452569	Hs.149804	ESTs	6.5
	437157	BE048860	Hs.120655	ESTs	6.5
	444050	AW138295	Hs.135024	ESTs	6.5
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	6.5
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	6.5
60	424433	H04607	Hs.9218	ESTs	6.4
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	6.4
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	6.4
	422544	AB018259	Hs.118140	KIAA0716 gene product	6.4
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	6.3
65	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	6.3
	417246	AI760098	Hs.21411	ESTs	6.3
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	6.3
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	6.3
	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
70	446002	AI346468	Hs.145789	ESTs	6.3
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	6.3
	424202	BE350295	Hs.15032	RAN binding protein 17	6.3
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.2
75	415511	AI732617	Hs.182362	ESTs	6.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.2
	416879	H98899	Hs.42599	ESTs	6.2
	432803	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	6.2
	442862	BE080429	Hs.15738	ESTs	6.2
80	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	6.2
	441082	AW444804	Hs.202655	ESTs	6.2
	404599				6.1
	453931	AL121278	Hs.25144	ESTs	6.1

	420252	AW270404	Hs.193161	ESTs	6.1
	431622	AW979271	Hs.293184	ESTs	6.1
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.1
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.0
5	424693	BE169810	Hs.47557	ESTs	6.0
	419172	AW338625	Hs.22120	ESTs	6.0
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.0
	453037	AA045175	Hs.177552	ESTs	6.0
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.0
10	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	6.0
	422352	AA766296	Hs.99200	ESTs	5.9
	433527	AW235613	Hs.133020	ESTs	5.9
	420077	AW512260	Hs.87767	ESTs	5.9
	429703	T93154	Hs.28705	ESTs	5.9
15	433096	AW190593	Hs.151143	ESTs	5.9
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	5.9
	449416	AI651016	Hs.246311	ESTs	5.9
	459023	AW968226	Hs.60798	ESTs	5.9
	450584	AA040403	Hs.60371	ESTs	5.9
20	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.9
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.9
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	5.9
	433479	AW511459	Hs.249972	ESTs	5.8
	443113	AI040666	Hs.132908	ESTs	5.8
25	430414	AW365665	Hs.120388	ESTs	5.8
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	5.8
	435420	AI928513	Hs.59203	ESTs	5.8
	404916				5.8
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.8
30	448253	H25899	Hs.201591	ESTs	5.8
	430899	BE016217	Hs.183528	hypothetical protein FLJ14906	5.8
	446967	AI699629	Hs.156781	ESTs	5.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	5.7
	436842	AA827176	Hs.124316	ESTs	5.7
35	437260	AA747807	Hs.149500	ESTs	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	428043	T92248	Hs.2240	uteroglobin	5.7
	408045	AW138959	Hs.245123	ESTs	5.7
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	5.7
40	428508	BE252383	Hs.184668	SBBI31 protein	5.7
	453393	AW956392	Hs.110376	ESTs	5.6
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	5.6
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.6
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	5.6
45	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	404043				5.5
	415094	D59513	Hs.330778	ESTs	5.5
	453049	BE537217	Hs.30343	ESTs	5.5
50	430153	AW968128	Hs.336679	ESTs	5.5
	410811	AW805687	Hs.300648	ESTs	5.5
	443903	AI220547	Hs.135223	ESTs	5.5
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	5.5
	444471	AB020684	Hs.11217	KIAA0877 protein	5.5
55	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.5
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.5
	432113	AA935065	Hs.152385	ESTs	5.5
	446608	N75217	Hs.257846	ESTs	5.5
	419945	AW290975	Hs.118923	ESTs	5.5
60	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	5.4
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	5.4
	439382	BE247684	Hs.103070	ESTs	5.4
	428895	AA437124	Hs.187247	ESTs	5.4
	446577	AB040933	Hs.15420	KIAA1500 protein	5.4
65	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	427778	AA412323	Hs.105323	ESTs	5.4
	437138	AI935622	Hs.271245	ESTs	5.4
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	5.4
	430437	AI758801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.4
70	435202	AI971313	Hs.170204	KIAA0551 protein	5.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	5.3
	434992	AA658501	Hs.283358	ESTs	5.3
	454039	AW079064	Hs.245540	ESTs	5.3
	456408	AI288348	Hs.23450	mitochondrial ribosomal protein S25	5.3
75	406554				5.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.3
	416769	AI339257	Hs.115436	ESTs, Moderately similar to I54374 gene	5.3
	414299	AA142989	Hs.71730	ESTs	5.3
	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.3
80	459664				5.3
	425509	AF079363	Hs.158213	sperm associated antigen 6	5.3
	401497				5.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	5.2

	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.2
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypotheti	5.2
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	5.2
	451050	AW937420	Hs.69662	ESTs	5.2
5	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	5.2
	404957				5.2
	452771	T05477	Hs.333265	ESTs	5.2
	438885	AI886558	Hs.184987	ESTs	5.2
	426244	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.2
10	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	5.2
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.2
	408729	AA195764	Hs.72639	ESTs	5.1
	457100	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	5.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.1
15	417154	AI674701	Hs.21388	ESTs	5.1
	411869	W20027	Hs.23439	ESTs	5.1
	427043	AA397679	Hs.3991	ESTs	5.1
	445635	AI769774	Hs.209631	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	5.1
20	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	5.1
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	5.1
	408677	AI279892	Hs.46801	sorting nexin 14	5.0
	404097				5.0
	437636	AA764781	Hs.291844	ESTs	5.0
25	452822	X85689	Hs.288617	hypothetical protein FLJ22621	5.0
	410733	D84284	Hs.66052	CD38 antigen (p45)	5.0
	439140	W85737	Hs.290830	ESTs	5.0
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	5.0
	405547				5.0
30	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	5.0
	449168	NM_016206	Hs.23142	colon carcinoma related protein	5.0
	455431	AW938484		gb:CM0-DT0057-290200-253-d06 DT0057 Homo	5.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.0
	411149	N68715	Hs.269128	ESTs	5.0
35	432441	AW292425	Hs.163484	ESTs	5.0
	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	450109	AI539295	Hs.115740	KIAA0210 gene product	5.0
	449695	AA164569	Hs.34550	ESTs	5.0
40	421764	AI681535	Hs.148135	serine/threonine kinase 33	4.9
	404593				4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (f	4.9
	419235	AW470411	Hs.288433	neurotrimin	4.9
45	436304	AA339622	Hs.108867	ESTs	4.9
	434613	AI821826		gb:ns92b10.x5 NCI_CGAP_Pr3 Homo sapiens	4.9
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	4.9
	415245	N59650	Hs.27252	ESTs	4.9
	428780	AI478578	Hs.50636	ESTs	4.9
50	406333				4.9
	445034	AW293376	Hs.143659	ESTs	4.8
	440202	AW516211	Hs.125300	ring finger protein 21, interferon-respo	4.8
	424638	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	4.8
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	4.8
55	427652	AI673025	Hs.43874	ESTs, Moderately similar to I54374 gene	4.8
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.8
	407327	AA467182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415261	T40928	Hs.8346	ESTs	4.8
60	453543	AA485425	Hs.48919	Homo sapiens cDNA FLJ11508 fis, clone HE	4.8
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HE	4.8
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	4.8
	441006	AW605267	Hs.7627	CGI-60 protein	4.8
	412222	AA526283	Hs.292737	ESTs	4.8
65	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypotheti	4.8
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.8
	439398	AA284267	Hs.221504	ESTs	4.8
	436397	AA715013	Hs.169835	ESTs	4.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	4.8
70	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	425916	NM_006786	Hs.162200	urotensin 2	4.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	4.8
	427457	AW779105	Hs.164682	ESTs	4.7
	451620	AW449888	Hs.257224	ESTs	4.7
75	408938	AA059013	Hs.22607	ESTs	4.7
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	4.7
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	4.7
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.7
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	4.7
80	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	435347	AW014873	Hs.116963	ESTs	4.7
	425458	H89317	Hs.182889	ESTs	4.7
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	4.7

436594	AI419982	Hs.156189	ESTs	4.7
421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	4.7
432731	R31178	Hs.287820	fibronectin 1	4.7
419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	4.7
426320	W47595	Hs.169300	transforming growth factor, beta 2	4.7
419751	AW195581	Hs.93121	KIAA0761 protein	4.6
433515	AA595800	Hs.190246	ESTs	4.6
451381	BE241831	Hs.172330	hypothetical protein MGC2705	4.6
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	4.6
438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	4.6
406992	S82472		gb:beta -pol=DNA polymerase beta (exon a	4.6
431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
435933	AA805520	Hs.192075	ESTs	4.6
447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	4.6
445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	4.6
426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypotheti	4.6
423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapi	4.6
424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.6
416258	N45661	Hs.90011	adenylosuccinate synthase	4.6
410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	4.6
454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	4.5
422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	4.5
433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
450192	AA263143	Hs.24596	RAD51-interacting protein	4.5
432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	4.5
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	4.5
409041	AB033025	Hs.50081	KIAA1199 protein	4.5
434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.5
452526	W38537	Hs.280740	hypothetical protein MGC3040	4.5
403271				4.5
450656	AA010539	Hs.18912	ESTs	4.5
446096	AI276454		gb:ql71a12.x1 Soares_NhHMPu_S1 Homo sapi	4.5
454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
437960	AI669586	Hs.222194	ESTs	4.5
440662	H39048	Hs.127432	ESTs	4.5
410615	AW772721		gb:hl95c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.5
413583	AL120806	Hs.5888	ESTs	4.5
419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	4.5
442324	R63578	Hs.28426	ESTs	4.4
453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
435747	AI079519	Hs.134398	ESTs	4.4
446509	AF169693	Hs.132892	protocadherin 20	4.4
448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.4
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.4
448089	AI467945	Hs.173696	ESTs	4.4
434367	AB020700	Hs.3830	KIAA0893 protein	4.4
434757	AI038997	Hs.132921	ESTs	4.4
413453	AA129640	Hs.128065	ESTs	4.4
454438	AA224053	Hs.172405	cell division cycle 27	4.4
458154	AW816379	Hs.335018	ESTs	4.4
430417	AA461045	Hs.50701	ESTs	4.4
434819	AA650099	Hs.291541	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.4
438796	W67821	Hs.109590	genethonin 1	4.4
415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.4
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.4
414812	X72755	Hs.77367	monokine induced by gamma interferon	4.4
451895	T93573	Hs.16970	ESTs	4.4
435434	AA680387	Hs.187850	ESTs	4.4
449623	C00719	Hs.120440	EST	4.4
433563	AI732637	Hs.277901	ESTs	4.3
444649	AW207523	Hs.197628	ESTs	4.3
441594	AL041080	Hs.208765	ESTs, Moderately similar to ALU7_HUMAN A	4.3
443314	AW771701	Hs.54646	ESTs	4.3
400292	AA250737	Hs.72472	ESTs	4.3
427972	AA864870	Hs.181304	putative gene product	4.3
446932	AA961459	Hs.125644	ESTs	4.3
445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.3
452393	H87398	Hs.99858	ribosomal protein L7a	4.3
443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	4.3
400608				4.3
411156	AW819939	Hs.273629	ESTs	4.3
435772	AA700019	Hs.132992	ATP-binding cassette, sub-family G (WHIT	4.3
439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	4.3
455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	4.3
443257	AI334040	Hs.11614	HSPC065 protein	4.3
436033	H75391	Hs.255748	ESTs	4.3
420214	AI146375	Hs.286073	ESTs, Moderately similar to ALU5_HUMAN A	4.3
410519	AW612264	Hs.131705	ESTs	4.3
401189				4.3
418852	BE537037	Hs.273294	hypothetical protein FLJ20069	4.3
425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3

	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	4.3
	434677	AW444575	Hs.130834	ESTs	4.3
	403310				4.3
	451830	H18433	Hs.21542	KIAA1035 protein	4.3
5	422222	AI699372	Hs.193247	hypothetical protein DKFZp434A171	4.3
	435627	W88774	Hs.118370	ESTs	4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	452166	AI948607	Hs.264680	ESTs	4.3
	413998	AW103807	Hs.243933	ESTs	4.2
10	416642	T96118	Hs.226313	ESTs	4.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	4.2
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	4.2
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	4.2
15	424641	AB001106	Hs.151413	glia maturation factor, beta	4.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
	458771	AW295151	Hs.163612	ESTs	4.2
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	4.2
20	436645	AW023424	Hs.156520	ESTs	4.2
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	4.2
	445268	AI218358	Hs.175048	ESTs	4.2
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.2
	431917	D16181	Hs.2868	peripheral myelin protein 2	4.2
25	443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	4.2
	443151	AI827193	Hs.132714	ESTs	4.2
	419255	AA235672	Hs.87491	ESTs	4.2
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
	452561	AI692181	Hs.49169	KIAA1634 protein	4.2
30	421106	AA877124	Hs.172844	ESTs	4.2
	424268	AA397653	Hs.307438	Human DNA sequence from clone 495O10 on	4.2
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.2
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	4.2
	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	4.2
35	426771	AB028992	Hs.193143	KIAA1069 protein	4.1
	445745	AB007924	Hs.13245	KIAA0455 gene product	4.1
	417009	AA191719	Hs.314714	ESTs	4.1
	436517	BE080932	Hs.135225	ESTs	4.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.1
40	414083	AL121282	Hs.257786	ESTs	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	4.1
	441802	AA968636	Hs.127877	ESTs	4.1
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.1
45	413875	BE175776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	4.1
	444009	AI380792	Hs.135104	ESTs	4.1
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	4.1
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
50	435256	AF193766	Hs.13872	cytokine-like protein C17	4.1
	428104	AA421350	Hs.191604	ESTs	4.1
	439648	AW780192	Hs.267596	ESTs	4.1
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	4.1
	446364	AB006624	Hs.14912	KIAA0286 protein	4.1
55	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E062 (fr	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	4.0
	404561				4.0
	401575				4.0
60	419296	AA236115	Hs.120785	ESTs	4.0
	432055	AW972359	Hs.293334	ESTs	4.0
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	4.0
	450320	AW291775	Hs.213793	ESTs	4.0
	447350	AI375572	Hs.172634	ESTs	4.0
65	441974	AI683782	Hs.128245	ESTs	4.0
	453142	AA033648	Hs.7473	ESTs	4.0
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.0
	410292	AA843087	Hs.124194	ESTs	4.0
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
70	420218	AW958037	Hs.286	ribosomal protein L4	4.0
	426625	T78300	Hs.300642	serologically defined colon cancer antig	4.0
	417708	N74392	Hs.50495	ESTs	4.0
	451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_	4.0
	411745	AW867626		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
75	422058	AA662231	Hs.334443	ESTs	4.0
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	4.0
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.0
	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.0
80	453096	AW294631	Hs.11325	ESTs	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
	421002	AF116030	Hs.100932	transcription factor 17	4.0
	445414	AV653692	Hs.146105	ESTs	4.0

447207	AA442233	Hs.17731	hypothetical protein FLJ12892	.4.0
451353	N21043	Hs.42932	ESTs	4.0
437075	AA743746	Hs.40758	ESTs	3.9
410505	AW752139	Hs.314323	ESTs	3.9
449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	3.9
426116	AA868729	Hs.144694	ESTs	3.9
415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	3.9
436298	AW293496	Hs.180138	ESTs	3.9
417718	T86540	Hs.193981	ESTs	3.9
436772	AW975688	Hs.74170	metallothionein 1E (functional)	3.9
401045				3.9
408767	AA057279	Hs.211928	ESTs	3.9
407303	AA016296	Hs.165200	ESTs, Weakly similar to A56194 thromboxa	3.9
432563	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	3.9
451623	H77818	Hs.268991	ESTs	3.9
450063	AI681509	Hs.277133	ESTs	3.9
416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.9
419276	BE165909	Hs.306881	MSTP043 protein	3.9
433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
436149	AI754308	Hs.159452	ESTs	3.9
422667	H25642	Hs.133471	ESTs	3.9
443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.9
458219	H22195	Hs.31874	ESTs	3.9
443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.9
439810	AL109710	Hs.85568	EST	3.9
436578	AI091435	Hs.134859	ESTs	3.9
415598	AI433165	Hs.9856	ESTs	3.9
425087	R62424	Hs.126059	ESTs	3.9
454111	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypothetl	3.9
409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	3.9
452466	N84635	Hs.29664	hypothetical protein DKFZp564B052	3.9
424962	NM_012288	Hs.153954	TRAM-like protein	3.9
435823	R07856	Hs.16355	ESTs	3.9
440633	AI140686	Hs.263320	ESTs	3.9
429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	3.9
444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.9
430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
417461	R38403	Hs.13305	ESTs	3.9
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.8
419140	AI982647	Hs.215725	ESTs	3.8
415652	T79213	Hs.272073	ESTs	3.8
430140	AW296771	Hs.221999	ESTs	3.8
446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.8
422165	AL041199	Hs.1481	histidine decarboxylase	3.8
417706	T90797	Hs.268623	ESTs	3.8
424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.8
450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.8
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.8
449729	R72032	Hs.29235	ESTs	3.8
414700	H63202	Hs.38163	ESTs	3.8
440899	AW449445	Hs.120021	DKFZP434I092 protein	3.8
439335	AA742597	Hs.62492	ESTs, Weakly similar to B39066 proline-r	3.8
408625	AW243323	Hs.266785	ESTs	3.8
421987	AI133161	Hs.286131	CGI-101 protein	3.8
418915	AI474778	Hs.118977	ESTs	3.8
410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.8
429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
442849	R10099	Hs.269805	ESTs	3.8
427191	BE221825	Hs.97691	ESTs	3.8
407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.8
437030	AA742577	Hs.303781	EST	3.8
427940	AA417812	Hs.38775	ESTs	3.7
443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
449679	AI823951	Hs.129700	tolloid-like 1	3.7
425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	3.7
456443	AW967500	Hs.133543	ESTs	3.7
439957	AI453184	Hs.66357	ESTs	3.7
446999	AA151520	Hs.334822	hypothetical protein MGC4485	3.7
428414	AL049980	Hs.184216	DKFZP564C152 protein	3.7
455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.7
418379	AA218940	Hs.137516	fidgetin-like 1	3.7
419720	AA249131	Hs.337778	hypothetical protein FLJ11068	3.7
443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.7
416185	AW975861	Hs.47367	KIAA1785 protein	3.7
417235	AA810278	Hs.24250	ESTs	3.7
441720	AI346487	Hs.28739	ESTs	3.7
451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
417355	D13168	Hs.82002	endothelin receptor type B	3.7
449321	AA001150	Hs.132937	ESTs	3.7
424806	AA362523	Hs.105689	MSTP031 protein	3.7
452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	3.7
409248	AB033035	Hs.51965	KIAA1209 protein	3.7

	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	429419	AB023226	Hs.202276	KIAA1009 protein	3.7
	447410	AI470235	Hs.172698	EST	3.7
	404274				3.7
	416320	H47867	Hs.34024	ESTs	3.7
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	3.7
10	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.7
	446025	AW305075	Hs.180948	KIAA0729 protein	3.7
	450458	AA009926		gb:zi07e05.r1 Soares_fetal_liver_spleen_	3.6
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	3.6
	438257	AW474419	Hs.224794	ESTs	3.6
15	440887	AI799488	Hs.135905	ESTs	3.6
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.6
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	3.6
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (fr	3.6
	407726	AA435679	Hs.88594	ESTs	3.6
20	436026	AI349764	Hs.217081	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	452293	AI871633	Hs.304609	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.6
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.6
25	429208	AA447990	Hs.190478	ESTs	3.6
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	3.6
	404476				3.6
	405848				3.6
	436209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.6
30	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	432408	N39127	Hs.332557	ESTs, Weakly similar to A46010 X-linked	3.6
	437641	AA811452	Hs.291911	ESTs	3.6
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.6
35	446102	AW168067	Hs.252956	ESTs	3.6
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
40	452055	AI377431	Hs.141693	hypothetical protein MGC10858	3.6
	440801	AA906366	Hs.190535	ESTs	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	440886	AW511032	Hs.190516	ESTs	3.6
	401049				3.6
45	449424	AW448937	Hs.197030	ESTs	3.6
	418076	R61388	Hs.6724	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	3.6
	438016	AI949638	Hs.336846	EST	3.6
50	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.6
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	3.5
	456536	AW135986	Hs.257859	ESTs	3.5
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
55	435344	AA700326	Hs.190599	ESTs	3.5
	445056	AB014530	Hs.12259	KIAA0630 protein	3.5
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.5
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
60	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	3.5
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.5
	428409	AW117207	Hs.98523	ESTs	3.5
	431087	H12723	Hs.290791	ESTs	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
65	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	437583	AA761190	Hs.244627	ESTs	3.5
	421599	AA293655	Hs.97293	ESTs	3.5
	433687	AA743991		gb:ny57g01.s1 NCI_CGAP_Pr18 Homo sapiens	3.5
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	3.5
70	430499	AW969408	Hs.231991	ESTs	3.5
	451531	AA018311	Hs.114762	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	410658	AW105231	Hs.192035	ESTs	3.5
	427865	AA416931	Hs.126065	ESTs	3.5
75	453390	AA862496	Hs.26482	ESTs	3.5
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	427718	AI798680	Hs.25933	ESTs	3.5
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.5
80	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	442080	AW444761	Hs.44565	ESTs	3.5
	406685	M18728		gb:Human nonspecific crossreacting antig	3.5

	404200				3.5
	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	432868	AW974093	Hs.292775	ESTs	3.5
5	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.4
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	3.4
	428775	AA434579	Hs.143691	ESTs	3.4
	410004	AI298027	Hs.5057	carboxypeptidase D	3.4
10	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	441736	AW292779	Hs.169799	ESTs	3.4
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	3.4
	405970				3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
15	459482	AA625339	Hs.237052	EST, Weakly similar to I38022 hypothetic	3.4
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.4
	410604	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.4
	402230				3.4
	436120	AI248193	Hs.119860	ESTs	3.4
20	405336				3.4
	434374	AA631439		gb:np85d02.s1 NCI_CGAP_Thy1 Homo sapiens	3.4
	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	3.4
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.4
	416057	AI927382	Hs.29857	ESTs	3.4
25	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	3.4
	436088	AA704687	Hs.191294	ESTs	3.4
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.4
	454076	AW204712	Hs.61957	ESTs	3.4
	431733	AW298410	Hs.21475	ESTs	3.4
30	432974	BE348793	Hs.233331	ESTs	3.4
	412576	AA447718	Hs.107057	ESTs	3.4
	446142	AI754693	Hs.145968	ESTs	3.4
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	3.4
	433384	AI021992	Hs.124244	ESTs	3.4
35	413621	AI808648	Hs.184156	ESTs	3.4
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	436111	AI803082	Hs.157212	ESTs	3.4
	421236	AI287622	Hs.151956	ESTs	3.4
	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	3.4
40	403515				3.4
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	3.4
	453375	AI990114	Hs.240091	ESTs	3.4
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	3.4
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
45	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	3.4
	409642	AW450809	Hs.257347	ESTs	3.4
	420092	AA814043	Hs.88045	ESTs	3.4
	453365	AA035211	Hs.17404	ESTs	3.3
	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti	3.3
50	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.3
	439024	R96696	Hs.35598	ESTs	3.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.3
	417991	AA731452	Hs.190008	ESTs	3.3
	403356				3.3
55	433650	AA603472	Hs.28456	ESTs	3.3
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.3
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	3.3
	413714	AI560944	Hs.71428	ESTs	3.3
	430887	N66801	Hs.260287	KIAA1841 protein	3.3
60	413618	BE154078		gb:PM0-HT0339-200400-010-F04 HT0339 Homo	3.3
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	405692				3.3
	432809	AA565509	Hs.131703	ESTs	3.3
65	433605	AA706910	Hs.112742	ESTs	3.3
	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	3.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heregulin	3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.3
70	410434	AF051152	Hs.63668	toll-like receptor 2	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	3.3
	444301	AK000136	Hs.10760	asporin (LRR class 1)	3.3
	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyll	3.3
75	458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.3
	435934	R19382	Hs.117869	ESTs	3.3
	400269				3.3
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.3
	412903	BE007967	Hs.155795	ESTs	3.3
80	400889				3.3
	449585	AI655321	Hs.197693	ESTs	3.3
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.3
	418557	BE140602	Hs.246645	ESTs	3.3

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	453204	R10799	Hs.191990	ESTs	3.3
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
5	446645	AI336596	Hs.156294	ESTs	3.3
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	3.3
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (defline not ava	3.3
	403895				3.2
10	414899	AW975433	Hs.36288	ESTs	3.2
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.2
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
15	437073	AI885608	Hs.94122	ESTs	3.2
	443830	AI142095	Hs.143273	ESTs	3.2
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_Ut2 Homo sapiens	3.2
	417561	AW974345		gb:EST386449 MAGE resequences, MAGM Homo	3.2
20	446063	AI720140	Hs.151079	ESTs	3.2
	423609	AA326348	Hs.218289	ESTs	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.2
	435808	AA702666	Hs.113150	ESTs	3.2
25	424001	W67883	Hs.137476	paternally expressed 10	3.2
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	3.2
	418946	AI798841	Hs.164526	ESTs	3.2
	431750	AA514986	Hs.283705	ESTs	3.2
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.2
30	428268	AA424957	Hs.294132	ESTs	3.2
	418878	W20090	Hs.6616	ESTs	3.2
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.2
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	3.2
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.2
35	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens	3.2
	407339	AA777542	Hs.132670	ESTs	3.2
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	3.2
40	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	421187	NM_014721	Hs.102471	KIAA0680 gene product	3.2
45	419929	U90268	Hs.93810	cerebral cavernous malformations 1	3.2
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.2
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.2
	438839	AW297945	Hs.128490	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
50	427961	AW293165	Hs.143134	ESTs	3.2
	429228	AI553633	Hs.337139	ESTs	3.2
	431548	AI834273	Hs.9711	novel protein	3.1
	441839	AW975512	Hs.29160	ESTs	3.1
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.1
55	441274	AW593781	Hs.131357	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	436154	AA764950	Hs.119898	ESTs	3.1
	406752	AI285598		gb:qu49f06.x1 NCI_CGAP_Lym6 Homo sapiens	3.1
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	3.1
60	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
	436739	BE208022	Hs.127685	KIAA1627 protein	3.1
	451674	AA019104	Hs.175483	Homo sapiens cDNA: FLJ22016 fis, clone H	3.1
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	3.1
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.1
65	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	3.1
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	3.1
	456551	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.1
70	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.1
	431814	BE256242	Hs.270847	delta-tubulin	3.1
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	436401	AI087958	Hs.29088	ESTs	3.1
	437439	H29796	Hs.269622	ESTs	3.1
75	403277				3.1
	408547	AA574291	Hs.57837	ESTs	3.1
	424131	AA335714	Hs.199665	ESTs	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	3.1
	434636	AA083764	Hs.6101	hypothetical protein MGC3178	3.1
80	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.1
	407905	AW103655	Hs.252905	ESTs	3.1
	452311	AW304029	Hs.252744	ESTs	3.1

	434849	AW292765	Hs.8053	ESTs	3.1
	446770	AV660309	Hs.154986	ESTs, Weakly similar to PLLP_HUMAN PLASM	3.1
	424238	AA337401	Hs.137635	ESTs	3.1
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.1
5	447829	AI433029	Hs.164104	ESTs	3.1
	406506				3.1
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.1
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.1
	451229	AW967707	Hs.48473	ESTs	3.1
10	401103				3.1
	433589	AA886530	Hs.188912	ESTs	3.1
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	3.1
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	3.1
	404288				3.1
15	406195				3.1
	438202	AW169287	Hs.22588	ESTs	3.1
	425516	BE000707	Hs.29567	ESTs	3.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.1
	422692	AA332376	Hs.24135	transmembrane protein vezatin; hypotheti	3.1
20	435414	AW270550	Hs.116957	ESTs	3.1
	418950	T78517	Hs.13941	ESTs	3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	3.1
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.1
25	459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	3.1
	421823	N40850	Hs.28625	ESTs	3.1
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.1
	452896	AA831508	Hs.32553	ESTs	3.1
	425895	AI269484	Hs.161427	zinc finger protein 215	3.1
30	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	3.1
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	3.1
	401862				3.1
	444325	AW152618	Hs.16757	ESTs	3.1
	408171	AA301228	Hs.43299	hypothetical protein FLJ12890	3.1
35	423949	AI014546	Hs.130912	ESTs	3.1
	419519	AI198719	Hs.176376	ESTs	3.0
	434683	AW298724	Hs.202639	ESTs	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	415086	AI597963	Hs.118726	ESTs	3.0
40	419220	AA811938	Hs.291759	ESTs	3.0
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	3.0
	405090				3.0
45	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	443253	AI041212	Hs.132117	ESTs	3.0
	444974	AI203500	Hs.151612	ESTs	3.0
	445717	AW664658	Hs.149332	ESTs	3.0
	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
50	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.0
	424406	D54120	Hs.146409	cell division cycle 42 (GTP-binding prot	3.0
	410371	AA084482	Hs.115850	ESTs	3.0
	426384	AI472078	Hs.303662	ESTs	3.0
55	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	3.0
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo	3.0
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	3.0
60	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.0
	447482	AB033059	Hs.18705	KIAA1233 protein	3.0
	439416	W58294	Hs.56254	ESTs	3.0
	436635	AW104325	Hs.272093	ESTs, Weakly similar to I78885 serine/th	3.0
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.0
65	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	3.0
	415452	F09134	Hs.12839	ESTs	3.0
	427874	AA732367	Hs.98198	ESTs	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	3.0
70	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Homo	3.0
	415122	D60708	Hs.22245	ESTs	3.0
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.0
	400227				3.0
	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	3.0
75	419503	AA243642	Hs.137422	ESTs	3.0
	446563	BE326588	Hs.141454	ESTs	3.0
	457285	AI038858	Hs.130522	Kv channel-interacting protein 1	3.0
	434998	AW975157	Hs.26037	ESTs	3.0
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.0
80	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	449856	AA203155	Hs.18200	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN A	3.0

	442994	AI026718	Hs.16954	ESTs	3.0
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	3.0
	421072	AI215069	Hs.89113	ESTs	3.0
	456273	AF154846	Hs.1148	zinc finger protein	3.0
5	404548				3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	445413	AA151342	Hs.12677	CGI-147 protein	3.0
	418717	AI334430	Hs.86984	ESTs	3.0
10	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.0
	407758	D50915	Hs.38365	KIAA0125 gene product	3.0
	431906	AW328038	Hs.37486	ESTs	3.0
	424968	AA349086	Hs.259746	ESTs, Weakly similar to A46010 X-linked	3.0
	431023	AI283133	Hs.297420	ESTs	3.0
15	432596	AJ224741	Hs.278461	matrilin 3	3.0
	452412	AA029608	Hs.61373	ESTs	3.0
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to T2D4_HUMAN TRANS	2.9
	408321	AW405882	Hs.44205	cortistatin	2.9
20	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN !	2.9
	400880				2.9
	417014	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!!	2.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.9
	406603				2.9
25	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	2.9
	427878	C05766	Hs.181022	CGI-07 protein	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.9
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.9
30	422634	NM_016010	Hs.118821	CGI-62 protein	2.9
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.9
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.9
	408525	AW206972	Hs.253595	ESTs	2.9
	412248	BE176480		gb:RC3-HT0585-160300-022-c02 HT0585 Homo	2.9
35	432507	BE391093	Hs.324667	ESTs	2.9
	447290	AI476732	Hs.263912	ESTs	2.9
	424188	AW954552	Hs.142634	zinc finger protein	2.9
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
40	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131975	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9
45	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	2.9
	444339	T96555	Hs.31562	ESTs	2.9
	446745	AW118189	Hs.156400	ESTs	2.9
	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
	430573	AA744550	Hs.136345	ESTs	2.9
50	451073	AI758905	Hs.206063	ESTs	2.9
	440575	AA889870	Hs.126006	ESTs	2.9
	402046				2.9
	426882	AA393108	Hs.97365	ESTs	2.9
	435738	AA699633	Hs.269543	ESTs, Weakly similar to A56194 thromboxa	2.9
55	420656	AA279098	Hs.187636	ESTs	2.9
	438323	AI985394	Hs.123369	ESTs	2.9
	453123	AI953718	Hs.221849	ESTs	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
60	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	2.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	2.9
	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.9
65	442118	AA976718	Hs.202242	ESTs	2.9
	420727	H75701	Hs.99886	complement component 4-binding protein,	2.9
	433849	BE465884	Hs.280728	ESTs	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	429826	N93266	Hs.40747	ESTs	2.9
70	437913	AI140825	Hs.121623	ESTs	2.9
	441330	AI692984	Hs.129354	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.9
75	444631	AW995395	Hs.84520	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.9
	458186	AA904244	Hs.153205	ESTs	2.9
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.9
	415757	AA830854	Hs.187810	ESTs	2.9
	449299	AA299919	Hs.84561	ESTs	2.9
80	457003	S78234	Hs.172405	cell division cycle 27	2.9
	408675	NM_015434	Hs.48604	DKFZP434B168 protein	2.9
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.9
	426174	AA547959	Hs.115838	ESTs	2.9

	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	2.9
	429950	AW081608	Hs.105053	ESTs	2.9
	412733	AA984472	Hs.74554	KIAA0080 protein	2.9
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
5	442655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	2.9
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	430447	W17064	Hs.332848	SWI/SNF related, matrix associated, acti	2.9
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	2.9
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.9
10	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.9
	401094				2.9
	401526				2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
15	418282	AA215535	Hs.98133	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	450006	AI241555	Hs.60171	ESTs	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	2.8
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	2.8
20	403329				2.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.8
	419038	AW134924	Hs.190325	ESTs	2.8
	440106	AA864968	Hs.127699	KIAA1603 protein	2.8
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.8
25	431745	AW972448	Hs.163425	ESTs	2.8
	421426	AA291101	Hs.33020	Homo sapiens, clone tMAGE:3939163, mRNA,	2.8
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.8
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.8
	441790	AW294909	Hs.132208	ESTs	2.8
30	404443				2.8
	428129	AI244311	Hs.26912	ESTs	2.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.8
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	2.8
	449327	AI638743	Hs.224672	ESTs	2.8
35	400983				2.8
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	2.8
	411213	AA676939	Hs.69285	neuropilin 1	2.8
	420896	AW149342	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	2.8
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.8
40	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	440192	AA872282	Hs.190596	ESTs	2.8
45	448466	AI522109	Hs.171066	ESTs	2.8
	414869	AA157291	Hs.21479	ubinuclein 1	2.8
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
50	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.8
	434812	AA649860	Hs.189496	ESTs	2.8
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	2.8
	455512	AW983608		gb:RC3-HN0001-240400-012-c01 HN0001 Homo	2.8
	408380	AF123050	Hs.44532	diubiquitin	2.8
55	435990	AI015862	Hs.131793	ESTs	2.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	432798	AA565309	Hs.194015	ESTs	2.8
	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	2.8
	438886	AA827728	Hs.128705	ESTs, Weakly similar to AF149422 2 unkno	2.8
60	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.8
	416940	N75620	Hs.43157	ESTs	2.8
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	2.8
	438398	AA806526	Hs.130277	ESTs	2.8
	435313	AI769400	Hs.189729	ESTs	2.8
65	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	2.8
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	2.8
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.8
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.8
	401323				2.8
70	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.8
	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	2.8
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.8
	406970	M29994		gb:Human alpha-I spectrin gene, exon 12.	2.8
75	426172	AA371307	Hs.125056	ESTs	2.8
	452114	N22687	Hs.8236	ESTs	2.8
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
80	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.8
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.8
	429881	T80112	Hs.192245	ESTs	2.8
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.8

409435	AI810721	Hs.95424	ESTs	2.8
442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.8
407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	2.8
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.8
412189	R60982	Hs.22581	ESTs	2.8
420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.8
448330	AL036449	Hs.207163	ESTs	2.8
418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
422505	AL120862	Hs.124165	ESTs	2.8
427752	AA470687	Hs.104772	ESTs	2.8
433513	AI566356	Hs.171437	ESTs	2.8
433703	AA210863	Hs.3532	nemo-like kinase	2.8
448912	D83781	Hs.22559	KIAA0197 protein	2.8
405621				2.8
430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.8
450400	AI694722	Hs.279744	ESTs	2.8
456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.8
418342	BE002723	Hs.226627	leptin receptor	2.8
420756	AA411800	Hs.189900	ESTs	2.8
423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	2.8
457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
439831	AW136488	Hs.25545	ESTs	2.8
425661	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	2.8
407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	2.8
418658	AW874263	Hs.32468	ESTs	2.8
409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
421340	F07783	Hs.1369	decay accelerating factor for complement	2.8
449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.8
409241	AF070602	Hs.51649	Homo sapiens clone 24504 mRNA sequence	2.8
448219	AA228092	Hs.42656	KIAA1681 protein	2.8
408936	AL138043	Hs.293549	ESTs	2.8
410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
426471	M22440	Hs.170009	transforming growth factor, alpha	2.8
454455	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	2.8
455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
401335				2.7
436577	W84774	Hs.17643	ESTs	2.7
409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.7
421003	T72080	Hs.95667	F-box protein 30	2.7
429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.7
436007	AI247716	Hs.232168	ESTs	2.7
408874	AW818091	Hs.252730	ESTs	2.7
418036	Z37976	Hs.83337	latent transforming growth factor beta b	2.7
435625	H50654	Hs.113999	ESTs	2.7
435766	R11673	Hs.186498	ESTs	2.7
410327	T33130	Hs.301746	RAP2A, member of RAS oncogene family	2.7
416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
427134	AA398409	Hs.173561	EST	2.7
428137	AA421792	Hs.170999	ESTs	2.7
429710	AI337113	Hs.146025	hypothetical protein FLJ23594	2.7
430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.7
441928	AI370188	Hs.211454	ESTs	2.7
409721	AW887732	Hs.257861	ESTs	2.7
427112	Z32887	Hs.290951	ESTs	2.7
403776				2.7
420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
427839	AA603823	Hs.98244	ESTs	2.7
432837	AA310693	Hs.87329	HSPC072 protein	2.7
438782	AA828380	Hs.126733	ESTs	2.7
449396	BE169100	Hs.195029	ESTs	2.7
458043	AW979009	Hs.326108	ESTs	2.7
438171	AW976507	Hs.293515	ESTs	2.7
452959	AI933416	Hs.189674	ESTs	2.7
439556	AI623752	Hs.163603	ESTs	2.7
446152	AI292036	Hs.150028	ESTs	2.7
434803	AW974640	Hs.303413	ESTs	2.7
407771	AL138272	Hs.62713	ESTs	2.7
411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.7
417543	AA203620	Hs.110153	ESTs	2.7
401517				2.7
403677				2.7
416337	H48713		gb:yq78d02.r1 Soares fetal liver spleen	2.7
423401	NM_001992	Hs.128087	coagulation factor II (thrombin) receptor	2.7
446800	AI341635	Hs.156486	ESTs	2.7
457906	AW975939	Hs.153290	Homo sapiens cDNA FLJ14318 fis, clone PL	2.7
452277	AL049013	Hs.28783	KIAA1223 protein	2.7
416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.7
416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	2.7

	408715	AA768873	Hs.112250	hypothetical protein FLJ23518	2.7
	410743	AA089474	Hs.272153	ESTs	2.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.7
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.7
5	427565	AI287280	Hs.97933	ESTs, Weakly similar to T46370 hypotheti	2.7
	406092				2.7
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	2.7
	438504	AW665281	Hs.224625	ESTs	2.7
	414783	AW069569	Hs.278270	unactive progesterone receptor, 23 kD	2.7
10	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.7
	418686	Z36830	Hs.87268	annexin A8	2.7
	413795	AL040178	Hs.142003	ESTs	2.7
	457528	AW973791	Hs.292784	ESTs	2.7
	444230	H95537	Hs.146067	ESTs	2.7
15	403760				2.7
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.7
	428904	AI312526	Hs.46640	ESTs	2.7
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	2.7
	458638	N78553	Hs.282204	nucleosomal binding protein 1	2.7
20	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	2.7
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.7
	433906	AI167816	Hs.43355	ESTs	2.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	2.7
25	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	2.7
	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2	2.7
	445158	AI992108	Hs.127206	ESTs	2.7
	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.7
	401793				2.7
30	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	451343	AW975057	Hs.293353	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wit	2.7
35	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	2.7
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.7
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	2.7
	451487	AA018072		gb:ze51g02.r1 Soares retina N2b4HR Homo	2.7
40	418269	AA806113	Hs.189025	ESTs	2.7
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	441963	AI733307	Hs.128002	ESTs	2.7
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.7
45	426902	AI125334	Hs.97408	ESTs	2.7
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	445265	AI218295	Hs.144942	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
50	428613	AB037749	Hs.186928	KIAA1328 protein	2.7
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	2.7
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	2.7
	402800				2.7
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.7
55	414729	BE466928	Hs.281901	ESTs	2.7
	453716	AA037675	Hs.152675	ESTs	2.7
	452693	T79153	Hs.48589	zinc finger protein 228	2.7
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	2.7
	443305	AI050693	Hs.133318	ESTs	2.7
60	416709	R99369	Hs.283108	hemoglobin, gamma G	2.7
	419077	AA233885	Hs.164526	ESTs	2.7
	453878	AW964440	Hs.19025	DC32	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	446817	AI700684	Hs.134166	ESTs	2.7
65	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	2.6
	410406	AI969703	Hs.1466	glycerol kinase	2.6
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.6
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	2.6
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.6
70	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	418217	AI910647	Hs.13442	ESTs	2.6
75	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
	414573	AI821846	Hs.71999	ESTs	2.6
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	2.6
80	428483	AI908539	Hs.321444	KIAA0344 gene product	2.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	405059				2.6
	425178	H16097	Hs.161027	ESTs	2.6

	442952	AI743261	Hs.131860	ESTs	2.6
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	2.6
	456179	H75490	Hs.271930	ESTs	2.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
5	459456	AA486036	Hs.190124	ESTs	2.6
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.6
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
10	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	438295	AI394151	Hs.37932	ESTs	2.6
	445550	AI242754	Hs.137306	ESTs	2.6
	450469	AI955049	Hs.281326	ESTs	2.6
	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
15	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	2.6
	429250	H56585	Hs.198308	tryptophan rich basic protein	2.6
	437906	AA771704	Hs.194626	ESTs	2.6
	426775	AA384564	Hs.108829	ESTs	2.6
	443372	AI792557	Hs.133107	ESTs	2.6
20	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	425465	L18964	Hs.1904	protein kinase C, iota	2.6
	422746	NM_004484	Hs.119651	glypican 3	2.6
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.6
	424527	AW138558	Hs.267158	ESTs, Weakly similar to I54374 gene NF2	2.6
25	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	2.6
	411402	BE297855	Hs.69855	NRAS-related gene	2.6
	445264	AI218263	Hs.323472	EST	2.6
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.6
	415227	AW821113	Hs.72402	ESTs	2.6
30	435429	AW592035	Hs.254414	ESTs, Weakly similar to 1805195B RNA-bin	2.6
	434445	AI349306	Hs.11782	ESTs	2.6
	448570	AI923944	Hs.30913	ESTs	2.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	422879	AI241409	Hs.188092	ESTs	2.6
35	409026	AL137554	Hs.49927	protein kinase NYD-SP15	2.6
	425717	X07282	Hs.171495	retinoic acid receptor, beta	2.6
	429127	AA749382	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.6
40	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
45	437939	AW298600	Hs.141840	ESTs, Weakly similar to S59501 interfero	2.6
	430719	AA488988	Hs.293796	ESTs	2.6
	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.6
	432095	AW022273	Hs.105769	ESTs	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
50	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	2.6
	423952	AW877787	Hs.136102	KIAA0853 protein	2.6
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	2.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.6
	430933	AW863635		gb:MR3-SN0010-270300-103-h02 SN0010 Homo	2.6
55	420691	AA829433	Hs.275343	ESTs	2.6
	429761	AI276780	Hs.135173	ESTs	2.6
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
60	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.6
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	2.6
	438647	AA813118	Hs.163230	ESTs	2.6
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.6
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.6
65	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.6
	428170	H05530	Hs.12565	ESTs	2.6
	457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	2.6
	424020	R76946	Hs.39738	ESTs	2.6
70	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.6
	411965	BE467339	Hs.280115	ESTs	2.6
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.6
	455488	AA102322		gb:zl90f03.r1 Stratagene colon (937204)	2.6
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.6
75	404285				2.6
	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	2.6
	454714	AW815098		gb:QV4-ST0212-091199-023-f10 ST0212 Homo	2.6
	429828	AB019494	Hs.225767	IDN3 protein	2.6
	436387	AA714760	Hs.240075	Homo sapiens cDNA FLJ13234 fis, clone OV	2.6
80	448587	AI539652	Hs.26338	KIAA1546 protein	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.6
	440479	AA886461	Hs.208161	ESTs	2.6
	443160	AI467915	Hs.36053	ESTs	2.6

	428978	AA442784	Hs.125445	ESTs	2.5
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.5
	453459	BE047032	Hs.257789	ESTs	2.5
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.5
5	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.5
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.5
	458760	AI498631	Hs.111334	ferritin, light polypeptide	2.5
	434131	AI858275	Hs.143659	ESTs	2.5
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
10	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	2.5
	417351	T90278	Hs.15049	ESTs	2.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sa	2.5
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	2.5
	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	2.5
15	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	453919	AW959912	Hs.7076	KIAA1705 protein	2.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.5
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
	427491	R43279	Hs.22574	ESTs, Weakly similar to I38022 hypotheti	2.5
20	435102	AW899053	Hs.76917	F-box only protein 8	2.5
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.5
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.5
	432887	AI926047	Hs.162859	ESTs	2.5
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5
25	401078				2.5
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.5
	425201	AA352111		gb:EST60061 Activated T-cells XX Homo sa	2.5
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
30	444542	AI161293	Hs.280380	aminopeptidase	2.5
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	2.5
	428497	BE010877	Hs.98584	ESTs	2.5
	457336	AW969657	Hs.291029	ESTs	2.5
	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	2.5
35	423782	AI472209	Hs.323117	ESTs	2.5
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	2.5
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	2.5
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.5
	417137	U46265	Hs.81261	mitochondrial ribosomal protein S21	2.5
40	436787	AA908554	Hs.192756	ESTs	2.5
	440331	AL046412	Hs.202151	ESTs	2.5
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.5
	417169	R13550	Hs.246773	ESTs	2.5
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	2.5
45	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
	446346	AI290205	Hs.309940	ESTs	2.5
50	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	2.5
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	2.5
	425523	AB007948	Hs.158244	KIAA0479 protein	2.5
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.5
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.5
55	425657	T89839	Hs.119471	ESTs	2.5
	401254				2.5
	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	2.5
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	2.5
	433138	AB029496	Hs.59729	semaphorin sem2	2.5
60	425804	BE501698	Hs.258189	ESTs	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	437267	AW511443	Hs.258110	ESTs	2.5
	454305	BE062633	Hs.28338	KIAA1546 protein	2.5
	455631	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	2.5
65	401878				2.5
	450350	T97817	Hs.174880	ESTs	2.5
	436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	2.5
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	2.5
	427304	AA761526	Hs.163853	ESTs	2.5
70	419721	NM_001650	Hs.288650	aquaporin 4	2.5
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.5
	434273	AA913143	Hs.26303	ESTs	2.5
75	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	2.5
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN !	2.5
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.5
	452232	AW020603	Hs.158423	radial spoke protein 3	2.5
	433764	AW753676	Hs.39982	ESTs	2.5
80	412050	H96503	Hs.109067	Homo sapiens cDNA: FLJ22845 fis, clone K	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	2.5
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.5

408813	AI580090	Hs.48295	RNA helicase family	2.5
414109	BE250744		gb:600943376F1 NIH_MGC_17 Homo sapiens c	2.5
451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.5
419985	H66373	Hs.15973	ESTs, Highly similar to bA393J16.3 [H.sa	2.5
417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.5
434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.5
448015	AI458065	Hs.23196	ESTs	2.5
454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
445865	AI262584	Hs.145575	ESTs	2.5
451800	AW977435	Hs.323867	ESTs	2.5
456987	AI557290	Hs.173536	ESTs	2.5
403568				2.5
435209	AW027809	Hs.187698	Homo sapiens cytomegalovirus partial fus	2.5
430371	D87466	Hs.240112	KIAA0276 protein	2.5
418033	W68180	Hs.259855	elongation factor-2 kinase	2.5
412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.5
453619	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	2.5
431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.5
409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	2.5
444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.4
417318	AW953937	Hs.12891	ESTs	2.4
413382	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.4
406748	AW339106	Hs.217493	annexin A2	2.4
445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.4
441817	AW969706	Hs.293332	ESTs	2.4
450551	AJ010046	Hs.25155	neuroepithelial cell transforming gene 1	2.4
457940	AL360159	Hs.306517	Homo sapiens TRIpartite motif protein ps	2.4
446135	AW130288	Hs.170318	hypothetical protein FLJ10147	2.4
436907	AA737171	Hs.131809	ESTs	2.4
429399	AA452244	Hs.16727	ESTs	2.4
448782	AL050295	Hs.22039	KIAA0758 protein	2.4
434404	AW445034	Hs.256578	ESTs	2.4
428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	2.4
442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.4
450705	U90304	Hs.25351	iroquois homeobox protein 5	2.4
425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (J	2.4
423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	2.4
458986	AI802772	Hs.208655	ESTs	2.4
443861	AW449462	Hs.134743	ESTs	2.4
412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
415250	F02614	Hs.27319	ESTs	2.4
434627	AI221894	Hs.39311	ESTs	2.4
443919	AI091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	2.4
440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.4
400385	NM_020389	Hs.283104	putative capacitative calcium channel	2.4
411322	AW887330	Hs.172405	cell division cycle 27	2.4
434638	H50758		gb:yp86e06.r1 Soares fetal liver spleen	2.4
435559	AF209198	Hs.42636	zinc finger protein 277	2.4
447849	AI538147	Hs.164277	ESTs	2.4
448005	AW207437	Hs.170378	ESTs	2.4
454201	AB023191	Hs.44131	KIAA0974 protein	2.4
456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.4
449486	AI652715	Hs.270811	ESTs	2.4
421516	AI362418	Hs.105379	FT005 protein	2.4
412167	AW897230		gb:CM0-NN0057-150400-335-a11 NN0057 Homo	2.4
426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.4
429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	2.4
400641				2.4
430576	AA767125	Hs.293574	ESTs	2.4
434423	NM_006769	Hs.3844	LIM domain only 4	2.4
412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.4
441499	AW298235	Hs.101689	ESTs	2.4
418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.4
417819	AI253112	Hs.133540	ESTs	2.4
431726	NM_007351	Hs.268107	multimerin	2.4
425025	AW953168	Hs.12407	ESTs	2.4
421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.4
409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.4
408867	AA437199	Hs.656	cell division cycle 25C	2.4
439446	AI927629	Hs.57873	ESTs	2.4
445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.4
428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.4
453864	AW021407	Hs.21068	hypothetical protein	2.4
426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.4
418203	X54942	Hs.83758	CDC28 protein kinase 2	2.4
426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	2.4

	447357	AI375922	Hs.159367	ESTs	2.4
	452631	AI188658	Hs.87496	ESTs	2.4
	405041				2.4
	405472				2.4
5	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	437119	AI379921	Hs.177043	ESTs	2.4
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.4
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.4
10	434936	AI285970	Hs.183817	ESTs	2.4
	408918	BE218603	Hs.279708	ESTs	2.4
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.4
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.4
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.4
15	446659	AI335361	Hs.226376	ESTs	2.4
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	2.4
	434995	AW974995		gb:EST387100 MAGE resequences, MAGN Homo	2.4
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.4
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	2.4
20	427131	AA448460	Hs.112017	GE36 gene	2.4
	442039	AW276240	Hs.128352	ESTs	2.4
	448595	AB014544	Hs.21572	KIAA0644 gene product	2.4
	432949	AA570749	Hs.298866	ESTs	2.4
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.4
25	417420	T85150	Hs.268814	ESTs	2.4
	427551	T96203		gb:ye48b07.r1 Soares fetal liver spleen	2.4
	420057	AA806899	Hs.184387	ESTs	2.4
	434950	AW974892		gb:EST386997 MAGE resequences, MAGN Homo	2.4
	425497	AA524596		gb:nh34b02.s1 NCI_CGAP_Pr3 Homo sapiens	2.4
30	438214	H06076	Hs.26320	TRABID protein	2.4
	416100	H18700	Hs.268799	ESTs	2.4
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	2.4
35	419179	AW275291	Hs.113009	hypothetical protein FLJ22527	2.4
	436391	AJ227892	Hs.146274	ESTs	2.4
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	2.4
	447499	AW262580	Hs.147674	protocadherin beta 16	2.4
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.4
40	412877	BE011168		gb:PM3-BN0218-100500-003-d08 BN0218 Homo	2.4
	435985	AA703154	Hs.191934	ESTs	2.4
	440674	BE561546		gb:601347208F1 NIH_MGC_8 Homo sapiens cD	2.4
	446476	AW294072	Hs.141376	ESTs	2.4
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.4
45	435731	AA699581	Hs.186811	ESTs	2.4
	437105	AA744554	Hs.222127	ESTs	2.4
	406091				2.4
	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
50	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	2.4
	424943	AU077260	Hs.153924	death-associated protein kinase 1	2.4
	444229	AV648613	Hs.282397	ESTs	2.4
	404860				2.4
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.4
55	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.4
	420843	H96982	Hs.42321	ESTs	2.4
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.4
	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
60	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	2.4
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	2.3
	418782	AI792648	Hs.14665	ESTs	2.3
65	447870	BE139479	Hs.161492	ESTs	2.3
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	2.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	2.3
	424049	AB014524	Hs.138380	KIAA0624 protein	2.3
70	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.3
	430702	U56979	Hs.250651	H factor 1 (complement)	2.3
	409620	AA076278	Hs.13277	hypothetical protein FLJ22054	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.3
75	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	2.3
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	2.3
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	2.3
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.3
80	404513				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	448506	AI524673	Hs.38170	ESTs	2.3
	434811	AW971205	Hs.114280	ESTs	2.3

	457065	AI476318	Hs.192480	ESTs	2.3
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	2.3
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.3
	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H.	2.3
5	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.3
	435867	AA954229	Hs.114052	ESTs	2.3
	440196	N72847	Hs.125221	ESTs	2.3
	401213				2.3
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo	2.3
10	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.3
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.3
	438138	R98299	Hs.177502	ESTs	2.3
	440283	AI732892	Hs.190489	ESTs	2.3
	447039	AV661798	Hs.282915	ESTs	2.3
15	412777	AI335773	Hs.270123	ESTs	2.3
	421424	AW452690	Hs.258775	ESTs	2.3
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.3
	440555	D31292	Hs.6853	hypothetical protein FLJ22167	2.3
	451516	AI800515	Hs.12024	ESTs	2.3
20	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	2.3
	421046	AA810854	Hs.89081	ESTs	2.3
	423604	AA486585	Hs.258901	ESTs	2.3
	409029	BE087807		gb:QV1-BT0681-290400-181-g02 BT0681 Homo	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
25	451836	T63673	Hs.173220	ESTs	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.3
	436671	AW137159	Hs.146151	ESTs	2.3
	434988	AI418055	Hs.161160	ESTs	2.3
30	452862	AW378065	Hs.8687	ESTs	2.3
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	2.3
	410606	AW418779	Hs.114889	ESTs	2.3
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.3
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	2.3
35	430217	N47863	Hs.336901	ribosomal protein S24	2.3
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
	438180	AA808189	Hs.272151	ESTs	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
40	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	2.3
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	2.3
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	2.3
	412953	Z45794	Hs.238809	ESTs	2.3
45	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	2.3
	428595	AB037795	Hs.186547	KIAA1374 protein	2.3
	437887	AA811524	Hs.29263	hypothetical protein FLJ11896	2.3
50	447720	AL038765	Hs.161304	ESTs	2.3
	452355	N54926	Hs.29202	G protein-coupled receptor 34	2.3
	408374	AW025430	Hs.155591	forkhead box F1	2.3
	440381	AA917808	Hs.190495	ESTs	2.3
	425478	AB007953	Hs.268840	ESTs	2.3
55	432231	AA339977	Hs.274127	CLST 11240 protein	2.3
	431757	AA196930	Hs.268526	Homo sapiens chromosome 21q22.1 anonymou	2.3
	417517	AF001176	Hs.82238	POP4 (processing of precursor , S. cerev	2.3
	452837	AL121053	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	2.3
	417426	NM_002291	Hs.82124	laminin, beta 1	2.3
60	423739	AA398155	Hs.97600	ESTs	2.3
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	2.3
	425876	AW005887	Hs.234058	ESTs	2.3
	457411	AW085961	Hs.130093	ESTs	2.3
	413136	BE066941		gb:PM0-BT0340-091299-002-a11 BT0340 Homo	2.3
65	420313	AB023230	Hs.96427	KIAA1013 protein	2.3
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
	436331	AI239495	Hs.120189	ESTs	2.3
	439275	AF086093	Hs.141566	ESTs	2.3
70	449272	AW137656	Hs.197645	ESTs	2.3
	454352	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	2.3
	407242	M18728		gb:Human nonspecific crossreacting antig	2.3
	445326	AI220072	Hs.165893	ESTs	2.3
75	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.3
	452607	AI160029	Hs.61438	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	418851	AI417828	Hs.192435	ESTs	2.3
	458332	AI000341	Hs.220491	ESTs	2.3
80	432565	AA553477	Hs.152428	ESTs	2.3
	437511	AI807500	Hs.125247	ESTs	2.3
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.3
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	2.3

	448225	AI476429	Hs.19238	ESTs	2.3
	408955	BE315170	Hs.8087	NAG-5 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
5	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	440348	AW015802	Hs.47023	ESTs	2.3
	436340	R42246	Hs.21606	ESTs	2.3
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.3
10	438462	AI624122	Hs.89578	general transcription factor IIH, polype	2.3
	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.3
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	2.3
	412505	AA974491	Hs.21734	ESTs	2.3
	418236	AW994005	Hs.337534	ESTs	2.3
15	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	2.3
	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.3
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.3
	433404	T32982	Hs.102720	ESTs	2.3
	409517	X90780	Hs.120036	troponin I, cardiac	2.3
20	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
	445641	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	2.3
	437770	AA767881	Hs.122897	ESTs	2.3
25	409064	AA062954	Hs.141883	ESTs	2.3
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.3
	449869	W57990	Hs.60059	Homo sapiens cDNA FLJ11478 fis, clone HE	2.3
	422108	AA297914	Hs.111749	postmeiotic segregation increased (S. ce	2.3
	418251	AA832123	Hs.177723	ESTs	2.3
30	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA P	2.3
	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.3
	415980	R52414		gb:yg80b05.r1 Soares infant brain 1NIB H	2.3
	449232	AW192780	Hs.196080	ESTs	2.3
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.3
35	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.3
	438089	W05391	Hs.83623	nuclear receptor subfamily 1, group I, m	2.3
	400238				2.3
	404488				2.3
	407809	AW082279	Hs.244106	ESTs	2.3
40	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518 (f	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
	426567	AA381579	Hs.182962	ESTs	2.3
45	435708	AI362949	Hs.75169	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
	445117	AI208754	Hs.147369	ESTs	2.3
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.3
	434226	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	2.2
50	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	2.2
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	2.2
	420653	AI224532	Hs.88550	ESTs	2.2
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.2
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	2.2
55	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.2
60	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446164	AW273539	Hs.288750	hypothetical protein FLJ23577	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	402745				2.2
65	434008	AA740878	Hs.112982	ESTs	2.2
	439492	AF086310	Hs.103159	ESTs	2.2
	436853	BE328074	Hs.148661	ESTs	2.2
	417648	R06552		gb:yf09e12.r1 Soares fetal liver spleen	2.2
	427690	AI253134	Hs.283410	ESTs	2.2
70	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.2
	450229	R18717	Hs.8929	hypothetical protein FLJ11362	2.2
	400756				2.2
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.2
	403388				2.2
75	433643	AI821787	Hs.179586	ESTs	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
	439920	H05430	Hs.288433	neurotrimin	2.2
80	432436	AW300248	Hs.181693	ESTs	2.2
	429493	AL134708	Hs.145998	ESTs	2.2
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	2.2

	442757	AI739528	Hs.28345	ESTs	2.2
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	2.2
	437146	AA730977		gb:nw55f05.s1 NCI_CGAP_Ew1 Homo sapiens	2.2
	432101	AI918950	Hs.123642	EphA3	2.2
5	459644				2.2
	453887	BE564037	Hs.36237	hypothetical protein	2.2
	431170	AW971246	Hs.291022	ESTs	2.2
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.2
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	2.2
10	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	2.2
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.2
	425810	AI923627	Hs.31903	ESTs	2.2
	433037	NM_014158	Hs.279938	HSPC067 protein	2.2
	407162	N63855	Hs.142634	zinc finger protein	2.2
15	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
	454766	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.2
	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.2
20	400639				2.2
	406149				2.2
	424027	AW337575	Hs.201591	ESTs	2.2
	427531	AA405097	Hs.97957	ESTs	2.2
	448353	BE407125	Hs.231510	ESTs	2.2
25	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	2.2
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	2.2
	452335	AW188944	Hs.61272	ESTs	2.2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
	447748	AI422023	Hs.161338	ESTs	2.2
30	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
	444540	AI693927	Hs.265165	ESTs	2.2
35	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.2
	439443	AF086261	Hs.127892	ESTs	2.2
	418824	AW751661	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	2.2
	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.2
40	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.2
	432702	AW973953	Hs.293744	ESTs	2.2
	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.2
	425570	AA359558		gb:EST68590 Fetal lung II Homo sapiens c	2.2
	414935	C15671		gb:C15671 Clontech human aorta polyA+ mR	2.2
45	453153	N53893	Hs.24360	ESTs	2.2
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	2.2
	439867	AA847510	Hs.161292	ESTs	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
	433420	AI674093	Hs.293961	ESTs, Moderately similar to putative DNA	2.2
50	434690	AI867679	Hs.148410	ESTs	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	431688	AA513906		gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens	2.2
	403133				2.2
55	414885	AA157531	Hs.269276	ESTs, Moderately similar to S65657 alpha	2.2
	432111	AW972777		gb:EST384871 MAGE resequences, MAGL Homo	2.2
	410073	AW408163	Hs.58488	catenin (cadherin-associated protein), a	2.2
	448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.2
60	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	2.2
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	2.2
	403378				2.2
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.2
65	438580	AA811262	Hs.299202	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspin	2.2
	412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	2.2
	411966	AA099113	Hs.118609	ESTs	2.2
	443915	Z40763	Hs.135292	ESTs	2.2
70	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.2
	446094	AK001760	Hs.13801	KIAA1685 protein	2.2
	436486	AA742221	Hs.120633	ESTs	2.2
	411139	AW819461		gb:RC5-ST0293-061299-031-C03 ST0293 Homo	2.2
	409070	AA063003	Hs.224560	ESTs	2.2
75	432713	AL118623	Hs.29494	PRO1912 protein	2.2
	419384	AA490866	Hs.39429	ESTs	2.2
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.2
	408444	AW661839	Hs.253204	ESTs	2.2
	432128	AA127221	Hs.117037	ESTs	2.2
80	418027	AB037807	Hs.83293	hypothetical protein	2.2
	446060	Z42061	Hs.27004	ESTs	2.2
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.2
	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.2

	443401	AI394067	Hs.160159	ESTs	2.2
	424665	AW368576	Hs.139851	caveolin 2	2.2
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	2.2
	426261	AW242243	Hs.166670	peroxisomal farnesylated protein	2.2
5	414564	AA164803	Hs.71994	ESTs, Weakly similar to I38022 hypotheti	2.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	2.2
	419160	AA911342	Hs.35524	KIAA1559 protein	2.2
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	2.2
	442879	AF032922	Hs.8813	syntaxin binding protein 3	2.2
10	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.2
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	2.2
	432074	AA525248	Hs.149723	ESTs	2.2
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	2.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.2
15	409723	AW885757	Hs.257862	ESTs	2.2
	425627	AF019612	Hs.297007	membrane-bound transcription factor prot	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	449369	AA001256	Hs.27260	ESTs	2.2
	425514	AF112345	Hs.158237	integrin, alpha 10	2.2
20	455821	BE143341		gb:MR0-HT0162-191099-002-d04 HT0162 Homo	2.2
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.2
	432284	AA532807	Hs.105822	ESTs	2.2
	403467				2.2
	436032	AA150797	Hs.109276	latexin protein	2.2
25	404356				2.2
	434205	AF119861	Hs.283032	hypothetical protein PRO2015	2.2
	405257				2.2
	402103				2.2
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.2
30	432985	T92363	Hs.178703	ESTs	2.2
	417649	AW239285	Hs.82359	tumor necrosis factor receptor superfami	2.2
	431277	AA501806	Hs.249965	ESTs	2.2
	454056	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	2.2
	401694				2.2
35	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	448390	AL035414	Hs.21068	hypothetical protein	2.2
	449939	T86420	Hs.272139	ESTs	2.2
40	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.2
	404555				2.2
	418186	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fis, clone H	2.2
	419981	AA897581	Hs.126773	ESTs	2.2
	449581	AI989517	Hs.181605	ESTs	2.2
45	419229	AI827237	Hs.282884	ESTs	2.2
	403691				2.2
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.2
	443479	AF027219	Hs.9443	zinc finger protein 202	2.2
	425329	AI961644	Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	2.2
50	453345	AA302862	Hs.90063	neurocalcin delta	2.2
	424335	AW021508	Hs.28170	ESTs	2.2
	451072	AA013451	Hs.117929	ESTs	2.2
	417845	AL117451	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	2.2
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.2
55	438035	AA938198	Hs.146123	poly(A) polymerase gamma	2.2
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.2
	400241				2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	2.2
60	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	2.1
	416441	BE407197		gb:601301552F1 NIH_MGC_21 Homo sapiens c	2.1
	414891	R27124	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	2.1
65	430172	AA468591	Hs.161889	ESTs	2.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.1
	422985	AU076411	Hs.1602	dihydropyrimidine dehydrogenase	2.1
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	2.1
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	2.1
70	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	2.1
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.1
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.1
75	415992	C05837	Hs.145807	hypothetical protein FLJ13593	2.1
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.1
	437132	AL049353	Hs.297268	ESTs	2.1
	415304	T66079	Hs.12799	ESTs	2.1
	450152	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	2.1
80	421147	AW592167	Hs.293299	ESTs	2.1
	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.1
	451750	AA280851	Hs.226930	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	2.1

	406945	K01383	Hs.173451	metallothionein 1A (functional)	2.1
	452449	AW068658	Hs.20943	ESTs	2.1
	436009	H57130	Hs.120925	ESTs	2.1
	418637	T86737	Hs.193536	ESTs	2.1
5	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	2.1
	449203	AI634578	Hs.282121	ESTs	2.1
	437751	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	428412	AA428240	Hs.126083	ESTs	2.1
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.1
10	441967	AA972742	Hs.209786	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
15	431229	AA496479	Hs.259929	ESTs	2.1
	435148	AI918049	Hs.124961	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
	448582	AI538880	Hs.94812	ESTs	2.1
20	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	2.1
	451874	AW963137	Hs.194233	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.1
	443484	AI091458	Hs.134559	ESTs	2.1
25	430686	NM_001942	Hs.2633	desmoglein 1	2.1
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	2.1
	407624	AW157431	Hs.248941	ESTs	2.1
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.1
	428923	BE047698	Hs.188785	ESTs	2.1
30	422496	AA311301	Hs.278827	ESTs	2.1
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.1
	408418	AW963897	Hs.44743	KIAA1435 protein	2.1
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.1
	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
35	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	459325	AW088369	Hs.282184	ESTs	2.1
	416996	W91892	Hs.59609	ESTs	2.1
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.1
	406000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	2.1
40	418894	W73921	Hs.50743	ESTs	2.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.1
	437378	AI198823	Hs.160473	ESTs	2.1
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	2.1
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	2.1
45	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	2.1
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.1
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	2.1
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	2.1
	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.1
50	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	2.1
	449911	AI262106	Hs.12653	ESTs	2.1
	449509	AA001615	Hs.84561	ESTs	2.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	2.1
	422839	AI674784	Hs.298908	ESTs	2.1
55	435040	AI932350	Hs.152825	ESTs	2.1
	401200				2.1
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.1
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.1
	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	2.1
60	453908	AW613920	Hs.282178	ESTs	2.1
	446965	BE242873	Hs.16677	WD repeat domain 15	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
65	455995	BE179408		gb:IL3-HT0618-060500-125-B07 HT0618 Homo	2.1
	422411	AW749443	Hs.22511	ESTs	2.1
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.1
	446893	AI610618	Hs.7110	ESTs	2.1
	442992	AI914699	Hs.13297	ESTs	2.1
70	407021	U52077		gb:Human mariner1 transposase gene, comp	2.1
	436938	AW139680	Hs.161393	ESTs	2.1
	433194	AB040883	Hs.83243	KIAA1450 protein	2.1
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.1
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	2.1
75	434739	AA804467	Hs.144130	ESTs	2.1
	406468				2.1
	457023	AA001732	Hs.173233	hypothetical protein FLJ10970	2.1
	416226	N55342	Hs.34372	ESTs	2.1
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.1
80	432810	AA863400	Hs.23054	ESTs	2.1
	412894	R09778	Hs.166510	ESTs	2.1
	430602	D13752	Hs.184927	cytochrome P450, subfamily XIB (steroid	2.1
	436981	AA740891	Hs.293316	ESTs	2.1

	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	2.1
	449838	AB020653	Hs.24024	KIAA0846 protein	2.1
	447160	AA330310	Hs.24181	ESTs	2.1
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	2.1
5	440137	AA866199	Hs.171397	ESTs	2.1
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	2.1
	436471	AA719813	Hs.117662	ESTs	2.1
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.1
	426782	R14614	Hs.191254	ESTs	2.1
10	430027	AB023197	Hs.227743	KIAA0980 protein	2.1
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.1
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	2.1
	427115	AW972853	Hs.112237	ESTs	2.1
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.1
15	400451				2.1
	435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	2.1
	442835	AI021989	Hs.131903	ESTs	2.1
20	400196				2.1
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.1
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.1
	438940	AF075045	Hs.271609	ESTs	2.1
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.1
25	448515	H68441	Hs.13528	hypothetical protein FLJ14054	2.1
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	2.1
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.1
	419088	AI538323	Hs.52620	integrin, beta 8	2.1
30	447373	AI381922	Hs.158781	ESTs	2.1
	457465	AW301344	Hs.122908	DNA replication factor	2.1
	413918	AW015898	Hs.71245	ESTs	2.1
	402820				2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
35	428552	AW274560	Hs.129520	ESTs	2.1
	435464	BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	2.1
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	2.1
	420838	AW118210	Hs.5244	ESTs	2.1
	428231	U17989	Hs.183105	nuclear autoantigen	2.1
40	434933	R91095	Hs.4276	KIAA1701 protein	2.1
	444870	AI200621	Hs.148504	ESTs	2.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.1
	429183	AB014604	Hs.197955	KIAA0704 protein	2.1
	439155	H81076	Hs.269001	ESTs	2.1
45	442787	W93048	Hs.250723	hypothetical protein MGC2747	2.1
	429864	AA460039	Hs.286	ribosomal protein L4	2.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.1
	437140	AA312799	Hs.283689	activator of CREM in testis	2.1
	421991	NM_014918	Hs.110488	KIAA0990 protein	2.1
50	446534	AI307356	Hs.175225	ESTs	2.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.1
	444838	AV651680	Hs.208558	ESTs	2.1
	402318				2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
55	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	421306	AA806207	Hs.125889	ESTs	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	429088	D61542	Hs.227716	KIAA0934 protein	2.1
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.1
60	428060	AA420616	Hs.249483	ESTs	2.1
	419953	BE267154	Hs.125752	ESTs	2.1
	443718	AI083580	Hs.221373	ESTs	2.1
	444187	AW138466	Hs.151274	ESTs	2.1
	428048	AA705745		gb:zf41b11.s1 Soares_fetal_heart_NbHH19W	2.1
65	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.1
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.1
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.1
	430335	D80007	Hs.239499	KIAA0185 protein	2.1
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.1
70	434029	AA621763	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.1
	410945	AW811552		gb:QV2-ST0145-071299-017-h10 ST0145 Homo	2.1
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.1
	433374	AI821409	Hs.332789	EST	2.1
	445644	R77766	Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.1
75	450271	AI693900	Hs.200920	ESTs	2.1
	448084	AI467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	2.1
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	2.1
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.1
	435542	AA687376	Hs.269533	ESTs	2.1
80	443544	AI076315	Hs.16359	ESTs	2.1
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	2.1
	405759				2.1
	446242	N66336	Hs.7360	ESTs	2.1

457938	AI373638	Hs.133900	ESTs	2.1
433017	Y15067	Hs.279914	zinc finger protein 232	2.1
436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	2.1
432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.1
439224	AW471088	Hs.145950	ESTs, Highly similar to T08692 hypotheti	2.1
410976	R36207	Hs.25092	hypothetical protein MGC10744	2.1
454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo	2.1
411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.1
452279	AA286844	Hs.61260	hypothetical protein FLJ13164	2.1
446891	AL036877	Hs.282878	ESTs	2.1
434294	AJ271379	Hs.76194	ribosomal protein S5	2.1
449057	AB037784	Hs.22941	KIAA1363 protein	2.1
432769	AA620814	Hs.144959	ESTs	2.1
441224	AU076964	Hs.7753	calumenin	2.1
407891	AA486620	Hs.41135	endomucin-2	2.1
429017	AA463605	Hs.66295	multi-PDZ-domain-containing protein	2.1
406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
430566	AA481282	Hs.190149	ESTs	2.1
449208	AW263635	Hs.48643	ESTs	2.1
451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.1
452042	H38857	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.1
444779	AI192105	Hs.147170	ESTs	2.0
433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	2.0
415954	AA171850	Hs.42251	ESTs	2.0
420273	AI652864	Hs.197257	ESTs	2.0
411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.0
422389	AF240635	Hs.115897	protocadherin 12	2.0
446994	AV650435	Hs.16755	MBIP protein	2.0
417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	2.0
422654	AA314316	Hs.163725	ESTs	2.0
425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	2.0
405634				2.0
451562	H04150	Hs.107708	ESTs	2.0
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.0
422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.0
442010	AI032680	Hs.132213	ESTs	2.0
442991	BE281238	Hs.8886	hypothetical protein FLJ20424	2.0
425312	AA354940	Hs.145958	ESTs	2.0
415191	AA190381	Hs.120810	ESTs	2.0
416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.0
425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1	2.0
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.0
452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	2.0
433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.0
417094	NM_006895	Hs.81182	histamine N-methyltransferase	2.0
409190	AU076536	Hs.50984	sarcoma amplified sequence	2.0
413783	AA314337	Hs.301547	ribosomal protein S7	2.0
423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
429418	AI381028	Hs.118769	ESTs	2.0
445829	AI452457	Hs.145526	ESTs	2.0
452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.0
446593	W79572	Hs.13277	hypothetical protein FLJ22054	2.0
400462				2.0
422003	AA361760	Hs.296326	ESTs	2.0
444585	AW170015	Hs.6594	ESTs	2.0
444898	AI201548	Hs.308338	ESTs	2.0
403525				2.0
443031	AW134696	Hs.49418	ESTs	2.0
430818	AI311928		gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	2.0
423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	2.0
440941	BE268362	Hs.7535	COBW-like protein	2.0
409627	AW997628	Hs.313637	ESTs	2.0
433258	AI806626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.0
412863	AA121673	Hs.59757	zinc finger protein 281	2.0
436476	AA326108	Hs.33829	bHLH protein DEC2	2.0
430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.0
417280	AW173116	Hs.262206	ESTs	2.0
423528	AB011137	Hs.300938	KIAA0565 gene product	2.0
424800	AL035588	Hs.153203	MyoD family inhibitor	2.0
446019	AI362520	Hs.279789	histone deacetylase 3	2.0
435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.0
424892	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.0
430473	AW130690	Hs.59962	ESTs	2.0
431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.0
438118	AW753311	Hs.259415	ESTs	2.0
400859				2.0
405829				2.0
415258	AW752247	Hs.293853	ESTs	2.0
420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
437733	AI792574	Hs.122876	ESTs	2.0
452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	2.0
453118	AW195849	Hs.252757	ESTs	2.0

	430706	NM_003540	Hs.247816	H4 histone family, member C	2.0
	420568	F09247	Hs.247735	protocadherin alpha 10	2.0
	452759	AW590773	Hs.258996	ESTs	2.0
	408496	AI683802	Hs.136182	ESTs	2.0
5	420674	NM_000055	Hs.1327	butyrylcholinesterase	2.0
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.0
	450086	AW016343	Hs.233301	ESTs	2.0
	410853	H04588	Hs.30469	ESTs	2.0
	438607	AW060237	Hs.252884	ESTs	2.0
10	422232	D43945	Hs.113274	transcription factor EC	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
	402490				2.0
	446551	AI308176	Hs.65636	ESTs	2.0
	438315	R56795	Hs.82419	ESTs	2.0
15	445261	T79759	Hs.282939	ESTs, Weakly similar to t38022 hypotheti	2.0
	401986				2.0
	420335	AA258771	Hs.43616	Homo sapiens mRNA for FLJ00029 protein,	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
	435413	AI267476	Hs.46569	ESTs	2.0
20	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to t38022 hypotheti	2.0
	417494	AI369494	Hs.222137	ESTs	2.0
	416045	H15990	Hs.31403	ESTs	2.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	2.0
25	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.0
	411578	AW238524		gb:xp27c05.x1 NCI_CGAP_HN10 Homo sapiens	2.0
	453116	AI276680	Hs.146086	ESTs	2.0
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.0
	435608	AW183971	Hs.250896	ESTs	2.0
30	402102				2.0
	458308	AI828155	Hs.211055	ESTs	2.0
	438177	BE327015	Hs.281391	ESTs	2.0
	415205	H71615	Hs.135233	ESTs	2.0
	427244	AA402400	Hs.178045	ESTs	2.0
35	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	2.0
	438979	AW976218	Hs.32565	ESTs	2.0
	400285				2.0
	405966				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
40	427739	AW196755	Hs.98105	NYD-SP14 protein	2.0
	433584	AW295399		gb:UI-H-BI2-ahv-h-03-0-UI.s1 NCI_CGAP_Su	2.0
	448956	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.0
	439474	AI824060	Hs.211501	ESTs	2.0
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.0
45	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.0
	418836	AI655499	Hs.161712	ESTs	2.0
	453108	AI311457	Hs.99472	ESTs	2.0
	447101	N72185	Hs.44189	ESTs	2.0
	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	2.0
50	426226	AA769045		gb:oa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	2.0
	401157				2.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.0
	425646	AW157044	Hs.158512	cyclin-dependent kinase-like 2 (CDC2-rel	2.0
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	2.0
55	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.0
	402855				2.0
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	2.0
	445672	AI907438	Hs.282862	ESTs	2.0
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.0
60	411941	AW876909	Hs.25201	ESTs, Weakly similar to FAT DROME CADHER	2.0
	430664	AW969834	Hs.303303	ESTs	2.0
	402812				2.0
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	2.0
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
65	402048				2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	437373	H67505	Hs.191979	KIAA1733 protein	2.0
70	439217	AF086041	Hs.42975	ESTs	2.0
	446609	BE395090	Hs.15535	Homo sapiens clone 24582 mRNA sequence	2.0

75 TABLE 3B: List of accession numbers for primekeys lacking unigeneID's for Table 3A. Forsuch such probeset is listed a gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession

408690	107490_1	AW864542 AA056567 AW882724
409029	1095422_1	BE067807 AW301579
409073	109851_1	AA063458 AA063018 AI444822
409519	113722_1	AA075368 AA075369
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
410008	116812_1	AA079552 BE142525 BE142527
410615	1212203_1	AW772721 AW873372 H89212
410672	1214882_1	AW794600 AW794730
410784	1221005_1	AW803201 BE079700 BE062940
410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
410888	1225955_1	AW861207 AW809508
410901	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
410934	1227240_1	AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157
410945	1227561_1	AW811552 AW811470 AW811523 AW811482 AW811514 AW811456 AW811525
410999	1228809_1	AW813004 AW812962 AW812961
411004	1228975_1	AW813242 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582
411018	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
411139	1233781_1	AW819461 AW819478 AW819479 AW819559 AW819505
411151	1234022_1	AW866497 AW819775 AW819868 AW866602 AW866561
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
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411578	125013_1	AW238524 AA094059 R59022
411745	1256160_1	AW867826 AW859896
411880	1263110_1	AW872477 BE088101 T05990
411905	1265181_1	BE265067 BE264978 AW875420
412167	1280605_1	AW897230 AW897252 AW897244 AW897231 AW897263
412209	1283610_1	AW901456 AW901450 AW901441
412248	1285000_1	BE176480 AW903298 AW903313
412282	1287679_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
412303	1288130_1	AW936336 AW936339
412566	1306469_1	AW962574 BE073261
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412879	1334272_1	BE092219 BE092361 BE006789
413087	1348720_1	BE064655 BE153953
413136	1350379_1	BE066941 BE066911 BE066979 BE066929 BE066925
413252	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
413382	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
413488	1373234_1	BE144017 BE185527 BE144023
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415236	1531080_1	R41400 H06659 Z38637 F02023 T16516
415635	1540853_1	F13168 R21289 T77628
415747	155189_1	AA381209 AA381245 AA167683
415980	1564218_1	R52414 R61681 H12009 T74429
416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
416337	1589299_1	H48713 H83057 H48694 H65247
416441	159480_1	BE407197 AA182474 AA180369 BE275628 BE276131
416548	1600181_1	H62953 N76608 N72413
416624	1604694_1	H69044 T47567 H75691 T50292
416871	1626761_1	H98716 N90792 N24283
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
416972	163668_1	BE019670 AA191284 AA191255
417561	168747_2	AW974345 BE145400 T97088 AA639076
417648	1691070_1	R06552 T98985 R08656
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417859	1703724_1	T26453 Z44226 R20425
418378	174656_1	AW962081 AA218925 AA354237
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419546	185766_1	AA244199 AA244272 H57440
419637	186639_1	W27493 AA248063 AA249685 AA429679
419807	188252_1	R77402 AA252462 AA250988 R06794
420111	190755_1	AA255652 AA280911 AW967920 AA262684
420621	195113_1	AA278808 BE082076 BE081812 BE081581
420637	195241_1	AW976153 AA278945 AA747691
421065	198936_1	AA329711 AA287436 AA283148
422063	210852_1	BE156476 BE156473 BE156474 BE156475 AA302839
422156	212379_1	N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 AI334966 W32951 H62656 H53902 R88904 AW835732
422342	215498_1	AA309272 AA309312 AW961837
422429	216469_1	AA310527 AW962295 Z44865 H06641
422977	223410_1	AA631498 AI017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510 AA319642 AW853758 H56414
423121	225175_1	AW864848 AA322213 AA322209 AW961624

423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235
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423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
423841	232507_1	AW753967 AA370795 AA331630 AW962550
423867	232732_1	AA331886 AW962659 AW962655 T89841
424872	244505_1	AA347923 AA347928 AW961769
425201	247933_1	AA352111 AW962247 AA429695
425497	252499_1	AA524596 AA358494 AA513507
425570	253248_1	AA359558 AA359819 AW963122
426226	262918_1	AA769045 AA372590 AW963633
426497	268121_1	AA379913 AA379981 AW963523
426603	269825_1	AA382291 AA994657
427551	280163_1	T96203 AA405343 T96121
428048	286394_1	AA705745 AA420850 AA420433
428679	294049_1	AA431765 AA432015
430212	314437_1	AA469153 AI718503 AA469225
430818	324239_1	AI311928 AA936030 T51931 AA609816 AA487195 AA664207
430844	324570_1	T94960 AA487679 T95013
430933	325757_1	AW863635 BE179901 BE179402 AW863789 AA489179 BE010747 BE010748
431071	327550_1	AA491379 H86020 AW969148
431169	328799_1	AW971240 AA493843 AA493723
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
431595	335512_1	AA508196 BE142920 AI280311 AI205616 D61709
431688	336609_1	AA513906 AA847734 AI357044
432111	341618_1	AW972777 AA526795 AA526305
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
432779	354024_1	AW979241 AA565006 AA847102
432803	354267_1	AA565398 AW894072 H97930
432869	355475_1	AW974094 AA569074 AA602574
433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
433492	367934_1	AW605849 AW262898 N41060 AA594852
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433644	371919_1	AW342028 AA641080 AA603282
433687	373061_1	AA743991 AA604852 AW272737
434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
434374	384889_1	AA631439 AI086355 AI082577
434613	389550_1	AI821826 AA640657 AA658836 AA650055 AI821079
434638	38990_1	H50758 AF147434 H50666
434950	396061_1	AW974892 AA654375
434995	397210_1	AW974995 AI821880 AI821932 AI791196 AA659617 AI821137 AA658925
435079	399783_1	AA664192 H60250 T71388
435463	406582_1	AA682507 AW851124
435634	409239_1	T82384 R05307 AA693714
436532	421802_1	AA721522 AW975443 T93070
437146	43371_1	AA730977 AI261584 AA334473 Z43283 AW875861 AW938044 BE150701 AW936262 AA306862 BE565575 BE567380 AA728920 AA167612 AI239729 AI251752 AA485791 BE568425 AW962958
438005	447553_1	BE151746 BE336853 D63271 T94955 AA774994
438458	457837_1	AW975186 AA807807 D29548
438909	46684_1	AF085839 R69137 AW188788 R69254
438993	467651_1	AA828995 AA834879 AI926361
440320	491930_1	AA879294 N67538 AI474541
440674	49997_1	BE561546 Z25124 AI307139 Z28800
443613	575391_1	AI079356 W23287
443657	576685_1	R14973 R14967 AI081006
444314	600667_1	AI140497 AW749625 AW749626 AW749644
444610	612257_1	AI174783 R83569 R12271
444910	624951_1	AI201849 BE069007 AW946544
446096	661959_1	AI276454 AI633717 AI275116
446901	697809_1	AI347274 AW844024
447197	711523_1	R36075 AI366546 R36167
448404	761515_1	BE089973 AI498612 AW805032
449540	80945_2	AA001713 H63836
450024	82296_1	AA005129 AA679084 AA694399
450458	83586_1	AA009926 BE149301
450522	837264_1	AI698839 AI909260 AI909259
451024	85565_1	AA442176 AA259181
451487	87131_1	AA018072 N46370 R84847
452453	918300_1	AI902519 AI902518 AI902516
452542	921410_1	AW812256 AW812257 AI906423 AI906422
453823	982526_1	AL137967 BE064160 BE064186
453901	986414_1	BE065902 AW749032 AW003637
454190	1049996_1	AW177821 AW177896 AW177867
454193	1050256_1	BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091 AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220 AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129 AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108 AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156 AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
454352	1129667_1	AW389668 AW389657 AW609198 AW389649
454359	1130674_1	N71277 AW390764
454389	115682_1	AW752571 AW847602 AA077979
454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093

454455	1206965_1	AW752710 BE180336 BE180186
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454574	1225636_1	AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
454600	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
454678	1228915_1	AW813089 W28102
454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
454714	1230493_1	AW815098 BE154843 BE154831
454766	1234022_1	AW866497 AW819775 AW819868 AW866602 AW866561
454784	1234630_1	AW820626 AW820621 AW820608
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454836	1236509_1	AW833711 AW833620 AW833699
454962	1246750_1	AW847645 AW847791 AW854083 AW853945
455047	1250536_1	AW852530 AW852527 AW852526
455092	1252971_1	BE152428 AW855572 AW855607
455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
455107	1253874_1	BE154113 AW856797 AW856847 AW861128 AW856817
455114	1254105_1	AW857121 AW857123 AW861238
455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
455226	1262534_1	AW902103 AW869012 AW869139
455252	1266222_1	AW876627 AW876630 AW876631 AW876625
455286	1273576_1	BE144384 AW887474 AW887403 BE144386
455310	1278158_1	AW893961 AW893998 AW894034 AW894019
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455488	129372_-1	AA102322
455511	1321229_1	BE144762 AW979091
455512	1321443_1	AW983608 AW983628 AW983610 AW983688 AW983601 AW983645 AW983607 AW983640 AW983625 AW983612 AW983642 AW983687 AW983602 AW983624 AW983634 AW983637 AW983632 AW983617 AW983635 AW983630 AW983636 AW983639 AW983616 AW983689 AW983641 AW983621 AW983603 AW983609 AW983623 AW983644 AW983618 AW983615 AW983611 AW983604 AW983686 AW983622 AW983619 AW983633 AW983589 AW983605 AW983626 AW983643 AW983631 AW983627 AW983613 AW983614 AW983685 AW983593 AW983590 AW983594 AW983620 AW983638 AW983592 AW983588
455571	1331885_1	BE003714 BE003721 BE003720 BE003716
455631	1347545_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
455678	1349716_1	BE066007 BE066017 BE066074
455685	1350393_1	BE066976 BE066928 BE066927
455807	1370914_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
455821	1372714_1	BE143341 BE143344 BE143378 BE143358
455866	1377119_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055
455992	1398552_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997
455995	1398903_1	BE179408 BE179798 BE179980
456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
458804	75803_1	AL157625 N72696 BE622492
458861	798085_1	AI630223 AI630470
459160	920051_1	AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
459201	925883_1	AW391177 W45021
459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 29C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400451	8113550	Minus	82189-82320
400462	9929659	Minus	197610-197785
400608	9887666	Minus	96756-97558
400639	9887597	Plus	23150-23580
400641	8117693	Plus	4786-4992
400756	8119084	Minus	38734-38857
400859	9757499	Minus	91888-92018,98131-98294,99474-99570
400880	9931121	Plus	29235-29336,36363-36580
400889	9958234	Minus	169782-170036
400983	8081198	Plus	107903-108832
401045	8117619	Plus	90044-90184,91111-91345
401049	7232177	Plus	149157-150692
401078	3687273	Plus	105052-105171
401094	9965511	Plus	137130-137302,139283-139506
401103	8568122	Minus	98330-98449
401157	9438289	Minus	114133-114247,114567-114645
401189	9690246	Minus	90815-90929

401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
401213	9858408	Plus	98243-98380,98489-98619
401254	9796309	Plus	152209-152383
401323	9212516	Plus	213509-214450
401335	9884881	Plus	15736-16352
401497	7381770	Plus	92607-92813
401517	7677912	Plus	29278-29770
401526	7770561	Plus	91570-93177
401575	7229804	Minus	76253-76364
401694	3540172	Minus	64056-64168
401793	7263888	Minus	102945-103083
401862	7770606	Minus	55839-55993,59145-59293
401878	8099802	Minus	162268-162474,163089-163195
401986	4406829	Minus	31137-31293
402046	8072415	Plus	166394-166556,168167-168395
402048	8072512	Plus	43936-44078
402102	8117771	Minus	174566-174740
402103	7249203	Plus	14453-15414
402230	9966312	Minus	29782-29932
402318	7582559	Minus	12843-13403
402490	9797648	Plus	149982-150929
402745	9212200	Minus	76516-76690
402800	6010175	Plus	43921-44049,46181-46273
402812	6010110	Plus	25026-25091,25844-25920
402820	6456853	Minus	82274-82443
402855	9662953	Minus	59763-59909
403133	7331427	Plus	38314-38634
403271	7230852	Plus	134283-134485
403277	8072597	Minus	27494-27642
403310	8139936	Minus	183883-184026
403329	8516120	Plus	96450-96598
403356	8569930	Plus	92839-93036
403378	9438244	Minus	44264-44443
403388	9438331	Plus	112733-113001,114599-114735
403467	9929556	Minus	73431-73602
403515	7656757	Minus	173358-179553
403525	7960440	Plus	152431-153243
403534	8076917	Minus	46652-47332
403568	8101145	Minus	85509-85658
403574	8101156	Plus	5542-6176
403637	8671936	Minus	142647-142771,145531-145762
403677	7331517	Minus	55008-55083,62860-63051
403691	7387384	Minus	88280-88463
403760	7712202	Minus	45910-46260,47563-47824
403776	7770611	Minus	1414-1513,1624-1756
403895	7381715	Minus	3502-4002,4070-4308
403937	7711761	Minus	12609-12773
404043	9558573	Plus	29042-29135,46597-46699
404097	7770701	Plus	55512-55781
404200	6010176	Minus	7066-7210
404249	8655533	Plus	64270-64633
404274	9885189	Plus	104127-104318
404285	2326514	Plus	32282-32416
404288	2769644	Plus	3512-3691
404356	7630858	Minus	126433-126623
404443	7579073	Minus	87198-87441
404476	8080699	Plus	101841-102043
404488	8113286	Minus	64835-64994
404513	8151941	Minus	112837-113339
404548	8570305	Minus	83896-84162
404555	7243881	Minus	63963-64157
404561	9795980	Minus	69039-70100
404588	6456726	Minus	40059-40210
404593	9944086	Minus	74922-75788
404599	8705107	Plus	110443-110733
404860	8979555	Plus	65852-66081
404916	7341826	Plus	91057-91188
404957	7407927	Plus	147512-148011
405041	7547195	Plus	121230-121714
405059	7656683	Plus	349-822
405090	8072525	Minus	38552-39202
405257	7329310	Plus	73121-73273
405336	6094635	Plus	33267-33563
405472	8439781	Plus	106297-106447,108462-108596
405494	8050952	Minus	70284-70518
405547	1054740	Plus	124361-124520,124914-125050
405621	5523811	Plus	59362-59607
405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
405654	4895155	Minus	53624-53759
405692	4314424	Plus	61379-62562
405759	3288022	Minus	18283-18399
405829	7109593	Minus	15628-16127
405848	7651809	Minus	28135-28244

	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
	406018	6758904	Minus	37795-38168
	406091	9123919	Minus	197370-197935
5	406092	9123919	Plus	251370-251797,252168-252882
	406149	7144791	Minus	44464-45164
	406195	7289992	Minus	36293-36827
	406333	9213235	Plus	64689-64798
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
10	406506	7711374	Minus	6843-8077
	406554	7711566	Plus	106956-107121
	406603	8272659	Minus	39506-39694

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TABLE 30A: ABOUT 1840 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO HYPERSENSITIVITY PNEUMONITIS (HP)

Table 30A lists about 1840 genes that are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with hypersensitivity pneumonitis (HP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 Gene Chip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" hypersensitivity pneumonitis sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" hypersensitivity pneumonitis level was set to the 90th percentile amongst hypersensitivity pneumonitis samples.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of IPF (idiopathic pulmonary fibrosis) to HP (hypersensitivity pneumonitis)

Pkey	ExAccn	Unigene ID	Unigene Title	R1
450478	AW451709	Hs.271200	ESTs	20.2
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
405654				11.8
440209	H05049	Hs.22269	neurexin 3	10.8
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	10.4
439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	10.2
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	9.5
416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	9.2
403574				9.1
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
419519	AI198719	Hs.176376	ESTs	8.2
435256	AF193766	Hs.13872	cytokine-like protein C17	8.1
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	8.1
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
405443				7.8
428766	AA477989	Hs.98800	ESTs	7.7
441802	AA968636	Hs.127877	ESTs	7.6
453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	7.5
447410	AI470235	Hs.172698	EST	7.2
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
405494				6.9
442377	AA993807	Hs.167367	ESTs	6.9
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	6.8
420407	AA814732	Hs.145010	lipopolysaccaride-specific response 5-li	6.8
415236	R41400		gb:yf94b12.s1 Soares infant brain 1NIB H	6.8
451562	H04150	Hs.107708	ESTs	6.8
403310				6.7
445189	AI936450	Hs.147482	ESTs	6.7
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.7
439780	AL109688		gb:Homo sapiens mRNA full length insert	6.6
402076				6.6
415025	AW207091	Hs.72307	ESTs	6.5
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	6.5
438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	6.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	6.4
409545	BE296182	Hs.19002	hypothetical protein MGC4675	6.4
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.4
411966	AA099113	Hs.118609	ESTs	6.4
440274	R24595	Hs.7122	scrapie responsive protein 1	6.3
442879	AF032922	Hs.8813	syntaxin binding protein 3	6.3
419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
420185	AL044056	Hs.158047	ESTs	6.3
415672	N53097	Hs.193579	ESTs	6.2
455488	AA102322		gb:zl90f03.r1 Stratagene colon (937204)	6.2
420026	AI831190	Hs.166676	ESTs	6.1
446868	AV660737	Hs.135100	ESTs	6.1
431622	AW979271	Hs.293184	ESTs	6.1
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	6.1
421300	AW297398	Hs.96617	ESTs	6.0
416045	H15990	Hs.31403	ESTs	6.0

	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	436397	AA715013	Hs.169835	ESTs	6.0
	440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.0
5	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.0
	403625				6.0
	418986	AI123555	Hs.81796	ESTs	5.9
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.9
	400292	AA250737	Hs.72472	ESTs	5.9
10	442849	R10099	Hs.269805	ESTs	5.9
	440887	AI799488	Hs.135905	ESTs	5.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	431374	BE258532	Hs.251871	CTP synthase	5.7
15	444963	AI916973	Hs.213603	ESTs	5.7
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	5.6
	444992	R37658	Hs.21375	ESTs	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
20	451830	H18433	Hs.21542	KIAA1035 protein	5.5
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	5.5
	404043				5.5
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	5.5
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	5.5
25	434683	AW298724	Hs.202639	ESTs	5.5
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	5.5
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	5.5
	428895	AA437124	Hs.187247	ESTs	5.4
	450018	AA421642	Hs.24309	hypothetical protein FLJ11106	5.4
30	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	403637				5.3
	414725	AA769791	Hs.125300	ring finger protein 21, interferon-respo	5.3
35	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	5.3
	403329				5.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	5.3
	459664				5.3
	401497				5.3
40	410797	AW857191		gb:RC2-CT0304-080100-011-b12 CT0304 Homo	5.2
	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	435202	AI971313	Hs.170204	KIAA0551 protein	5.1
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.1
45	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	5.1
	434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.1
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.0
50	437636	AA764781	Hs.291844	ESTs	5.0
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.0
	418771	AA807881	Hs.25329	ESTs	5.0
	434820	AI821863		gb:ns90f05.x5 NCI_CGAP_Pr3 Homo sapiens	5.0
55	440615	AI733055	Hs.130806	ESTs	5.0
	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	4.9
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	423607	AA328329	Hs.5591	ESTs	4.9
60	407415	AF073328		gb:Homo sapiens tetracyline transporter-	4.9
	401878				4.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	4.9
	451325	AA021283	Hs.59788	ESTs	4.9
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	4.9
65	406333				4.9
	409105	AW467539	Hs.255877	ESTs	4.8
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.8
	421482	AL135462	Hs.104715	inversin	4.8
	442757	AI739528	Hs.28345	ESTs	4.8
70	459717				4.8
	436637	AI783629	Hs.26766	ESTs	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
75	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
	441640	AI733345	Hs.144104	ESTs	4.8
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	4.8
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
80	411965	BE467339	Hs.280115	ESTs	4.7
	403341				4.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	4.7
	443271	BE568568	Hs.195704	ESTs	4.7

	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	426097	BE327369	Hs.112238	ESTs	4.7
	439199	R40373	Hs.26299	ESTs	4.7
	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	4.6
5	434381	AA631834		gb:np77h05.s1 NCI_CGAP_Pr2 Homo sapiens	4.6
	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	431242	AA987742	Hs.251278	KIAA1201 protein	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
10	442360	AI374621	Hs.29055	ESTs	4.6
	452171	AI863302	Hs.211930	EST	4.6
	440801	AA906366	Hs.190535	ESTs	4.5
	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
	431447	AA505138	Hs.291341	ESTs	4.5
15	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	401365				4.5
	408281	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	4.5
	411657	AW855583		gb:CM4-CT0278-221099-027-f07 CT0278 Homo	4.5
	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	4.5
20	428528	AI004034	Hs.98638	ESTs	4.5
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	417252	AA195014	Hs.85971	ESTs	4.5
	417135	AA422067	Hs.50547	ESTs	4.5
	403089				4.4
25	420691	AA829433	Hs.275343	ESTs	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	4.4
	454438	AA224053	Hs.172405	cell division cycle 27	4.4
30	435434	AA680387	Hs.187850	ESTs	4.4
	420828	AA280778	Hs.186878	ESTs	4.3
	435586	AI279137	Hs.151498	ESTs	4.3
	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	416170	H42454	Hs.220645	ESTs	4.3
35	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	4.3
	428912	AW103117	Hs.98949	ESTs, Weakly similar to MEA6 [H.sapiens]	4.3
	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	4.3
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	4.3
	401189				4.3
40	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288685	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	422654	AA314316	Hs.163725	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
	417919	AI928203	Hs.86379	ESTs	4.3
45	405784				4.3
	431853	AA521034	Hs.70834	ESTs	4.3
	409629	AW449589	Hs.279724	ESTs	4.2
	403281				4.2
	427173	BE255017	Hs.97540	ESTs	4.2
50	433717	AF063536		gb:AF063536 Homo sapiens library (Yu Y)	4.2
	406777	T23625	Hs.150580	putative translation initiation factor	4.2
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	4.2
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.2
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
55	449762	N93057	Hs.54888	ESTs	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	439382	BE247684	Hs.103070	ESTs	4.1
	404957				4.1
	436332	AL049679	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	4.1
60	446393	AW014174	Hs.301956	zinc finger protein	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	456386	W28481		gb:47e1 Human retina cDNA randomly prime	4.1
	406288	AW068311	Hs.311054	Homo sapiens mRNA full length insert cDN	4.1
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
65	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	403344				4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.1
	401596	AA172106	Hs.110950	Rag C protein	4.1
70	418693	AI750878	Hs.87409	thrombospondin 1	4.1
	414299	AA142989	Hs.71730	ESTs	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	458552	AW136139	Hs.245856	ESTs	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
75	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	441201	AW118822	Hs.128757	ESTs	4.0
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	4.0
	440472	AA886169	Hs.169071	ESTs	4.0
	418379	AA218940	Hs.137516	fidgetin-like 1	4.0
80	435878	R08330	Hs.20152	ESTs	4.0
	437263	AA747822		gb:nx97a04.s1 NCI_CGAP_GCB1 Homo sapiens	4.0
	444087	AV647899	Hs.282375	ESTs	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0

	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
	405521				4.0
	411597	AW852925		gb:PM0-CT0248-131099-001-f10 CT0248 Homo	4.0
	415655	W05433	Hs.49890	ESTs	4.0
5	404822				4.0
	441107	AA917075	Hs.190520	ESTs	4.0
	404834				4.0
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	4.0
	428102	AA968441	Hs.126866	ESTs	4.0
10	436511	AA721252	Hs.291502	ESTs	4.0
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	4.0
	453098	Z25935	Hs.86379	ESTs	3.9
	410811	AW805687	Hs.300648	ESTs	3.9
	425048	H05468	Hs.164502	ESTs	3.9
15	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	452768	AW069459	Hs.61539	ESTs	3.9
	455241	AW876249		gb:PM4-PT0019-131299-006-B05 PT0019 Homo	3.9
20	409070	AA063003	Hs.224560	ESTs	3.9
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
	403188				3.9
25	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	3.9
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
30	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.9
	451221	AI949701	Hs.210589	ESTs	3.9
	455475	AW948126		gb:RC0-MT0013-280300-031-a12 MT0013 Homo	3.9
	433197	AB040889	Hs.281022	KIAA1456 protein	3.9
35	429881	T80112	Hs.192245	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	431220	N52937	Hs.102679	ESTs	3.9
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
40	404443				3.9
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.9
	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	3.9
	427167	AI239607	Hs.99196	hypothetical protein MGC11324	3.9
45	438090	AA777534	Hs.191992	ESTs	3.8
	407938	AA905097	Hs.85050	phospholamban	3.8
	440454	AI733037	Hs.129990	ESTs	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
50	407762	AW235638	Hs.29475	ESTs	3.8
	420727	H75701	Hs.99886	complement component 4-binding protein,	3.8
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	3.8
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	3.8
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
55	459429	AA278779	Hs.335696	EST	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	437458	AL390131	Hs.128751	Homo sapiens cDNA FLJ12235 fis, clone MA	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	3.8
60	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	444414	AW293214	Hs.8752	transmembrane protein 4	3.8
	402615				3.7
	410585	AW770523	Hs.337501	ESTs	3.7
	425168	R96366		gb:yq37d04.s1 Soares fetal liver spleen	3.7
65	449729	R72032	Hs.29235	ESTs	3.7
	459359	N99545		gb:za40a05.r1 Soares fetal liver spleen	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439001	AF075068		gb:Homo sapiens full length insert cDNA	3.7
	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	3.7
70	404193				3.7
	416379	N38857	Hs.203933	ESTs	3.7
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	3.7
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	3.7
	412589	R28660	Hs.24305	ESTs	3.7
75	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heregulin	3.7
80	451882	AI821324	Hs.100445	ESTs	3.7
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.7
	405001	U58196	Hs.296281	interleukin enhancer binding factor 1	3.7
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	3.7

	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.7
	432781	NM_014133	Hs.278940	PRO0618 protein	3.7
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.7
	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
5	430682	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.7
	430503	AA533574	Hs.152274	ESTs	3.7
	443305	AI050693	Hs.133318	ESTs	3.7
10	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.7
	452280	AI911410	Hs.167224	ESTs	3.6
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	3.6
	406992	S82472		gb:beta -pol=DNA polymerase beta (exon a	3.6
	441416	AI990139	Hs.148609	ESTs	3.6
15	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	413998	AW103807	Hs.243933	ESTs	3.6
	440385	AA884283	Hs.192136	ESTs	3.6
	431673	AW971302	Hs.293233	ESTs	3.6
	401887				3.6
20	404793				3.6
	422054	AA322506		gb:EST25146 Cerebellum II Homo sapiens c	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
	449645	AI961092	Hs.196155	ESTs	3.6
	404476				3.6
25	449336	AL119995	Hs.15260	ESTs, Highly similar to AC007228 2 BC372	3.6
	401200				3.6
	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	443394	AI055865	Hs.133485	ESTs	3.6
30	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	436269	AA707472	Hs.190760	ESTs	3.6
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	3.6
35	416394	H64111		gb:yr57f03.r1 Soares fetal liver spleen	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	435766	R11673	Hs.186498	ESTs	3.6
40	448067	R68568	Hs.183373	src homology 3 domain-containing protein	3.6
	441605	AA984647	Hs.128801	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.5
45	450350	T97817	Hs.174880	ESTs	3.5
	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	459037	AW439497	Hs.290656	EST	3.5
	419247	S65791	Hs.89764	fragile X mental retardation 1	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
50	426724	AA383623	Hs.293616	ESTs	3.5
	434273	AA913143	Hs.26303	ESTs	3.5
	438042	AW296971	Hs.255593	ESTs	3.5
	410500	R09442		gb:yf26c09.r1 Soares fetal liver spleen	3.5
	416154	Z46122		gb:HSC0VB031 normalized infant brain cDN	3.5
55	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.5
	454447	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	444338	AI937026	Hs.146642	ESTs	3.5
	427687	AW003867	Hs.1570	histamine receptor H1	3.5
60	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	3.5
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.5
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	3.5
	403515				3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
65	439953	AA918129	Hs.124638	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	3.5
	453931	AL121278	Hs.25144	ESTs	3.5
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.5
70	413468	BE504766		gb:hz40g01.x1 NCI_CGAP_GC6 Homo sapiens	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.5
	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	3.5
	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.5
75	410908	AA121686	Hs.10592	ESTs	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
	406190				3.5
	430762	AI343652	Hs.105667	ESTs	3.5
	451182	D52562	Hs.296317	KIAA1789 protein	3.4
80	432437	W07088	Hs.293685	ESTs	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
	407676	AW064111	Hs.279823	ESTs	3.4

	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
	459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	3.4
5	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	3.4
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.4
	420430	AI703192		gb:wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	3.4
	443921	AI091310	Hs.134848	ESTs	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
10	443475	AI066470	Hs.134482	ESTs	3.4
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.4
	453263	R91778	Hs.99369	ESTs	3.4
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	3.4
	456303	AA224872	Hs.115088	ESTs	3.4
15	431474	AL133990	Hs.190642	ESTs	3.4
	439702	AW085525	Hs.134182	ESTs	3.4
	458797	AW001835	Hs.13323	hypothetical protein FLJ22059	3.4
	430140	AW296771	Hs.221999	ESTs	3.4
	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	3.4
20	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.4
	446672	T05514		gb:EST03403 Fetal brain, Stratagene (cat	3.4
	431548	AI834273	Hs.9711	novel protein	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
25	417663	R07483	Hs.180461	ESTs	3.3
	405455				3.3
	426235	AI631964	Hs.34447	ESTs	3.3
	439567	AI056618	Hs.134314	ESTs	3.3
	444848	AW451176	Hs.195954	ESTs	3.3
30	451426	AW205003	Hs.208063	ESTs	3.3
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.3
	401626				3.3
	405780				3.3
	417991	AA731452	Hs.190008	ESTs	3.3
35	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	3.3
	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.3
40	445510	AA946676	Hs.282824	ESTs	3.3
	418663	AK001100	Hs.41690	desmocollin 3	3.3
	447617	AI400762	Hs.176675	ESTs	3.3
	448150	AI472167	Hs.302739	ESTs	3.3
	410140	AL134435	Hs.22269	neurexin 3	3.3
45	443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens c	3.3
	454777	AW820027		gb:QV0-ST0294-240300-173-g04 ST0294 Homo	3.3
	410767	AJ001873	Hs.66185	Homo Sapiens mRNA, partial cDNA sequence	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
50	438456	AA913381	Hs.190513	ESTs	3.3
	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.3
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	3.3
	433567	AF073299	Hs.103132	solute carrier family 9 (sodium/hydrogen	3.3
	433805	AA706910	Hs.112742	ESTs	3.3
55	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	456555	AW592167	Hs.293299	ESTs	3.3
	419189	T95862	Hs.112318	6.2 kd protein	3.3
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfami	3.3
60	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.3
	413200	AA127395	Hs.222414	ESTs	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	416737	AF154335	Hs.79691	LIM domain protein	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
65	429216	AI369472	Hs.65407	ESTs	3.3
	432488	AA551010	Hs.216640	ESTs	3.3
	433386	AW360833		gb:PM1-CT0243-201099-004-d08 CT0243 Homo	3.3
	400889				3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
70	446190	AI279299	Hs.256564	ESTs	3.3
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	3.3
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
75	446645	AI336596	Hs.156294	ESTs	3.3
	434294	AJ271379	Hs.76194	ribosomal protein S5	3.3
	452372	AI885742	Hs.228474	ESTs	3.3
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	3.2
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.2
80	430548	AW450575	Hs.163203	ESTs, Weakly similar to B34087 hypotheti	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	437845	AA769578	Hs.90488	ESTs	3.2

	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.2
	417175	R44558	Hs.94002	ESTs	3.2
	456536	AW135986	Hs.257859	ESTs	3.2
5	401132				3.2
	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	450947	AI745400	Hs.204662	ESTs	3.2
	456605	AI827786	Hs.259044	ESTs	3.2
10	452879	AW905328	Hs.180842	ribosomal protein L13	3.2
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.2
	429479	AA453488	Hs.99333	ESTs	3.2
	448090	AI608821	Hs.270289	ESTs	3.2
	401324				3.2
15	404731				3.2
	419936	AI792788		gb:ol91d05.y5 NCI_CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	433990	AA889328	Hs.112950	ESTs	3.2
	415239	R42608	Hs.139270	ESTs	3.2
20	418878	W20090	Hs.6616	ESTs	3.2
	438079	R09664	Hs.191223	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	3.2
	454145	AA046872	Hs.62798	ESTs	3.2
25	446577	AB040933	Hs.15420	KIAA1500 protein	3.2
	430664	AW969834	Hs.303303	ESTs	3.2
	404588				3.2
	407834	AW084991	Hs.26100	ESTs	3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
30	440790	AW593050	Hs.128580	ESTs	3.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	3.2
	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone L	3.2
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
35	444771	AB023201	Hs.11912	KIAA0984 protein	3.2
	445233	AV653034	Hs.297559	ESTs	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
40	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.2
	403623				3.2
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.2
	444050	AW138295	Hs.135024	ESTs	3.2
	421036	AA810560	Hs.303577	ESTs	3.2
45	401459				3.1
	404404				3.1
	450438	AI696071	Hs.253800	ESTs	3.1
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	3.1
50	441274	AW593781	Hs.131357	ESTs	3.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
55	431906	AW328038	Hs.37486	ESTs	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	450271	AI693900	Hs.200920	ESTs	3.1
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	3.1
	415273	Z39840	Hs.22229	ESTs	3.1
60	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.1
	446364	AB006624	Hs.14912	KIAA0286 protein	3.1
	436638	AI271945	Hs.134984	ESTs	3.1
	418079	R40058	Hs.6911	ESTs	3.1
65	448466	AI522109	Hs.171066	ESTs	3.1
	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
	415046	R40018	Hs.56400	ESTs	3.1
	448134	AI470790	Hs.34494	ESTs	3.1
	456027	BE327387	Hs.13913	KIAA1577 protein	3.1
70	458023	AW978161	Hs.268555	5'-3' exoribonuclease 2	3.1
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.1
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	449138	AW294215	Hs.195631	ESTs	3.1
75	455756	BE079307		gb:RC1-BT0623-120200-011-g09 BT0623 Homo	3.1
	428170	H05530	Hs.12565	ESTs	3.1
	429878	AA460188	Hs.127263	ESTs	3.1
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	3.1
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptid	3.1
80	415840	R15955	Hs.21758	ESTs	3.1
	444955	AW002844	Hs.148641	ESTs	3.1
	436020	AA778177	Hs.121724	ESTs	3.1
	453051	AW196690	Hs.224269	ESTs	3.1

	425178	H16097	Hs.161027	ESTs	3.1
	402145				3.1
	410685	AA497117	Hs.129600	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	449238	AA426229	Hs.331561	muscle-specific RING-finger protein 3	3.1
5	456737	BE247203	Hs.124831	CGI-67 protein	3.1
	438214	H06076	Hs.26320	TRABID protein	3.1
	436250	AY004867	Hs.85844	neurotrophic tyrosine kinase, receptor,	3.1
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
10	449357	AI076363	Hs.288806	Homo sapiens cDNA FLJ11778 fis, clone HE	3.0
	418950	T78517	Hs.13941	ESTs	3.0
	431508	NM_012481	Hs.182979	ribosomal protein L12	3.0
	405090				3.0
	445409	AI949081	Hs.147862	ESTs	3.0
15	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.0
	408235	AA053361	Hs.75969	proline-rich protein with nuclear target	3.0
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	3.0
	452073	AA625150	Hs.82098	ESTs	3.0
20	427050	AA397789	Hs.161803	ESTs	3.0
	427244	AA402400	Hs.178045	ESTs	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sap	3.0
	421376	AA287948	Hs.134110	ESTs	3.0
25	441519	AA972740	Hs.127092	ESTs	3.0
	404367				3.0
	453502	AL039786	Hs.21273	transcription factor NYD-sp10	3.0
	421948	L42583	Hs.334309	keratin 6A	3.0
	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
30	400608				3.0
	404042				3.0
	405229				3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
	415452	F09134	Hs.12839	ESTs	3.0
35	430371	D87466	Hs.240112	KIAA0276 protein	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	429014	AI800518	Hs.118158	ESTs	3.0
	405605				3.0
40	400227				3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	427533	R36022	Hs.179566	hypothetical protein FLJ22624	3.0
	418355	L42563	Hs.1165	ATPase, H+/K+ transporting, nongastric,	3.0
45	433536	AI732163	Hs.188909	ESTs, Weakly similar to alternatively sp	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	449623	C00719	Hs.120440	EST	3.0
	445568	H00918	Hs.268744	KIAA1796 protein	3.0
	440448	AA885428	Hs.125646	ESTs	3.0
50	428201	AA424158	Hs.206461	ESTs	3.0
	444148	AW003204	Hs.151167	ESTs	3.0
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	3.0
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	3.0
	440925	AW511090	Hs.130419	ESTs	3.0
55	428398	AI249368	Hs.98558	ESTs	3.0
	415913	H70302		gb:yr95f07.r1 Soares fetal liver spleen	3.0
	418145	AF121260	Hs.83577	cysteine and glycine-rich protein 3 (car	3.0
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	3.0
	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	3.0
60	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	437980	R50393	Hs.278436	KIAA1474 protein	3.0
	455955	BE162394		gb:PM2-HT0451-170100-004-a08 HT0451 Homo	3.0
	414899	AW975433	Hs.36288	ESTs	2.9
65	403786				2.9
	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.9
70	457041	AA399018	Hs.250835	ESTs	2.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.9
	422336	AI761322	Hs.115285	dihydrolipoamide S-acetyltransferase (E2	2.9
	451664	AA889081	Hs.153952	5' nucleotidase (CD73)	2.9
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.9
75	455249	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.9
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.9
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	2.9
	405302				2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
80	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9

	425793	AA363946	Hs.20969	ESTs	2.9
	401462				2.9
	458817	AI522129	Hs.173119	ESTs	2.9
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.9
5	419875	AA853410	Hs.93557	proenkephalin	2.9
	423047	NM_005323	Hs.123064	H1 histone family, member T (testis-spec	2.9
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.9
	401368				2.9
	418531	R96760	Hs.183758	ESTs	2.9
10	447290	AI476732	Hs.263912	ESTs	2.9
	441143	AI027604	Hs.159650	ESTs	2.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	2.9
	405783				2.9
	444459	AI680624	Hs.148676	ESTs	2.9
15	402112	R58624	Hs.2186	eukaryotic translation elongation factor	2.9
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.9
	444827	R09764	Hs.20416	ESTs	2.9
	451195	U10492	Hs.438	mesenchyme homeo box 1	2.9
	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.9
20	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	455699	BE068121		gb:CM1-BT0368-061299-060-a02 BT0368 Homo	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
25	428632	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
	443185	NM_006134	Hs.284142	chromosome 21 open reading frame 4	2.9
30	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	2.9
	437183	AI928184	Hs.122011	ESTs	2.9
	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
	442726	AW136066	Hs.19145	ESTs	2.9
35	456189	H91010	Hs.44940	ESTs	2.9
	441115	R69910	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	2.9
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.9
	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
40	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypotheti	2.9
	450877	AI799608	Hs.29178	ESTs	2.9
	439063	AF085922	Hs.113968	ESTs	2.9
	401526				2.9
	408751	N91553	Hs.258343	ESTs	2.9
45	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.9
	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
50	452589	BE159915	Hs.61406	ESTs, Weakly similar to 2004399A chromos	2.8
	403011				2.8
	436154	AA764950	Hs.119898	ESTs	2.8
	408221	AA912183	Hs.47447	ESTs	2.8
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.8
55	415399	T26994	Hs.177198	ESTs	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	443556	AA256769	Hs.94949	methylmalonyl-CoA epimerase	2.8
	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo	2.8
	439703	AF086538	Hs.196245	ESTs	2.8
60	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.8
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.8
	434715	BE005346	Hs.116410	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
65	453736	AL118674	Hs.34871	zinc finger homeobox 1B	2.8
	404967				2.8
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.8
	426942	AA393551	Hs.97450	ESTs	2.8
70	403513				2.8
	419077	AA233885	Hs.164526	ESTs	2.8
	421823	N40850	Hs.28625	ESTs	2.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	2.8
	451007	H38108	Hs.32759	ESTs	2.8
75	407803	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	2.8
	409642	AW450809	Hs.257347	ESTs	2.8
	439492	AF086310	Hs.103159	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	2.8
80	428350	AW873520	Hs.112017	GE36 gene	2.8
	405456				2.8
	442459	AI264628	Hs.125428	ESTs	2.8
	415763	Z42285	Hs.5181	proliferation-associated 2G4, 38kD	2.8

	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	449539	W80363	Hs.58446	ESTs	2.8
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.8
5	408749	H65489	Hs.250659	ESTs	2.8
	404652				2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	2.8
	402131				2.8
10	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	444217	AV648751	Hs.282395	ESTs	2.8
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	2.8
15	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	451496	AW503407		gb:UI-HF-BN0-akw-d-11-0-UI.r1 NIH_MGC_50	2.8
	420273	AI652864	Hs.197257	ESTs	2.8
20	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	425012	T77666	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	2.8
	441609	AA946764	Hs.133460	ESTs	2.8
25	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypotheti	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	2.8
30	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	459450	AA426429	Hs.98463	EST	2.8
	424188	AW954552	Hs.142634	zinc finger protein	2.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	2.7
	427443	AA402713	Hs.97872	ESTs	2.7
35	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.7
	413091	BE065063		gb:RC1-BT0313-110500-017-e02 BT0313 Homo	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
40	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.7
	408243	Y00787	Hs.624	interleukin 8	2.7
	407308	H67394	Hs.331325	ESTs, Weakly similar to I38022 hypotheti	2.7
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.7
	404587	M99587	Hs.104134	homeo box (H6 family) 1	2.7
45	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.7
	416431	AW384459	Hs.172004	titin	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	427134	AA398409	Hs.173561	EST	2.7
50	428137	AA421792	Hs.170999	ESTs	2.7
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	441218	BE327561	Hs.202345	ESTs	2.7
	440911	AA909536	Hs.143562	ESTs	2.7
	411131	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo	2.7
55	438602	AI167149	Hs.123374	ESTs, Weakly similar to mariner transpos	2.7
	441191	AI693930	Hs.148816	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
60	429905	AL080128	Hs.225998	DKFZP434C153 protein	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	450777	AA255646	Hs.60478	ESTs, Moderately similar to S47073 finge	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
	405523				2.7
65	434849	AW292765	Hs.8053	ESTs	2.7
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	2.7
	438055	AA776655	Hs.270942	ESTs	2.7
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	2.7
	405738				2.7
70	417806	AI867277	Hs.183733	ESTs	2.7
	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	2.7
	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	446092	N33522	Hs.145894	ESTs	2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
75	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.7
	444931	AV652066	Hs.75113	general transcription factor IIIA	2.7
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.7
	453264	AA034137	Hs.271955	ESTs	2.7
	438370	AA843242	Hs.48523	ESTs	2.7
80	406092				2.7
	454874	AW836407	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7

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	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.7
	441884	AW172630	Hs.144884	ESTs	2.7
	416211	R14625		gb:yg45c03.r1 Soares infant brain 1NIB H	2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
5	452259	AA317439	Hs.28707	signal sequence receptor, gamma (transio	2.7
	453696	AI989482	Hs.146286	kinesin family member 13A	2.7
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.7
	425876	AW005887	Hs.234058	ESTs	2.7
	450458	AA009926		gb:zi07e05.r1 Soares_fetal_liver_spleen_	2.7
10	406603				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	410871	D78367	Hs.66739	keratin 12 (Meesmann corneal dystrophy)	2.7
	412706	R97106	Hs.167546	ESTs	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
15	436329	AI798750	Hs.163960	Homo sapiens heat shock transcription fa	2.7
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	2.7
	419296	AA236115	Hs.120785	ESTs	2.7
20	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	411409	AW844803		gb:RC3-CN0056-170300-015-f08 CN0056 Homo	2.7
	426662	AA879474	Hs.122710	ESTs	2.7
	400268				2.7
25	438782	AA828380	Hs.126733	ESTs	2.7
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	2.7
	412486	AF210650	Hs.150858	NAG19 protein	2.7
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	2.7
	457900	AW976692	Hs.291665	ESTs	2.7
30	417376	AA253314	Hs.154103	LIM protein (similar to rat protein klna	2.7
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	435608	AW183971	Hs.250896	ESTs	2.7
	413627	BE182082	Hs.246973	ESTs	2.7
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.7
35	445660	AI702668	Hs.201955	ESTs	2.7
	441396	AW293677	Hs.186890	ESTs	2.6
	452046	AB018345	Hs.27657	KIAA0802 protein	2.6
	454936	AW846082		gb:MR3-CT0176-081099-002-d01 CT0176 Homo	2.6
	454434	AA083558	Hs.261286	ESTs	2.6
40	436888	AI942357	Hs.187870	ESTs	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	416690	H84078	Hs.108551	ESTs	2.6
	436471	AA719813	Hs.117662	ESTs	2.6
45	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.6
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.6
	455544	AW993880		gb:RC3-BN0034-240400-017-d09 BN0034 Homo	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
50	452821	AW471181	Hs.160874	ESTs	2.6
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	2.6
	429864	AA460039	Hs.286	ribosomal protein L4	2.6
	456273	AF154846	Hs.1148	zinc finger protein	2.6
	402603				2.6
55	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
	438295	AI394151	Hs.37932	ESTs	2.6
60	450181	H05254	Hs.201198	ESTs	2.6
	433764	AW753676	Hs.39982	ESTs	2.6
	433229	AB040925	Hs.91625	KIAA1492 protein	2.6
	443718	AI083580	Hs.221373	ESTs	2.6
	418246	AI472179	Hs.121276	ESTs, Weakly similar to R5HU7A ribosomal	2.6
65	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	2.6
	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.6
	419318	AW969742	Hs.291005	ESTs	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	404414				2.6
70	446444	AI743737	Hs.24370	ESTs	2.6
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.6
	418310	AA814100	Hs.86693	ESTs	2.6
	454481	AW794878	Hs.314230	ESTs, Highly similar to clock [H.sapiens	2.6
75	441216	BE299830	Hs.192908	ESTs	2.6
	438257	AW474419	Hs.224794	ESTs	2.6
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	419505	AA243660	Hs.143061	ESTs	2.6
	417596	R07343	Hs.226823	ESTs, Moderately similar to I54374 gene	2.6
80	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	454867	AW835924		gb:PM1-LT0018-250200-002-e09 LT0018 Homo	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6

	457630	AI680803	Hs.112627	ESTs	2.6
	424210	T71397	Hs.222707	KIAA1718 protein	2.6
	447748	AI422023	Hs.161338	ESTs	2.6
	411970	AA099142	Hs.13804	hypothetical protein dJ462O23.2	2.6
5	441233	AA972965	Hs.135568	ESTs	2.6
	400706				2.6
	436033	H75391	Hs.255748	ESTs	2.6
	440836	AW370882	Hs.222080	ESTs	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
10	455110	BE154505		gb:PM0-HT0343-281299-003-e06 HT0343 Homo	2.6
	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.6
	413088	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.6
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.6
15	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.6
	442690	AI014727	Hs.160047	ESTs, Weakly similar to B28096 line-1 pr	2.6
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	2.6
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.6
	403271				2.6
20	429761	AI276780	Hs.135173	ESTs	2.6
	437085	AA743935	Hs.202329	ESTs	2.6
	450822	AW771860	Hs.205130	ESTs	2.6
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	2.6
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	2.6
25	430357	AW976789	Hs.165607	ESTs	2.6
	417249	N58198	Hs.182898	ESTs	2.6
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.6
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
30	446302	AI285848	Hs.149757	ESTs	2.6
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6
	428944	AA780181	Hs.41182	Homo sapiens DC47 mRNA, complete cds	2.6
	419647	AA348947	Hs.91816	hypothetical protein	2.6
	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	2.6
35	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	2.6
	452450	AW854891	Hs.194720	ATP-binding cassette, sub-family G (WHIT	2.6
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	2.6
	436421	AI678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	2.6
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.6
40	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.6
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.5
	447624	AI640326	Hs.62713	ESTs	2.5
45	411736	AW859089		gb:MR1-CT0350-150200-002-d02 CT0350 Homo	2.5
	416334	H53139	Hs.36271	ESTs	2.5
	446818	AI342668	Hs.279765	ESTs	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	442278	AI733477	Hs.166313	ESTs	2.5
50	453393	AW956392	Hs.110376	ESTs	2.5
	420854	AW296927		gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCI_CGAP_Su	2.5
	408729	AA195764	Hs.72639	ESTs	2.5
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	2.5
	411660	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
55	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	409156	N76186	Hs.173518	M-phase phosphoprotein homolog	2.5
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.5
	430291	AV660345	Hs.238126	CGI-49 protein	2.5
	401785				2.5
60	402369				2.5
	439079	AF085937	Hs.38348	ESTs	2.5
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	2.5
	411463	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	2.5
	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.5
65	404988				2.5
	409446	AI561173	Hs.67688	ESTs	2.5
	412613	AA653507	Hs.285711	hypothetical protein FLJ13089	2.5
	417909	R35614		gb:yg66e08.r1 Soares infant brain 1NIB H	2.5
	454743	AW818456	Hs.79347	KIAA0211 gene product	2.5
70	406364				2.5
	404108				2.5
	411934	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
	443526	AW792804	Hs.134002	ESTs	2.5
75	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.5
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	2.5
	458771	AW295151	Hs.163612	ESTs	2.5
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	426589	AW954460		gb:EST366530 MAGE resequences, MAGC Homo	2.5
80	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	2.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	2.5
	434784	AA649051	Hs.164007	ESTs	2.5

	429322	D86984	Hs.199243	KIAA0231 protein	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
5	449410	AA001356	Hs.18159	ESTs	2.5
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.5
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.5
	416944	N22809		gb:yw41e07.s1 Weizmann Olfactory Epithel	2.5
	423010	W25436	Hs.90725	ESTs, Moderately similar to I38022 hypot	2.5
10	412505	AA974491	Hs.21734	ESTs	2.5
	446399	AI298405	Hs.150080	ESTs	2.5
	412139	BE044976		gb:hn25b10.x1 NCI_CGAP_Thy7 Homo sapiens	2.5
	403691				2.5
	424025	AI701852	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	2.5
15	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.5
	457770	BE065030	Hs.124179	ESTs	2.5
	427731	AA411750	Hs.20943	ESTs	2.5
20	426920	AA393351	Hs.132121	ESTs	2.5
	427794	AA709186	Hs.282963	ESTs	2.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo sapiens c	2.5
25	436391	AJ227892	Hs.146274	ESTs	2.5
	401989				2.5
	423346	AI267677	Hs.127416	synaptojanin 1	2.5
	444905	AW135863	Hs.209228	ESTs	2.5
	424539	L02911	Hs.150402	activin A receptor, type I	2.5
30	400861				2.5
	458426	AI084514	Hs.249587	ESTs	2.5
	429520	AA160142	Hs.205058	hypothetical protein FLJ20075	2.5
	403568				2.5
	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.5
35	451078	AI927694	Hs.204470	ESTs	2.5
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.5
	427888	AA417088	Hs.137598	ESTs	2.5
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.5
	422840	U44059	Hs.121481	thyrotrophic embryonic factor	2.5
40	404708				2.5
	405008				2.5
	453772	BE281431	Hs.16323	Homo sapiens, Similar to G antigen 8, cl	2.5
	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
45	449311	AI657014		gb:tt49a12.x1 NCI_CGAP_GC6 Homo sapiens	2.5
	454277	AW295069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	2.4
50	407851	NM_014496	Hs.40434	ribosomal protein S6 kinase, 90kD, polyp	2.4
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.4
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	2.4
	406468				2.4
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.4
55	408617	R61736	Hs.124128	ESTs	2.4
	409627	AW997628	Hs.313637	ESTs	2.4
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen	2.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.4
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	2.4
60	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	2.4
	429654	AI435046	Hs.164318	ESTs	2.4
	432253	AW090822	Hs.274174	transcription elongation factor (SII) e	2.4
	439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDN	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
65	453052	R63050	Hs.223813	ESTs	2.4
	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.4
	452843	AI796769	Hs.208320	ESTs	2.4
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	2.4
70	449695	AA164569	Hs.34550	ESTs	2.4
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.4
	400641				2.4
	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.4
75	432808	NM_015985	Hs.278973	angiopoietin-3	2.4
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411561	H81164	Hs.285017	hypothetical protein FLJ21799	2.4
	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
	423513	AF035960	Hs.129719	transglutaminase 5	2.4
80	434627	AI221894	Hs.39311	ESTs	2.4
	435663	AI023707	Hs.134273	ESTs	2.4
	455879	BE153275		gb:PM0-HT0335-180400-008-e11 HT0335 Homo	2.4
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.4

	409041	AB033025	Hs.50081	KIAA1199 protein	2.4
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.4
	448889	BE140902		gb:IL1-HT0028-240699-001-C11 HT0028 Homo	2.4
5	439481	AF086294	Hs.125844	ESTs	2.4
	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	409298	AA070211		gb:zm68c04.s1 Stratagene neuroepithelium	2.4
	411322	AW887330	Hs.172405	cell division cycle 27	2.4
10	447640	AI417187		gb:tg75g11.x1 Soares_NhHMPu_S1 Homo sapi	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	458763	AI693417	Hs.293309	ESTs	2.4
	404638				2.4
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.4
15	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.4
	408238	W95901		gb:ze43d11.r1 Soares retina N2b4HR Homo	2.4
	436747	AW977192	Hs.291343	ESTs	2.4
	437048	AA743240	Hs.91582	ESTs	2.4
20	413143	BE067232		gb:PM3-BT0347-170200-001-b05 BT0347 Homo	2.4
	404561				2.4
	444009	AI380792	Hs.135104	ESTs	2.4
	400250				2.4
	403891				2.4
25	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	441227	AW295407	Hs.128893	ESTs	2.4
	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
30	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	2.4
	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.4
	450068	AW207212	Hs.280925	ESTs	2.4
35	444750	AW242684	Hs.243623	ESTs	2.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	407264	L34727		gb:Homo sapiens T-cell receptor beta (TC	2.4
	443169	AI038687	Hs.133338	ESTs	2.4
	426536	AI949749	Hs.44441	ESTs	2.4
40	449752	AI668626	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	2.4
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pol. ORF 1 [	2.4
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
	430484	D82880	Hs.241548	RAS p21 protein activator 2	2.4
45	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.4
	447375	AI376660	Hs.257822	ESTs	2.4
	444230	H95537	Hs.146067	ESTs	2.4
	439911	AA854024	Hs.189110	ESTs	2.4
	421296	NM_002666	Hs.103253	perilipin	2.4
50	449385	AI650471	Hs.270370	ESTs	2.4
	430044	AA464510	Hs.152812	ESTs	2.4
	427131	AA448460	Hs.112017	GE36 gene	2.4
	409103	AF251237	Hs.112208	XAGE-1 protein	2.4
	421354	AA766485	Hs.269664	ESTs	2.4
55	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	2.4
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein	2.4
	441358	AW173212	Hs.129041	ESTs	2.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.4
	414290	AI568801	Hs.71721	ESTs	2.4
60	427342	AL110150	Hs.176680	Homo sapiens mRNA; cDNA DKFZp586D0724 (f	2.4
	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	2.4
	434638	H50758		gb:yp86e06.r1 Soares fetal liver spleen	2.4
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.4
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
65	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	458734	AI554946	Hs.158794	ESTs	2.4
	449529	AI990559	Hs.232033	ESTs	2.4
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.4
70	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.4
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.4
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.4
	418188	AW139413	Hs.151880	ESTs	2.4
	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.4
75	454324	AW608930	Hs.52184	hypothetical protein FLJ20618	2.4
	437369	AA765230	Hs.121742	ESTs	2.4
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	2.4
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.4
	400462				2.4
80	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	424195	U50536	Hs.142907	Human BRCA2 region, mRNA sequence CG011	2.4
	434163	AW974720	Hs.25206	group XII secreted phospholipase A2	2.4

	435985	AA703154	Hs.191934	ESTs	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	458661	AI299789	Hs.166999	ESTs, Moderately similar to I38344 titin	2.4
	459023	AW968226	Hs.60798	ESTs	2.4
5	406005				2.4
	456561	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypotheti	2.4
	452161	R43077	Hs.221747	ESTs	2.4
	436590	AI393115	Hs.127655	ESTs	2.4
	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo	2.4
10	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	433479	AW511459	Hs.249972	ESTs	2.4
	441676	BE564206	Hs.49889	ESTs	2.4
	407965	W21483	Hs.41707	heat shock 27kD protein 3	2.4
	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
15	452958	AA883929	Hs.40527	ESTs	2.4
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	2.4
	405347				2.4
	440577	AA889945	Hs.326381	EST	2.4
	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
20	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
	437511	AI807500	Hs.125247	ESTs	2.4
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.4
	425146	AW954627		gb:EST366697 MAGE resequences, MAGC Homo	2.4
25	428277	AA425220	Hs.179203	ESTs	2.4
	444870	AI200621	Hs.148504	ESTs	2.4
	402090				2.4
	458507	AI185703	Hs.206957	ESTs	2.4
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.4
30	446534	AI307356	Hs.175225	ESTs	2.4
	453111	AB014598	Hs.31720	hephaestin	2.4
	405230				2.4
	405935				2.4
	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
35	420724	AA279694	Hs.191540	ESTs	2.4
	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.3
	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRN	2.3
40	440621	AW296024	Hs.150434	ESTs	2.3
	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	2.3
	424131	AA335714	Hs.199665	ESTs	2.3
	450737	AW007152	Hs.203330	ESTs	2.3
	453687	T55674	Hs.283108	hemoglobin, gamma G	2.3
45	442704	AI015463	Hs.130987	ESTs	2.3
	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.3
	412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo	2.3
	418998	F13215	Hs.287849	ESTs, Weakly similar to T22074 hypotheti	2.3
	419751	AW195581	Hs.93121	KIAA0761 protein	2.3
50	429485	AW197086	Hs.99338	ESTs	2.3
	433377	AI752713	Hs.43845	ESTs	2.3
	434896	AW022054	Hs.136591	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	444711	AI188739	Hs.148488	ESTs	2.3
55	445621	AI733818	Hs.145549	ESTs	2.3
	449182	AW292381	Hs.224150	ESTs	2.3
	430987	Y08564	Hs.248190	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.3
	404068				2.3
	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.3
60	438315	R56795	Hs.82419	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	447998	AI768289	Hs.304389	ESTs	2.3
	410150	AW382942	Hs.6774	ESTs	2.3
	432792	AA448114	Hs.278950	protocadherin beta 1	2.3
65	443363	AI792629	Hs.133293	ESTs	2.3
	440729	AA904739	Hs.128204	ESTs	2.3
	411045	AW854691	Hs.115325	RAB7, member RAS oncogene family-like 1	2.3
	459207	AW138410	Hs.45051	ESTs	2.3
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.3
70	458684	BE281115	Hs.98855	hypothetical protein FLJ20909	2.3
	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.3
	401899				2.3
	432116	AA902953	Hs.308538	ESTs	2.3
	404196				2.3
75	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	413308	W28131		gb:42f7 Human retina cDNA randomly prime	2.3
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	2.3
	443482	AW188093	Hs.250385	ESTs	2.3
	453305	R39224	Hs.267997	EHM2 gene	2.3
80	451963	AI825440	Hs.224952	ESTs	2.3
	453043	AW136440	Hs.224277	ESTs	2.3
	435559	AF209198	Hs.42636	zinc finger protein 277	2.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	2.3

	434120	AI436050	Hs.143937	ESTs	2.3
	429768	AA805719	Hs.192154	ESTs	2.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.3
	455841	BE145836		gb:MR0-HT0208-101299-202-b08 HT0208 Homo	2.3
5	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
	430706	NM_003540	Hs.247816	H4 histone family, member C	2.3
	428268	AA424957	Hs.294132	ESTs	2.3
	458833	AW236702	Hs.171431	ESTs, Weakly similar to A46010 X-linked	2.3
	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	2.3
10	444109	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.3
	428411	AW291464	Hs.10338	ESTs	2.3
	433098	AW190593	Hs.151143	ESTs	2.3
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.3
	453178	AA496086	Hs.61648	ESTs	2.3
15	404569				2.3
	413841	M34276	Hs.75576	plasminogen	2.3
	424068	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	2.3
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	2.3
	442710	AI015631	Hs.23210	ESTs	2.3
20	444206	AW301017	Hs.146492	ESTs	2.3
	451264	AI768235		gb:wg82g08.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	429080	AA446228	Hs.99057	ESTs	2.3
	404166				2.3
25	416327	R99822	Hs.36172	ESTs	2.3
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.3
	438504	AW665281	Hs.224625	ESTs	2.3
	435325	AI038388	Hs.119309	ESTs	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
30	427046	BE246180	Hs.121385	ESTs	2.3
	432711	AA563785	Hs.152465	ESTs, Weakly similar to I38022 hypotheti	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
	448458	AW614367	Hs.171054	ESTs	2.3
35	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	2.3
	417768	R24732	Hs.175139	ESTs	2.3
	427374	AI150033	Hs.143686	ESTs	2.3
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.3
	423600	AI633559	Hs.310359	ESTs	2.3
40	413006	W03857	Hs.34298	ESTs	2.3
	434698	BE044674		gb:hm46f02.x1 NCI_CGAP_RDF1 Homo sapiens	2.3
	407639	AW205369	Hs.312830	ESTs	2.3
	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
	448117	H49129	Hs.172982	ESTs	2.3
45	443931	H23213	Hs.22657	ESTs	2.3
	450795	AW173371	Hs.50435	ESTs	2.3
	418632	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.3
	419441	AW023731	Hs.274368	MSTP032 protein	2.3
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	2.3
50	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.3
	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.3
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
	449272	AW137656	Hs.197645	ESTs	2.3
55	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	2.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.3
	444715	AV650947	Hs.282464	ESTs	2.3
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	2.3
	444140	AV648089	Hs.282383	ESTs	2.3
60	423949	AI014546	Hs.130912	ESTs	2.3
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	445711	T79611	Hs.193691	ESTs	2.3
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	2.3
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.3
65	429180	AA806287	Hs.58893	ESTs	2.3
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.3
	425523	AB007948	Hs.158244	KIAA0479 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419337	AW291112	Hs.209978	ESTs	2.3
70	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	436294	AA708310		gb:zg07b07.s1 Soares_pineal_gland_N3HPG	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	433939	AL133887	Hs.254122	hypothetical protein	2.3
75	450048	AI693269	Hs.202273	ESTs	2.3
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	2.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	2.3
	405920				2.3
	405747				2.3
80	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.3
	420457	AA482280	Hs.191656	ESTs	2.3
	407726	AA435679	Hs.88594	ESTs	2.3
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.3

	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	435352	AI056599	Hs.120893	ESTs	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
5	449276	AW241510	Hs.252713	ESTs	2.3
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.3
	449015	AL038958	Hs.22868	protein tyrosine phosphatase, non-recept	2.3
	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	2.3
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.3
10	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.3
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
15	445117	AI208754	Hs.147369	ESTs	2.3
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.2
	420230	AL034344	Hs.284186	forkhead box C1	2.2
	411517	AW850267		gb:IL3-CT0219-161199-031-A09 CT0219 Homo	2.2
	403678				2.2
20	457003	S78234	Hs.172405	cell division cycle 27	2.2
	404531	Z25884	Hs.121483	chloride channel 1 , skeletal muscle (Th	2.2
	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	2.2
	409427	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.2
	434745	AW974445	Hs.185155	ESTs, Weakly similar to T12482 hypotheti	2.2
25	400696				2.2
	407259	L02256		gb:Human Fab fragment binding syncytial	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
30	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	458303	AI264628	Hs.125428	ESTs	2.2
	405692				2.2
	403572				2.2
	415380	F07953	Hs.16085	putative G-protein coupled receptor	2.2
35	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.2
	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.2
	456472	AK001714	Hs.95744	hypothetical protein similar to ankyrin	2.2
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.2
	428231	U17989	Hs.183105	nuclear autoantigen	2.2
40	454086	AW885909	Hs.6975	PRO1073 protein	2.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.2
	416348	H65887	Hs.272163	ESTs	2.2
	403780				2.2
	414262	AW975616	Hs.291469	ESTs	2.2
45	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
	416588	H66558		gb:yu16e04.r1 Soares fetal liver spleen	2.2
50	425368	AB014595	Hs.155976	cullin 4B	2.2
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.2
	441638	AW293202	Hs.133451	ESTs	2.2
	446845	AI343645	Hs.156108	ESTs	2.2
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	2.2
55	436574	AW293527	Hs.126465	ESTs	2.2
	424584	H10692	Hs.13310	ESTs	2.2
	456347	U00803	Hs.89426	fyn-related kinase	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
	459364	W69284		gb:zd46c03.r1 Soares_fetal_heart_NbHH19W	2.2
60	430686	NM_001942	Hs.2633	desmoglein 1	2.2
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	2.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.2
	403525				2.2
	453343	AA905353	Hs.121622	ESTs	2.2
65	421574	AJ000152	Hs.105924	defensin, beta 2	2.2
	449327	AI638743	Hs.224672	ESTs	2.2
	454769	AW819848		gb:QV0-ST0294-070300-151-b04 ST0294 Homo	2.2
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	2.2
	401614				2.2
70	404767				2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	436193	AA706059	Hs.255286	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
75	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
	441453	AW176106	Hs.285459	ESTs	2.2
	424946	M64572	Hs.153932	protein tyrosine phosphatase, non-recept	2.2
	437332	AA814943		gb:oc07d06.s1 NCI_CGAP_GCB1 Homo sapiens	2.2
	454419	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	2.2
80	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	2.2
	450579	AW136774	Hs.48614	ESTs	2.2
	400664				2.2
	447613	AL041057	Hs.33363	DKFZP434N093 protein	2.2

	402689	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	2.2
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.2
	432797	AA565264	Hs.136443	ESTs	2.2
	405608				2.2
5	426365	AA376667	Hs.10283	RNA binding motif protein 8B	2.2
	405634				2.2
	423646	H02364		gb:yj35d06.r1 Soares placenta Nb2HP Homo	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
10	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
	433781	AA609379	Hs.192083	ESTs	2.2
15	450587	AI828854	Hs.258538	striatin, calmodulin-binding protein	2.2
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	2.2
	448756	AI739241	Hs.171480	ESTs	2.2
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.2
	454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.2
20	419107	AW085152	Hs.292987	ESTs	2.2
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.2
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	2.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.2
	456056	AA463550	Hs.337532	ESTs, Weakly similar to A47582 B-cell gr	2.2
25	409998	M78345	Hs.98265	KIAA1877 protein	2.2
	422352	AA766296	Hs.99200	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspin	2.2
	433919	AA746311		gb:oa56d12.r1 NCI_CGAP_GCB1 Homo sapiens	2.2
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	2.2
30	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	2.2
	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.2
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	2.2
	458037	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	2.2
	434239	AF119910	Hs.283047	hypothetical protein PRO2964	2.2
35	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	2.2
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.2
	400697				2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
	447039	AV661798	Hs.282915	ESTs	2.2
40	404593				2.2
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.2
	421976	AL138443	Hs.23450	mitochondrial ribosomal protein S25	2.2
	401673				2.2
	425001	U55184	Hs.154145	hypothetical protein FLJ11585	2.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	2.2
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	2.2
	419118	AA234223	Hs.139204	ESTs	2.2
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
50	454749	AW818649		gb:RC1-ST0278-040400-018-e02 ST0278 Homo	2.2
	456933	AA363946	Hs.20969	ESTs	2.2
	402942				2.2
	437064	AI023264		gb:ov64h08.s1 Soares_testis_NHT Homo sap	2.2
	458623	AI305223	Hs.148056	ESTs	2.2
55	415257	F03016	Hs.27513	ESTs	2.2
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	2.2
	442783	AI017586	Hs.131181	ESTs	2.2
	444313	AI140494	Hs.197955	KIAA0704 protein	2.2
	453444	AL036531		gb:DKFZp564I1162_r1 564 (synonym: hfbr2)	2.2
60	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
	430013	AA463833	Hs.151275	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.2
	437138	AI935622	Hs.271245	ESTs	2.2
	406298				2.2
	409723	AW885757	Hs.257862	ESTs	2.2
65	414481	AW451956	Hs.8383	bromodomain adjacent to zinc finger doma	2.2
	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
	445061	AI253094	Hs.145227	ESTs	2.2
70	442617	AW340093	Hs.130538	ESTs	2.2
	438298	H23542	Hs.181788	ESTs	2.2
	454916	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	2.2
	428017	AA424983	Hs.98312	ESTs	2.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	2.2
75	418076	R61388	Hs.6724	ESTs	2.2
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmi	2.2
	441811	AI073548	Hs.164597	ESTs	2.2
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	2.2
	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.2
80	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.2
	415424	Z44766		gb:HSC28G081 normalized infant brain cDN	2.2
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	2.2
	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	2.2

	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.2
	448700	BE614182	Hs.123075	ESTs	2.2
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.2
	437927	AI039789	Hs.25982	hypothetical protein FLJ21031	2.2
5	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	436640	AA724411	Hs.156065	ESTs	2.2
	438290	AA843719	Hs.122341	ESTs	2.2
10	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	455735	BE161124		gb:PM0-HT0425-141299-001-A06 HT0425 Homo	2.2
	458455	AV648310	Hs.213488	ESTs	2.2
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.2
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	2.2
15	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	2.2
	441874	AA970389	Hs.128055	ESTs	2.2
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	433629	R13140	Hs.13359	ESTs	2.2
	415266	AA164199	Hs.270152	ESTs	2.2
20	440633	AI140686	Hs.263320	ESTs	2.2
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.2
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.2
	401240				2.2
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
	436992	AA741074	Hs.120750	ESTs	2.2
	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
30	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.1
	400040				2.1
	458762	AW802754		gb:IL2-UM0076-030400-061-H01 UM0076 Homo	2.1
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	2.1
	419953	BE267154	Hs.125752	ESTs	2.1
35	410648	AW792909		gb:CM0-UM0001-010300-258-c05 UM0001 Homo	2.1
	423717	AA330036	Hs.152003	ESTs	2.1
	436683	AW991278	Hs.57787	ESTs	2.1
	445225	AI216555	Hs.202398	ESTs	2.1
	410991	AW812790		gb:RC3-ST0186-141299-014-g08 ST0186 Homo	2.1
40	412639	AW961284	Hs.296235	ESTs	2.1
	447777	AI424223		gb:te95a05.x1 NCI_CGAP_Pr28 Homo sapiens	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	404526	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	2.1
	452492	BE063096		gb:CM4-BT0266-091199-039-a02 BT0266 Homo	2.1
45	417154	AI674701	Hs.21388	ESTs	2.1
	428152	AA422030		gb:zv26h05.r1 Soares_NhHMPu_S1 Homo sapi	2.1
	442312	AI820617	Hs.129216	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	456513	AA279143	Hs.88561	ESTs	2.1
	430712	AW044647	Hs.196284	ESTs	2.1
50	441445	AI221959	Hs.187937	ESTs	2.1
	420288	AW071225	Hs.245556	ESTs	2.1
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.1
	447033	AI357412	Hs.157601	ESTs	2.1
	436853	BE328074	Hs.148661	ESTs	2.1
55	455189	AW864176		gb:PM0-SN0014-260400-002-b08 SN0014 Homo	2.1
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	2.1
	458356	AI024855	Hs.131575	ESTs	2.1
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.1
	424480	AA341442	Hs.205299	ESTs	2.1
60	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
65	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
	417725	R25257	Hs.21503	ESTs	2.1
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.1
	439474	AI824060	Hs.211501	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
70	448582	AI538880	Hs.94812	ESTs	2.1
	452783	AA028167	Hs.61486	ESTs	2.1
	442430	R89164	Hs.48320	double ring-finger protein, Dorfin	2.1
	428908	AW303529	Hs.144955	ESTs	2.1
	427335	AA448542	Hs.251677	G antigen 7B	2.1
75	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.1
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.1
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.1
	439950	AW937417	Hs.293561	ESTs	2.1
	458227	Z40670	Hs.181340	ESTs	2.1
80	447179	AW015633	Hs.157299	ESTs	2.1
	454950	AW847460		gb:RC3-CT0208-270999-021-e04 CT0208 Homo	2.1
	404453				2.1
	420844	AA595522		gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sapiens	2.1

	426456	AA580748	Hs.130658	ESTs	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	430879	BE149423	Hs.10554	hypothetical protein FLJ12761	2.1
	444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.1
5	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	414083	AL121282	Hs.257786	ESTs	2.1
	401645				2.1
	436577	W84774	Hs.17643	ESTs	2.1
10	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.1
	409168	N94037	Hs.312938	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	410276	AI554545	Hs.68301	ESTs	2.1
	443372	AI792557	Hs.133107	ESTs	2.1
	422093	AF151852	Hs.111449	CGI-94 protein	2.1
15	402333				2.1
	409374	R87083	Hs.19081	ESTs	2.1
	412011	NM_000406	Hs.73064	gonadotropin-releasing hormone receptor	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
20	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	452374	AL037405	Hs.339639	ESTs	2.1
	450061	AI797034	Hs.201115	ESTs	2.1
	450180	AW449644	Hs.257182	ESTs	2.1
25	405120				2.1
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.1
	458890	AW865523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.1
	435600	AL047034	Hs.119747	ESTs	2.1
	440964	AI733106	Hs.130218	ESTs	2.1
30	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.1
	436461	AW511956	Hs.293261	ESTs	2.1
	436777	AA731199	Hs.293130	ESTs	2.1
	427521	AW973352	Hs.290585	ESTs	2.1
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.1
35	413231	D87461	Hs.75244	BCL2-like 2	2.1
	423969	AI830571	Hs.331633	hypothetical protein DKFZp566N034	2.1
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.1
	443777	AV646510	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	2.1
	416148	H22453	Hs.169187	ESTs	2.1
40	402528				2.1
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	446209	AI375025	Hs.153368	ESTs	2.1
	453362	H14988	Hs.107375	ESTs	2.1
45	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.1
	401069				2.1
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.1
	410966	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo	2.1
	447124	AW976438	Hs.17428	RBP1-like protein	2.1
50	449939	T86420	Hs.272139	ESTs	2.1
	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.1
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	2.1
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	2.1
55	404694				2.1
	406668	T62745	Hs.184411	albumin	2.1
	441092	T99289	Hs.126556	EST	2.1
	454643	BE006345		gb:RC2-BN0127-240300-011-d05 BN0127 Homo	2.1
	426646	AA382787	Hs.122713	ESTs	2.1
60	431605	AW972407		gb:EST384498 MAGE resequences, MAGL Homo	2.1
	414452	AA454038	Hs.29032	ESTs	2.1
	401991				2.1
	457176	AA436837		gb:zv57g07.s1 Soares_testis_NHT Homo sap	2.1
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
65	428208	AA442327	Hs.104854	ESTs	2.1
	445049	AV652718		gb:AV652718 GLC Homo sapiens cDNA clone	2.1
	419116	AF292402	Hs.283093	neuromedin U receptor 2	2.1
	427894	AL135709	Hs.28921	zinc finger protein	2.1
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.1
70	424323	AA338791	Hs.177788	ESTs	2.1
	404582				2.1
	418631	AA225921	Hs.115105	ESTs	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	452539	AW105321	Hs.49367	ESTs	2.1
75	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	440310	AA878939	Hs.125406	ESTs	2.1
	433297	AV658581	Hs.282633	ESTs	2.1
	410900	AW810169		gb:MR4-ST0124-040500-007-h07 ST0124 Homo	2.1
	419386	AA236867	Hs.143868	ESTs, Weakly similar to I38022 hypotheti	2.1
80	402451				2.1
	447842	AW160804	Hs.247302	twisted gastrulation	2.1
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	2.1
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1NIB H	2.1

	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.1
	400612				2.1
	402318				2.1
	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	2.1
5	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	412029	AW886238		gb:RC5-OT0078-280300-022-F01 OT0078 Homo	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	444498	AI151413	Hs.26330	ESTs	2.1
10	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	2.1
	425324	M89470	Hs.155644	paired box gene 2	2.1
	430719	AA488988	Hs.293796	ESTs	2.1
	432577	BE208545	Hs.317590	hypothetical protein FLJ14640	2.1
	407593	AW044083	Hs.237008	ESTs	2.1
15	401098				2.1
	440299	AI871778	Hs.250112	ESTs	2.1
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	2.1
	428627	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	2.1
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	2.1
20	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	2.1
	439831	AW136488	Hs.25545	ESTs	2.1
	451829	AW964081	Hs.247377	ESTs	2.1
	404595				2.1
	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
25	456083	U46922	Hs.77252	fragile histidine triad gene	2.1
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	2.1
	406413				2.1
	439483	T69980	Hs.58323	Homo sapiens cDNA FLJ11613 fis, clone HE	2.1
	446242	N66336	Hs.7360	ESTs	2.1
30	449625	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	2.1
	457938	AI373638	Hs.133900	ESTs	2.1
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	2.1
	408350	AW183350	Hs.250127	ESTs	2.1
	419812	NM_000562	Hs.93210	complement component 8, alpha polypeptid	2.1
35	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A recepto	2.1
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.1
	409955	U60665	Hs.57692	chromosome 6 open reading frame 10	2.1
	435579	AI332373	Hs.156924	ESTs	2.1
	436088	AA704687	Hs.191294	ESTs	2.1
40	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.1
	416100	H18700	Hs.268799	ESTs	2.1
	403218	AL134878	Hs.119500	ribosomal protein, large P2	2.1
	409747	H60964	Hs.331250	ESTs	2.1
	428764	W21550		gb:zb52f12.r1 Soares_fetal_lung_NbHL19W	2.1
45	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.1
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.1
	428299	AL038004	Hs.29419	ESTs	2.1
	406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
50	412446	AI758015	Hs.92127	ESTs	2.1
	414012	AW452334	Hs.128148	ESTs	2.1
	421966	AA904519	Hs.130710	ESTs	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
	456606	AA292862	Hs.275369	ESTs	2.1
55	451604	T65365	Hs.172851	arginase, type II	2.0
	440926	AW196772	Hs.131323	ESTs	2.0
	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.0
	459082	BE551721	Hs.282149	ESTs	2.0
	413241	BE073771	Hs.302414	Homo sapiens clone FLB8945 PRO2411 mRNA,	2.0
60	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0
	447552	AI394125	Hs.160413	ESTs	2.0
	420905	AA521307	Hs.186651	ESTs	2.0
	428052	AA420477	Hs.26993	ESTs	2.0
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.0
65	432527	AW975028	Hs.102754	ESTs	2.0
	430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen	2.0
	446610	AV659433	Hs.282984	ESTs, Weakly similar to I38022 hypotheti	2.0
	427961	AW293165	Hs.143134	ESTs	2.0
	455290	U75810		gb:HSU75810 Human Homo sapiens cDNA clon	2.0
70	445564	AB028957	Hs.12896	KIAA1034 protein	2.0
	412811	H06382	Hs.21400	ESTs	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
	429418	AI381028	Hs.118769	ESTs	2.0
75	431511	NM_012386	Hs.258581	Homo sapiens p95 paxillin-kinase linker	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	453123	AI953718	Hs.221849	ESTs	2.0
	455401	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	2.0
80	406666	V00495	Hs.184411	albumin	2.0
	445688	AI248205	Hs.153244	ESTs	2.0
	446131	NM_000929	Hs.290	phospholipase A2, group V	2.0
	440388	AI693520	Hs.223000	ESTs	2.0

	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.0
	404416				2.0
	444187	AW138466	Hs.151274	ESTs	2.0
	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	2.0
5	455814	BE141689		gb:CM1-HT0092-220999-016-b09 HT0092 Homo	2.0
	454759	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	2.0
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.0
	404420				2.0
	408112	AW451982	Hs.248613	ESTs	2.0
10	432702	AW973953	Hs.293744	ESTs	2.0
	448587	AI539652	Hs.28338	KIAA1546 protein	2.0
	446854	BE268103	Hs.208914	hypothetical protein MGC10999	2.0
	410569	AA766825	Hs.205675	ESTs	2.0
	432596	AJ224741	Hs.278461	matrilin 3	2.0
15	402341				2.0
	452919	AW962167		gb:EST374240 MAGE resequences, MAGG Homo	2.0
	433632	AA649921	Hs.112553	ESTs	2.0
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.0
	451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	2.0
20	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.0
	450895	N66727	Hs.10957	ESTs	2.0
	408459	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypotheti	2.0
	400842				2.0
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.0
25	400859				2.0
	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN !	2.0
30	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
35	454578	AW809178		gb:MR4-ST0118-261099-012-c07 ST0118 Homo	2.0
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0
	415173	AW501735	Hs.253015	ESTs	2.0
	449011	AI655376	Hs.192693	ESTs	2.0
40	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.0
	416057	AI927382	Hs.29857	ESTs	2.0
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.0
	408531	AW207553	Hs.253639	ESTs	2.0
	434663	AA641972	Hs.130058	ESTs	2.0
45	428085	AA421081	Hs.12388	ESTs	2.0
	425006	R38685	Hs.332622	ESTs	2.0
	446139	H77395	Hs.39749	ESTs	2.0
	400049				2.0
	428333	AW972668	Hs.293044	ESTs	2.0
50	429458	BE161832	Hs.292689	ESTs	2.0
	425087	R62424	Hs.126059	ESTs	2.0
	457122	AI026157	Hs.33728	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	400310	X63966	Hs.135631	H.sapiens synthetic gene for platelet-de	2.0
	451805	AI968300	Hs.208220	ESTs	2.0
55	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
60	429110	L29301	Hs.2353	opioid receptor, mu 1	2.0
	433755	AW085934	Hs.120868	ESTs	2.0
	434118	AF116715	Hs.256256	Homo sapiens PRO2829 mRNA, complete cds	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
	443748	AW206447		gb:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su	2.0
65	445205	D83776	Hs.12413	KIAA0191 protein	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
	446419	AW576760	Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE	2.0
	441627	AA947552	Hs.58086	ESTs	2.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.0
70	455614	AI693369	Hs.202274	ESTs	2.0
	449899	AI610700	Hs.103280	ESTs	2.0
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	2.0
	437354	AA749215	Hs.291886	ESTs	2.0
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.0
75	419691	W03298	Hs.193521	ESTs	2.0
	439724	AF086565	Hs.60351	EST	2.0
	413362	BE088812		gb:CM2-BT0693-230300-129-d08 BT0693 Homo	2.0
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	2.0
	434361	AF129755	Hs.117772	ESTs	2.0
80	442479	AF069484		gb:AF069484 Homo sapiens astrocytoma IIb	2.0
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	2.0
	459323	AW062490		gb:MR0-CT0065-100899-001-d01 CT0065 Homo	2.0
	449438	AA927317	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	2.0

	400285				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
	417383	W02642	Hs.136102	KIAA0853 protein	2.0
5	447153	AA805202	Hs.315562	ESTs	2.0
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
	456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
	449815	AI671000	Hs.199739	ESTs	2.0
10	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.0
	400238				2.0
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.0
	445073	AW291389	Hs.13056	hypothetical protein FLJ13920	2.0
	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.0
15	413174	AA723564	Hs.191343	ESTs	2.0
	435810	BE349853	Hs.2785	keratin 17	2.0
	418687	R61650	Hs.22581	ESTs	2.0
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.0
	431750	AA514986	Hs.283705	ESTs	2.0
20	453242	T98327	Hs.18343	ESTs	2.0
	437074	AI286235	Hs.128905	hypothetical protein FLJ13204	2.0
	459411	N52920		gb:yv34h09.s1 Soares fetal liver spleen	2.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.0
	409929	R38772	Hs.172619	myelin transcription factor 1-like	2.0
25	406378				2.0
	459208	BE261314	Hs.149039	ESTs, Weakly similar to I38022 hypotheti	2.0
	445260	AI218133	Hs.147617	ESTs	2.0
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.0
	445020	AI205655	Hs.147221	ESTs	2.0
30	402048				2.0
	412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	2.0
	416408	R94725	Hs.35354	ESTs	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	427836	AA416642	Hs.116176	ESTs	2.0
35	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	436902	AW247145	Hs.192729	ESTs	2.0
	440122	AI733011	Hs.127678	ESTs	2.0
	442901	AI023654	Hs.114191	ESTs	2.0
	444097	AW517412	Hs.150757	ESTs	2.0
40	447278	AI934935	Hs.158669	ESTs	2.0
	451361	AA053854		gb:zf52f02.r1 Soares retina N2b4HR Homo	2.0
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.0
	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0
	458801	N98648	Hs.276860	ESTs, Weakly similar to C Chain C, Human	2.0

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TABLE 30B

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Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
407593	1003161_1	AW044083 AW044094 AW370634
407594	1003220_1	AW057584 AW057585 AW044153 R34370
407639	1006924_1	AW205369 AW058599 AW207608
407676	1008294_1	AW064111 AW064450 AW064429
407721	10108_1	Y12735 NM_003582 AW238970 R38268 R41411 R41419 T16717 AA002193 H62028 AI359545 AW105201 AW087158 AA699728 AI095264 AA002065 H62029 AI289101 AA884804 AA904950 AA609672 AI139874 H77896
407726	101126_1	AA435679 AA470655 H22526 AA044031 AA876426 W63767 AI421140 AI418990 H42329 H88910 AL041066 H88909 W94610 AW352277 W94648 W94167 AW952568 AI419653 AA335501 AA393641 AA044353 H41626 H22525 R58582 AW297645 C75230 AW368034 AW468904 AI272755
407762	101439_1	AW235638 AA346882 AW866803 AA361281 AW963163 AA044373 AA136755
407764	1014849_1	BE008347 BE008320 BE083307 BE083311 AW075968
407788	10163_1	BE514982 BE614814 AW393078 AW238480 AA055637 N27644 AA641158 M87068 AA161019 AA161003 AA587315 AA716746 AA593632 AI354870 AW183492 Y07755 NM_005978 AW872948 AI608987 H64656 AF086003 AA643149 AI819402 H64555 AA858398 AA594885 AI436747 BE122811 AA587026 AW857106 AI950679 AA596012 AA654004 AW236238 AI971395 AA459074 AA458884 AI608591 BE181995 BE181970 AW195797 C00271 BE182043
407803	1017498_1	AW081681 N36967 N36959
407809	1017982_1	AW082279 AW082688
407811	10180_1	AW190902 AI802788 AI041650 AI037867 AF110137 NM_013372 H99469 N35377 AW151676 AI578451 AW078795 AW087935 AI884505 AW044602 AB032372 AF045800 AI621183 AI750578 AA376403 AI910477 AA373348 AA373673 AI752124 AL359060 W48619 AA373298 AA373975 AW604409 AW604404 AW368603 AA545734 AW361415 AA373557 AW956164 AW853798 AI750595 AL359059 AA344024 N31127 AW580737 N27040 AA071138 AI753050 AA599801 W48852 AA669811 AA112124 AI940705 W52686 AA084001 C01826 AI940729 AA373544 AW957491 AW383224 AW383164 AW383192 AW383125 AW383194 AW842507 AI940795 H80042 AW631119 W47324 W42884 AI750594 AI754387 AI753734 AA372833 AW069006 AI750577 AW473621 AI888605 AA600082 AI041803 W51909 W25447 AI521673 AI087351 AA670070 W47325 AA071381 W42791 AI090390 AI085102 AI302125 AA788723 AW069430 AW069485 AI754608 AA373014 BE140150 BE140166 BE140102 BE140143 BE140157 BE140117 BE140098 AW005943 BE140108 BE140176 BE140171 BE140144 BE140175 BE140160 BE140152 BE140099 BE140177 BE140167 BE140145 BE140109 BE140163 BE140172 BE140161 BE140179 BE140147 BE140107 BE140146 BE140155 BE140173 BE140148 BE140174 BE140158 BE140149 BE140116 BE140156 BE140105 BE140103 BE140164 AW138508 BE140153 AW806557 BE140121 BE140162 C01953 AW806500 BE140124 AA329219 AW955642 AW069165 AI968107 N21113 AI754594 AW069264 AI754660 BE551937 AA543066 AA703927 AW130486 AI814434 AI924946 AA789056 AW173667 AW069841 AI022286 AI753523 AI753558 AI753482 AW068940 AI753002 AA669866

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			AI753593 AI753469 AI753506 AW008360 AI753255 AI949111 AI752123 W19275 AI679005 AI888455 AI677772 AI589279 AI968546 AW069588 AI754028 N20040 AI754354 AI752878 AA836970 AW631283 AI440410 AW016646 AI801326 AI610424 AI521669 AI446171 AI453455 AI753087 AA670062 AA599863 AI753621 AI802571 AI537325 AA669978 AI921732 AI811571 AI309543 H80043 AI623845 AI623852 AI075634 AI919521 AA729459 C01795 AA577421 AA668620 AA600003 AA653400 AI445339 AW468974 AW130343 AA600104 AW970482 AW806615 BE140122
	407834	1020170_1	AW084991 R54179 N64486
	407851	10212_1	NM_014496 AF184965 H82896 H82897
	407884	1023626_1	BE075316 AW090150 AW589417 H47391 D61911 BE173252
	407938	102759_1	AA905097 AI734242 BE044545 N86431 AA344041 C03245 AW963097 AI567324 AA045934 AW079233 R58274 AI744425 AI167427 R58176 R58598 AI969945 AI921684 AW013864 AI204559 AA909648 N84115 AA897468 AI668637 BE221753 AI355307 AI139542 N80934
	407965	10298_1	W21483 U15590 NM_006308 N56314 AA126678 AA426507 Y17782 W24740 W05062 W21042 AA649552 AA093507 AA092088 AA476830 N88299 AA429090 AA095643 AI224915 AA443775 AI204315 AI333690 AA586584 AI275037 AI193915 AA659647 T82641 AA136048 T82643 T82647 F36041 N74099 AI572217 T82650 T82642 T82640 R47360 R47361 R47357 N74672 R47356 R47355 N93086 R47354 R47353 R47342 R47362 R47358 N93441 N56384 N93566 T82622 T82618
	407995	103177_1	AI094748 AW241797 AI759976 T10509 AI814441 AI421977 AI423762 N73686 T11392 AA046406
	408000	1031_1	L11690 NM_001723 M69225 H99965 AI750335 BE000199 M63618 N31521 AA112876 AW265395 AA088909 N21507 X58677 U04850 AW864903 AI830854 AW361101 AW379356 AA301170 T29232 AW965998 H26216 H44230 H44784 AA808916 AA514765 H44575 AA705179 AA586735 AW589403 H25843 AA654993 AI783826 BE087370
	408112	1039850_1	AW451982 AW157117 AW161544
	408172	1044105_1	W02488 AW167479 AW361027 AW833243
	408221	104826_1	AA912183 AA541622 AI673341 AI266109 AI335896 AI421010 AA053327 AI982962 AI372854 AI674348 AA531087 AI801016 AI372855 AI817816 N52151 D62928 AI401633 AI378549 AI378800 AI337972 D62536 AW972977 AA135826 BE222491 D62195 BE326453 AA225293 AA236461 R85586 AA625141 AA058641 AA135825 AA234644 H50784 R71863
	408235	104868_-1	AA053381
	408238	104872_1	W95901 AA053387 AA121501
	408243	1048_1	Y00787 M28130 D14283 BE439795 BE439924 AA362187 BE439515 M17017 C05929 AA381897 AA346136 AA381472 C06304 AA381670 AA381679 AA381965 T11274 AA381318 AA381601 AA381700 AA381952 AW950718 AA381992 D82198 AA381914 AV653399 AA362140 AA381592 AA381967 AA381454 M26383 AA362188 AA382057 AA381781 AA362246 AA381669 AA381395 AA381845 AA381848 AA381603 W40425 AW663238 AA381702 AA381355 AA381356 AA381653 AA362127 AA374516 AA381426 AA381767 AA362270 AA381459 AA362358 AA362160 AA304441 T27482 D83848 AA381877 AA381623 D83851 AA362133 AA381999 AA372837 AA362192 AA362196 AA381806 D82132 AA362107 AA363589 AA296403 T11316 D82218 AA381456 W56111 AA381435 W40163 T11379 W40283 D82615 AA382121 W40401 AA381699 T68485 D82618 W52968 W39356 T27467 D83813 Z11686 T10915 AW367405 AW604306 AA363550 AA363514 BE004230 AA381218 W40279 AA363545 AW377023 AA363453 AA363559 AA381833 AW850620 AA381813 AA381710 AA381584 AA381577 AA381715 AW376990 T11334 AA305271 AA363554 W52491 AW631242 AA363599 D82254 AA363540 AA363596 AW951160 BE122704 AA380965 AW850702 AW630501 AA381229 AA381228 AA381576 AA381795 AA381816 AI274317 AA360958 AA381517 AA381618 AA381891 AI310352 T11037 BE122702 AA634388 W38334 C01358 AW059870 AA371394 AW075978 AI922031 AA381189 AW468452 AI375262 AI870149 C06055 AA381309 AA381625 AA381252 AI620395 AW467642 AJ227913 AW780131 AI742278 AI564251 C75559 AW272612 AI634748 AW339521 AI079248 C75557 AI569162 C75493 AW591509 AW769268 C75524 AI469809 AI579895 C75486 AI697109 AI475413 AI355474 AI282685 AI087873 AI469815 C06100 AA568576 AW014817 C05914 AW272671 C75615 AW337841 AI380580 AW467270 AA847352 W46290 AW780211 AW440851 W45324 C06017 C75643 AI346866 W45040 C05698 C05704 AA381931 AA381177 AA382015 AI476632 AA381274 C05758 C75413 W45362 AW951601 C05910 C75382 W60423 AA095727 C75410 AW188453 AW341742 W60450 AW613454 AI469266 AI473944 BE042737 AW273112 AW467973 C05693 AW272835 W45409 C05668 AI431254 T29157 AI953422 AW510601 W45271 C75538 BE138893 AW662358 AA102526 AI457250 AW615017 AW662707 AW051250 AW470168 AI952442 AA362337 AW015490 AA362269 BE122713 C06363 C06353 AW779405 T68419 AA381217 AA362139 T11140 T11198 AA363591 AA362138 AA362357 AA362344 D56519 AA362132 AA361981 AA362159 AA362110 D83856 D82102 D83842 AW959358 AI373550 AA362225
	408281	1050256_1	BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091 AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220 AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129 AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108 AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156 AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
	408332	1052056_1	H91230 AW182672
	408334	1052079_1	AW514652 AW612492 AW182695
	408350	1052676_1	AW183350 C03487 C05115
	408408	10566_1	AF070571 H70949 AW149569 AI804276 AA936447 AA987912 N35082 N35065 N43822 N43804 H69776 T80170
	408459	1059830_1	H09701 R35799 R19028 AW196589
	408531	1064578_1	AW207553 BE221925 BE551043
	408617	1070070_1	R61736 AW242757 R53961 T33418 Z45363
	408691	1074933_1	AW250525 BE265117
	408729	107722_1	AA195764 AA167076 AW937980 AA166917 AA056984 AI206035 AW023639 AA195520 AA329676 AA678589 AI784331
	408749	1078708_1	H65489 AW876581 AW876552 AW268587
	408751	1078907_1	N91553 AW268820 AW566003 W19061
	408812	1083877_1	BE397160 AW274839
	408908	10893_2	BE296227 AF008551 Z43879 AA313688 AW409753 AA298501 AW957623 BE299015 BE093498 AA431134 N64029 AI038260 AW732512 AI917458 AA628301 AA291514 BE092461 H63889 AI126792 BE092286 H72166 H57643 AI884785 R96793 AW516673 W78726 H78488 BE011847 AI638439 AA834453 AW014897 AI004050 AA804577 AI207188 AW365050 AI689761 AA432153 AA767736 AI738674 R19158 BE503915 AA629662 BE465533 AA602467 AI859635 N58083 AI828708 AI859629 AI148444 R97724 AI652950 BE243218 AI318096 AA704673 AI318060 BE465518 AA745859 AI026750 AW409660 AI266728 AA748628 H58486 AA486497 AI750284 H79032 H54313 H78390 H63492 AW272138 AA488685 R07581 AA736853 AW594462 AI500164 AA832386 Z39943 AA598643 W80533 AA243133 AF011468 NM_003600 AA373999 H54104 AW136695 BE547389 H70678
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	409044	109648_1	AI129586 AA455078 BE536256 AA834910 AI264121 AA715165 AI675186 AA878884 AI937502 H41127 AI613527 AA136856 AI858126 AA062762 AI351420 AW195729 AI493903 W78038 BE143223 AA136950 AA193470 AA082447 AW796079 AW996023 BE065712
	409070	109839_1	AA063003 AI880645 AI880644
	409073	109851_1	AA063458 AA063018 AI444822
	409103	109_1	AF251237 AA412359 T19106 AW975988 AA948244 AI954712 AA620697 AA758618 AI631681 AA648117 BE620755 BE620196 AW386187 AA747475 AI205793 AA730288
	409105	1100052_1	AW467539 AW468376 AW467312 AW337844 AW337833 AW467317 AW467401 AW468247 AW440988 AW440830 AW467337

409156	110362_1	N76186 R69723 AW444682 BE220376 W49490 AA961099 BE218202 N53704 W73451 AI823360 AW675687 N64773 AA064629 AA064753 AA527475 AW473807 AA199658 AI090198 AI374757 AI769715 AI026060 AI801785 W49491 R72390 R63399 AI742199 AI190947 R69629 AI287331 AI769707 AI219372 D20803 AI187711 AI472100 W73390
409168	110474_1	N94037 N94055 AA064789 AW835560 T84873
409191	1107176_1	AW818390 AW818237 AW858911 AW858977 BE072544 W26498
409298	111658_1	AA070211 AA070030 AA070114 AA070198 AA070217 AA070106 AA070265 AA070334 AA070101 AA070302 AA070278 AA070231
409374	1124155_1	R87083 R01811 T81648 AW383308
409427	1129667_1	AW389668 AW389657 AW609198 AW389649
409432	11298_1	D49372 Z75668 Z92709 NM_002986 U46572 U46573 AA125790 AW294260 AA127067 AI080514 U34780 AI867933 AA910483 AI446061 AI913625 AI913629 AI537716 AI357416 W69211 AW805343 C21564
409434	112_1	AF278761 AA461577 AA460289
409446	113166_1	AI561173 AA600224 AA074612 AW382145 AL045940
409517	11370_1	X90780 C03339 C03114 W07136 C02994 C03103 C04896 C05070 W17389 C04180 C05502 W19390 C04558 C04543 AA311399 C05351 C04551 C04456 X54163 NM_000363 C02730 C05613 C05482 R57607 BE140258 M64247 C04434 AI265781 AI950215 AI634065 AI760600 AI367238 AI864649 C03467 AA992938 C05063 C03065 AI185229 AI003859 AI193201 AI355654 AA935234 AW207185 C03193 N91524 C04315 AI657074 C05024 C04608 C03333 AI193911 AW003240 AW003043 AI650950 AA092543 T12017 N90905 N90947 AI652255 AI969724 T12391 T29798 T12073 AA158797 N93687 AI369979
409545	1138823_1	BE296182 AW629821
409627	1144175_1	AW997628 AW449319 BE068930
409629	1144421_1	AW449589 BE219028 BE503053
409632	11445_1	W74001 AA316156 U04313 NM_002639 T27595 AA294992 AW951580 AW814845 BE122694 W72351 AI989728 AW362665 AW379980 AI656538 AI633911 AI656426 BE122695 W93572 BE152369 AI589723 AI435384 AW274531 AW173600 AW151556 AI559971 AA583423 AA583421 AI042520 AI041742 AI863998 AI924540 AI168755 AF086216 C00555 W93726 AI081348 AW609782 W30956 AA284290 AA662428 AI276525 AI242306 W02802 AI913973 AI913861
409642	1145579_1	AW450809 H06661 AW860936
409718	11505_1	D86640 NM_003149 AA451622 AA558394 H14661 BE262331 AI741761 AW137199 W49541 AI288524 BE220310 AI800206 AI471117 AA450217 AI370524 W49772
409723	1150962_1	AW885757 AW885748 AW885693 AW885549 AW572414 AW470595
409747	1152417_1	H60964 H57755 AW473583
409928	11601_1	AL137163 AA101422 AW367010 Z83826 BE167397 AA813575 AI280253 AI277959 R28517 R28131 AA375127 R76478 W21429 T62693 AI433432 AI401346 T62844 BE552077 AI277896 AW338135 AI435513 AA873621 AA528626 AI961880 AW338124 AA127501 AI918990 AA876737 AI365181 N92911 AI077290 C00153 AI580500
409929	1160241_1	R38772 AW510843 H16714
409955	11619_1	U60665 AL034394 AA897135 AL035445 AW665839 AI935027 AA936514 AA629287
409998	1167032_1	M78345 T07132 AW566007 R83578 T36151 H08587 Z45984 R61252 AW966442 BE180035
410085	11757_1	AA428482 AB024518 W79345 AA449389 AL080211 AA249114 W05152 AA345239 W79445 AI146674 D60585 AA046754 W07067 AA315195 AW954874 T69187 AI150705 N78517 R35444 R33255 R33248 N78928 D61726 AI636918 AI675380 D62188 AI935469 AI375549 D79309 AI610794 AI281303 T69129 AI587330 AA046641 AA479893 AI085845 AI474465 AW028856 H12424 D60584 AI016160 AI766477 N92986 AA582759 R67773
410140	117882_1	AL134435 N99191 AA081918 D81425 D60802 D81310 D52972 D52986 Z45092 H00118
410150	117913_1	AW382942 AA249770 AA249043 AL133837 N85732 AA249732 AA081961 R19529 R13631 Z43675 H11407 AA376302 T25307
410181	118146_1	AI468210 R54453 AW291931 AA814911 AA828285 AA731670 AA553734 H17613 AW780162 AW780176 AW182524 AI743107 AI635064 T32609 AW192433 AI307672 AA994018 AA082285 AI671334 AI862698 AW583237 BE219648 AI985157 AI610704 BE328117 Z38374 AI083538 AA099352 T35606 BE088282 F08855
410276	119050_1	AI554545 AA083514 AI633826 AI765524 AW169852 AI656026 AI363822
410286	11912_2	AI739159 AA040433 AL047873 AA037778 AI205645
410307	11935_1	AF022913 Y07596 R18975 AA366192 AI904896 W05406 AW130797 W38804 AW628276 AL035409 N70544 AI123406 AA330449 AW950460 AI926246 R44860 AA746741 AW612942 AI539700 N69061 AA481761 AI559559 N93182 AI245742 AA814787 AA464862
410318	119440_1	AA084050 AA084064 AA084174
410365	11974_7	AI287518 AI243745 AW196535 AW102813 AA834941 H24627 AL050199 W21139 N53879 H84695 AA424083 AI872323 AI475291 W69379 AI919258 AA557197 AI581597 N66899 AW604533 W69378 R16586 AA559860 AA559908
410481	1204955_1	R34107 AW750133 AW750120 R21663
410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
410500	1206323_1	R09442 AW846115 AW846108 AW751967 AW846083 AW846087 AW846090
410534	1207247_1	AW905138 AW753008 R13818 Z43519
410566	120846_1	AA373210 H91768 BE172318 AA371497 AA085843 AI307247 AI824005 AW261982 AI625754 N27830 AI679467 AI078259 AW594323 AI335252 AA122264 AA994930 AA111902 N21680 AI498311 AA633551 AA455980 AI625756 AA938642
410569	120893_1	AA766825 AA811180 AA085906 AI752946 AW977820
410585	1210225_1	AW770523 BE503941 BE219626
410594	1210463_1	AW770778 BE551458 BE550838 BE549582 BE328860 BE550143
410648	1213842_1	AW792909 AW876101 AW792964 AW876100 AW876099 AW792910
410685	121605_1	AA497117 AA497039 AA996105 AI042190 AI910528 AA088543 AI733733 AA732081 AI269879
410767	12201_1	AJ001873 R58869 AJ001874 AW301235 AA496916 Z41363
410797	1221640_1	AW857191 AW857192 AW804060
410811	1222814_1	AW805687 H88503 H88502
410845	1223881_1	AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283
410871	12252_1	D78367 NM_000223 AF137286 AB007119 C00499
410878	1225667_1	AW809201 AW809176 AW809258 AW809266 AW809236 AW809213 AW809243 AW809187 AW809235 AW809142 AW809186 AW809152 AW809146 AW809144 AW809141 AW809145 AW809170 AW809248 AW809149
410888	1225955_1	AW861207 AW809508
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	456303	176684_1	AA224872 AI791642 AA228308 AI821503 AA230172 AA224838
	456347	18004_1	U00803 NM_002031 AW195632 C05922
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	456443	188540_1	AW967500 AW966876 AW976565 AI417020 AI057022 AA251316 AA744820 AI806037 AW966871 AA251713 AF080576 T49825 AA281037 T49826
	456472	19126_1	AK001714 AW960785 AK001831 BE075311 AW273355 AA928445 AI698734 AW977909 AW268863 AI392846 AA811609 AI555035 AW007245 AI754385 AI092244 AA906509 AW438768 AW751668 AA459681 AA861761 AW118314 D63077 AI537049 AA782718 AW050550 AA430988 AA130556 AA383461 AA337522 AA130593
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	456555	199748_1	AW592167 AA284280 W47266 AW972765 AW069452 W47267 AI186593 AA526308 AA525432
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	457122	287827_1	AI026157 AA838752 AI146272 AA910825 AI266100 N24580 H97503 BE327388 AI697814 W56675 AA423842 AA423880 H40134

	457128	28930_1	AI932995 BE064464 AW371902 AW371841 AI885885 BE064457 AA524113 AA721037 AA504343 AA778099 AI800598 AI693112 AI864633 AI690228 AI400990 AW969089 AW371927 AW371912 AW383562 BE151089 AW383568 BE218503 AW383570 AW371899 BE151097 AW371900 AW293095 AW292008 AA434179 AA714780 R45868 W01182 AW957767 AW119223 AI207864 W01578 AA354403 AA805177 AI613299 AW269636 AA481528 AW079101 AF131777 R60489 T81289 AA481594 BE161020 AA465433 AW808125 T84992 AA749191
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	457225	30546_1	AW820035 T20260 T20259 AL049415 AA737756 W46965 W00799 AW340968 AW027417 AW263261 AI420674 AA814921 AA736509 N69991 AW368643 W47065 AI090172 AI924139 BE468071 AA375842 AA375767 AW628849 AI422731 AA494558 AA969233 AI142954 AI161089 AI167233 W94484 AI681576 AA249694 AI695943 AA832347 AA476621 AA937792 AI702870 AA455748 AW195100 AI638530 BE502479 AI383418 AA039630 C20777
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	457630	373784_1	AI680803 AI703329 AA609004 AI305245 AI457796 AW295787
	457652	37972_1	AF116656 AI114583 AW838134 AW838525 AW885447 H83251 AW836349 AW838378 AW838175 H83252
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	457900	434061_1	AW976692 AA806542 AA745856
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	458023	463717_1	AW978161 AW978165 AI016938 AI539270 AW294958 AW511089 AA814849
	458037	46627_1	AF074982 R27906 R31333 R31591 R27812
	458043	466952_1	AW979009 AA828036 AA828148
	458067	46875_2	AA393603 Z19481 AA252342 AI807614 AI913804 AA040176 AA971879 H53388 AF085972 AI291424 H53349 AW015078 AA768307 AA127921 AA723700 AA040841 AA993954 AA213655 AA127972 AA913063 BE327712 AI017585 AA988186 AA628183 AI205930 AA833558 AA974107 AI004390 H48931 AA724004
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	458356	555234_1	AI024855 AI024877
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	458552	633259_1	AW136139 AI216724
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	458624	662652_1	AI362790 AI275996 N48887
	458661	677016_1	AI299789 BE551384
	458684	68549_1	BE281115 T53860 AV659439 AV659421 BE539929
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	458762	73076_1	AW802754 BE619228
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	458771	737397_1	AW295151 AI425004 AW470228 AI693738 H50554 R99198 H50553 R99197
	458797	75398_2	AW001835 AW612725 AW136670 AI798956 BE467368 AA280216 AI216754 BE622057 AL121193 AW853470 AW853450 AW369075 AW369108 AW578479 AW369106 AW361242 AW361190 N79183
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	458861	798085_1	AI630223 AI630470
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	459082	889533_1	BE551721 H51878 AI823338 C01488 AW813562
	459124	916575_1	AW301478 AW301560 AI889207
	459207	926704_1	AW138410 AI912712 N40186
	459208	92717_1	BE261314 AI243406 AA027322
	459275	97318_1	AI808913 AW028342 W81290 AI571379 AI382808 AA037071 W79688 R48751 N31808 AI870233 R48752 AW024895 AI333754
	459278	9751_1	AW294659 AI204928 AA351653 H51220 R86843 AA993182 U79298 R15294 F05089 Z42963 R17818 T77498 AA332319 W56049 AA331586 AW881873 AW881865 AW881876 R52345 AI652070 AA400044 AA401512 T08151 W05486 N68378 T33846 AI190920 R43021 AI949980 Z39084 T63413 W37269 F01343 R86669 AI621055 AW117593 AI193211 AW297932 AI500709 AA400056

Table 30C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position

400462	9929659	Minus	197610-197785
400608	9887666	Minus	96756-97558
400612	9929646	Minus	151513-151662
400631	8247025	Minus	56203-56313,56424-56482,57073-57185,57513-57593,57747-57941
400641	8117693	Plus	4786-4992
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400696	8118812	Minus	77737-77899
400697	8118812	Minus	79073-79198
400706	7249204	Minus	78299-78686
400816	8569993	Plus	161221-162078
400842	1927148	Plus	90462-90673
400859	9757499	Minus	91888-92018,98131-98294,99474-99570
400861	9757506	Plus	163855-164016
400889	9958234	Minus	169782-170036
401069	3927852	Minus	45682-45831
401098	9965518	Minus	85632-86174
401132	8705350	Minus	85679-85795
401189	9690246	Minus	90815-90929
401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
401240	3355450	Plus	77433-77636
401324	9863791	Plus	234057-234174
401365	9796180	Minus	119572-119672
401368	8670914	Minus	65508-65662
401459	9212270	Minus	182001-183323
401462	6682291	Plus	112763-112909
401497	7381770	Plus	92607-92813
401526	7770561	Plus	91570-93177
401596	3293210	Plus	63639-63890
401614	7839924	Plus	17350-17735
401626	8575943	Minus	238100-238432
401645	7657839	Minus	34986-35133
401673	7689903	Minus	122587-122705,122765-123047
401694	3540172	Minus	64056-64168
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401878	8099802	Minus	162268-162474,163089-163195
401887	7229981	Plus	93973-94120
401899	7230209	Minus	155620-155815
401986	4406829	Minus	31137-31293
401989	4309964	Minus	118611-118821
401991	4156128	Plus	2398-2513
402048	8072512	Plus	43936-44078
402076	8117410	Plus	128316-128627
402090	7249154	Minus	104806-104939,106898-107052
402112	8139750	Plus	10507-10713
402131	7704961	Minus	33114-33209,33496-33678
402145	8018280	Plus	113086-114800
402318	7582559	Minus	12843-13403
402333	8844110	Minus	165693-165856
402341	7656696	Plus	22583-23699
402369	9558577	Minus	50417-50522
402451	9796677	Minus	48137-48343
402528	7630857	Minus	169609-169742
402603	9909396	Minus	141663-141852
402615	9926801	Plus	131390-132157
402689	8348025	Minus	5885-6209
402942	9368398	Plus	102152-102386
403011	6693597	Minus	3468-3623
403053	8746888	Plus	146568-146659,147539-147811
403089	8954241	Plus	171964-172239
403188	9838289	Minus	157618-157755
403218	7630969	Plus	58039-58149
403271	7230852	Plus	134283-134485
403281	8072630	Minus	7521-7728
403306	8099945	Plus	127100-127251
403310	8139936	Minus	183883-184026
403317	8318526	Minus	50623-50834
403329	8516120	Plus	96450-96598
403341	8569175	Plus	30699-30910
403344	8569726	Plus	70823-70990
403356	8569930	Plus	92839-93036
403513	7656757	Minus	155310-155436,158402-158535
403515	7656757	Minus	173358-179553
403525	7960440	Plus	152431-153243
403534	8076917	Minus	46652-47332
403568	8101145	Minus	85509-85658
403572	8101156	Minus	1253-1675
403574	8101156	Plus	5542-6176
403623	8569879	Minus	3519-5426
403625	8569879	Plus	6551-7111
403637	8671936	Minus	142647-142771,145531-145762
403678	7331517	Minus	119573-120430
403691	7387384	Minus	88280-88463

403776	7770611	Minus	1414-1513,1624-1756
403780	8076989	Plus	93160-93409
403786	8083636	Minus	73028-73217
403891	7331467	Minus	191508-193220
403937	7711761	Minus	12609-12773
404042	9558573	Plus	5140-5208,8633-8763
404043	9558573	Plus	29042-29135,46597-46699
404068	3168621	Minus	18123-18766
404108	8247074	Minus	63603-64942
404166	7596822	Plus	86147-86509
404193	3881948	Minus	94185-94322
404196	3805917	Minus	67928-68109
404249	8655533	Plus	64270-64633
404367	9965011	Minus	114391-114628
404404	7272262	Plus	82112-82244
404414	7382165	Plus	143127-143398
404416	7382420	Minus	143042-143216,144704-144853,145800-146048
404420	7407952	Minus	129817-130586
404443	7579073	Minus	87198-87441
404453	7657714	Plus	27768-29179
404476	8080699	Plus	101841-102043
404518	8151988	Plus	84494-84603
404526	8152087	Plus	121918-122123,125198-125348
404531	8247909	Plus	20152-20362
404561	9795980	Minus	69039-70100
404569	7249169	Minus	104257-104348,104822-104970
404582	9739220	Plus	53230-53424
404587	8698840	Minus	69781-70096
404588	6456726	Minus	40059-40210
404593	9944086	Minus	74922-75788
404595	9958262	Minus	16764-16900
404638	9796751	Minus	99433-99528,100035-100161
404652	9796969	Minus	108172-108296
404694	9799957	Minus	128092-128227
404708	9800828	Plus	77522-77658
404731	7230299	Minus	168609-168781,182951-183081
404767	7882827	Minus	23244-23759
404793	7232206	Minus	61087-61590
404822	3810614	Plus	7541-8132
404834	6911603	Minus	37948-38226
404957	7407927	Plus	147512-148011
404967	7523744	Minus	89944-90729
404988	4662677	Minus	72406-72600,72779-72856
405001	6015406	Minus	104646-104819
405008	6088019	Minus	64091-64267
405090	8072525	Minus	38552-39202
405120	8099940	Plus	140176-140340
405229	7249019	Plus	51081-51701
405230	7249032	Minus	97493-97682
405302	2078453	Minus	121688-121840
405347	2979602	Minus	977-1116
405443	7408143	Plus	90716-90887,101420-101577
405455	7656675	Plus	134112-134671
405456	7656676	Plus	150052-150208
405494	8050952	Minus	70284-70518
405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405605	5836195	Minus	117070-117270
405608	5815499	Minus	66822-66925
405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
405654	4895155	Minus	53624-53759
405692	4314424	Plus	61379-62562
405738	9943998	Plus	44370-45410
405747	8469069	Minus	153933-154060
405780	7248203	Minus	48204-48371
405783	5738434	Minus	27238-27885
405784	7417368	Minus	77798-78000
405829	7109593	Minus	15628-16127
405920	6758795	Plus	120621-120971
405935	6758795	Minus	163112-163652
405970	8247789	Minus	45795-46295
406005	8247801	Minus	39912-40220
406018	6758904	Minus	37795-38168
406076	9123123	Plus	89972-90319
406092	9123919	Plus	251370-251797,252168-252682
406190	7289992	Minus	22395-22901
406288	7549620	Plus	111718-112008
406298	5686278	Minus	30084-30770
406333	9213235	Plus	64689-64798
406364	9256114	Minus	50715-50833
406378	9256142	Minus	126408-126800
406413	9256407	Plus	43858-44003,46993-47136
406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880

406603 8272659 Minus 39506-39694

TABLE 31A: ABOUT 1884 GENES UP-REGULATED IN IPF COMPARED TO NSIP

Table 31A lists about 1884 geneswhose expression levels are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with non-specific interstitial pneumonia (NSIP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" non-specific interstitial pneumonia sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" non-specific interstitial pneumonia level was set to the 90th percentile amongst non-specific interstitial pneumonia samples.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of IPF (idiopahic pulmonary fibrosis) to NSIP (non-specific interstitial pneumonia)

Pkey	ExAccn	Unigene ID	Unigene Title	R1
450478	AW451709	Hs.271200	ESTs	20.2
405654				16.1
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
403637				11.2
431548	AI834273	Hs.9711	novel protein	10.8
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	10.4
439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
403574				10.1
416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
441233	AA972965	Hs.135568	ESTs	9.1
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	8.4
432437	W07088	Hs.293685	ESTs	8.3
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	8.2
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	8.1
403329				8.0
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
441519	AA972740	Hs.127092	ESTs	7.9
453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	7.8
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	7.7
416379	N38857	Hs.203933	ESTs	7.7
428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.5
407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	7.2
434683	AW298724	Hs.202639	ESTs	7.2
441802	AA968636	Hs.127877	ESTs	6.9
431242	AA987742	Hs.251278	KIAA1201 protein	6.9
442377	AA993807	Hs.167367	ESTs	6.9
420407	AA814732	Hs.145010	lipopolysaccaride-specific response 5-li	6.8
428908	AW303529	Hs.144955	ESTs	6.8
445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.7
457673	AA551569	Hs.272034	hypothetical protein PRO2822	6.7
458771	AW295151	Hs.163612	ESTs	6.6
426800	AA385085		gb:EST98959 Thyroid Homo sapiens cDNA 5'	6.6
440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.6
415025	AW207091	Hs.72307	ESTs	6.5
438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
416128	AA173632	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	6.4
457242	AA457011		gb:aa90c11.r1 Stratagene fetal retina 93	6.3
423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	6.3
404793				6.2
435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	6.2
415672	N53097	Hs.193579	ESTs	6.2
455488	AA102322		gb:zl90f03.r1 Stratagene colon (937204)	6.2
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	6.1
412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	6.1
431622	AW979271	Hs.293184	ESTs	6.1
405523				6.0
424693	BE169810	Hs.47557	ESTs	6.0
436397	AA715013	Hs.169835	ESTs	6.0
456476	AA256753		gb:zs22b12.r1 NCI_CGAP_GCB1 Homo sapiens	5.9
434784	AA649051	Hs.164007	ESTs	5.9
422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	5.9
442849	R10099	Hs.269805	ESTs	5.9
451519	AI800600	Hs.209573	ESTs	5.8
412474	AI791451		gb:ni50c09.y5 NCI_CGAP_Ov2 Homo sapiens	5.8
457081	AA916785	Hs.180610	splicing factor proline/glutamine rich (	5.8
444827	R09764	Hs.20416	ESTs	5.8
404822				5.7
402430				5.7
457900	AW976692	Hs.291665	ESTs	5.7
400292	AA250737	Hs.72472	ESTs	5.7
410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
440172	AA868584	Hs.126154	ESTs	5.7

	431374	BE258532	Hs.251871	CTP synthase	5.7
	409816	AW500954		gb:UI-HF-BP0p-air-h-12-0-UI.r1 NIH_MGC_5	5.6
	447613	AL041057	Hs.33363	DKFZP434N093 protein	5.6
	417919	AI928203	Hs.86379	ESTs	5.6
5	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.6
	439063	AF085922	Hs.113968	ESTs	5.6
	406053				5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
10	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.5
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	5.5
	459458	AW270957	Hs.254577	ESTs, Weakly similar to B34087 hypotheti	5.5
	416154	Z46122		gb:HSC0VB031 normalized infant brain cDN	5.5
	404561				5.4
15	428895	AA437124	Hs.187247	ESTs	5.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	5.4
	440925	AW511090	Hs.130419	ESTs	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
20	448477	BE612572		gb:601452090F1 NIH_MGC_66 Homo sapiens c	5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	459664				5.3
	401497				5.3
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.3
25	444931	AV652066	Hs.75113	general transcription factor IIIA	5.3
	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (fr	5.3
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.2
	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	404957				5.2
30	436445	AA922213	Hs.121735	ESTs	5.2
	442617	AW340093	Hs.130538	ESTs	5.2
	416045	H15990	Hs.31403	ESTs	5.2
	425178	H16097	Hs.161027	ESTs	5.2
	441918	AI733373	Hs.128119	ESTs	5.2
35	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.2
	420929	AI694143	Hs.296251	programmed cell death 4	5.2
	448644	AI581519	Hs.177164	ESTs	5.2
	430686	NM_001942	Hs.2633	desmoglein 1	5.2
	405229				5.1
40	417641	AA205015	Hs.54617	hypothetical protein FLJ20060	5.1
	434167	AA626334	Hs.116153	ESTs	5.1
	450438	AI696071	Hs.253800	ESTs	5.1
	456394	W28506		gb:48f1 Human retina cDNA randomly prime	5.0
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
45	417420	T85150	Hs.268814	ESTs	5.0
	409545	BE296182	Hs.19002	hypothetical protein MGC4675	5.0
	426750	AA383950		gb:EST97403 Thymus II Homo sapiens cDNA	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	408959	AW890878	Hs.211610	CUG triplet repeat, RNA-binding protein	4.9
50	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	452046	AB018345	Hs.27657	KIAA0802 protein	4.9
	407415	AF073328		gb:Homo sapiens tetracyline transporter-	4.9
	450090	AW448940	Hs.202259	ESTs	4.9
55	406333				4.9
	434188	AI765848	Hs.281680	peroxisomal trans 2-enoyl CoA reductase;	4.8
	403344				4.8
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	4.8
	405455				4.8
60	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	4.8
	426097	BE327369	Hs.112238	ESTs	4.8
	427768	T78402	Hs.174880	ESTs	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415257	F03016	Hs.27513	ESTs	4.8
65	441107	AA917075	Hs.190520	ESTs	4.8
	419519	AI198719	Hs.176376	ESTs	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
	424188	AW954552	Hs.142634	zinc finger protein	4.8
70	456987	AI557290	Hs.173536	ESTs	4.8
	405303				4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	451620	AW449888	Hs.257224	ESTs	4.7
	421948	L42583	Hs.334309	keratin 6A	4.7
75	424780	U39576	Hs.153056	butyrophilin, subfamily 1, member A1	4.7
	443271	BE568568	Hs.195704	ESTs	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	402230				4.7
	422246	AA461032	Hs.5306	hypothetical protein DKFZp586F1122 simil	4.7
80	431508	NM_012481	Hs.182979	ribosomal protein L12	4.7
	415236	R41400		gb:yf94b12.s1 Soares infant brain 1NIB H	4.7
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	4.6
	444774	AW052174	Hs.196030	ESTs	4.6

	444414	AW293214	Hs.8752	transmembrane protein 4	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	436853	BE328074	Hs.148661	ESTs	4.6
	445334	AI610081	Hs.9475	glucose transporter protein 10	4.6
5	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	404638				4.6
	447617	AI400762	Hs.176675	ESTs	4.6
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	4.6
10	442360	AI374621	Hs.29055	ESTs	4.6
	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
	444157	AI125785	Hs.153351	ESTs	4.5
	401365				4.5
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF I [	4.5
15	436269	AA707472	Hs.190760	ESTs	4.5
	459448	AA416773	Hs.275012	EST	4.5
	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	4.5
	414899	AW975433	Hs.36288	ESTs	4.5
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	4.5
20	444898	AI201548	Hs.308338	ESTs	4.5
	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	405605				4.5
	457982	AW856093	Hs.183617	ESTs	4.5
25	427731	AA411750	Hs.20943	ESTs	4.4
	420691	AA829433	Hs.275343	ESTs	4.4
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
30	435747	AI079519	Hs.134398	ESTs	4.4
	453824	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	4.4
	458865	T05095	Hs.19597	KIAA1694 protein	4.4
	459037	AW439497	Hs.290656	EST	4.4
	403310				4.4
35	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
	427500	AW970017	Hs.293948	ESTs, Weakly similar to S65657 alpha-1C-	4.4
	432020	AJ251509	Hs.272345	phosphodiesterase 11A	4.4
	453043	AW136440	Hs.224277	ESTs	4.4
	456293	AW131715	Hs.311561	ESTs, Weakly similar to CYA7_HUMAN ADENY	4.4
40	447879	BE503405	Hs.170437	ESTs, Weakly similar to PRP4_HUMAN SALIV	4.4
	426646	AA382787	Hs.122713	ESTs	4.4
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	4.4
	404898				4.4
	435434	AA680387	Hs.187850	ESTs	4.4
45	443314	AW771701	Hs.54646	ESTs	4.3
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.3
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	4.3
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	4.3
	404767				4.3
50	445189	AI936450	Hs.147482	ESTs	4.3
	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	428740	AA433838		gb:zw53e12.r1 Soares_total_fetus_Nb2HF8_	4.3
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	4.3
	410615	AW772721		gb:hl95c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.3
55	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.3
	406073				4.3
	405692				4.3
	436033	H75391	Hs.255748	ESTs	4.3
	410733	D84284	Hs.66052	CD38 antigen (p45)	4.3
60	455587	BE007829		gb:QV0-BN0147-280400-213-d03 BN0147 Homo	4.3
	459084	H01699	Hs.27289	CGI-125 protein	4.3
	401189				4.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heregulin	4.3
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.3
65	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	436659	AI217900	Hs.144464	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	4.3
70	439481	AF086294	Hs.125844	ESTs	4.3
	405287				4.3
	405784				4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	437636	AA764781	Hs.291844	ESTs	4.2
75	409629	AW449589	Hs.279724	ESTs	4.2
	412999	BE046255		gb:hn38g10.x2 NCI_CGAP_RDF2 Homo sapiens	4.2
	403281				4.2
	427531	AA405097	Hs.97957	ESTs	4.2
	451882	AI821324	Hs.100445	ESTs	4.2
80	418856	AA362858		gb:EST72900 Ovary II Homo sapiens cDNA 5	4.2
	405494				4.2
	456027	BE327387	Hs.13913	KIAA1577 protein	4.2
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	4.2

	421106	AA877124	Hs.172844	ESTs	4.2
	409076	N57559	Hs.82273	hypothetical protein	4.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	4.2
	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	4.1
5	416614	T83391	Hs.111849	ESTs	4.1
	454434	AA083558	Hs.261286	ESTs	4.1
	404526	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	405302				4.1
10	432669	AL043482	Hs.267115	ESTs	4.1
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	430484	D82880	Hs.241548	RAS p21 protein activator 2	4.1
15	403895				4.1
	420457	AA482280	Hs.191656	ESTs	4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	458421	AI279978	Hs.22547	ESTs	4.1
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.1
20	411382	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	4.1
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	4.1
	430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral relat	4.1
	403625				4.1
	401887				4.1
25	403667				4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	432792	AA448114	Hs.278950	protocadherin beta 1	4.0
30	405443				4.0
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	4.0
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens	4.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.0
	448324	AI571356	Hs.34174	ESTs, Moderately similar to ALU8_HUMAN A	4.0
35	456536	AW135986	Hs.257859	ESTs	4.0
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
	449327	AI638743	Hs.224672	ESTs	4.0
40	426062	N57014	Hs.75874	pregnancy-associated plasma protein A	4.0
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.0
	434849	AW292765	Hs.8053	ESTs	4.0
	400268				4.0
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	4.0
45	445414	AV653692	Hs.146105	ESTs	4.0
	406470				3.9
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (	3.9
	453098	Z25935	Hs.86379	ESTs	3.9
	402867				3.9
50	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
55	426076	AW962714		gb:EST374787 MAGE resequences, MAGG Homo	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3.9
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogen	3.9
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.9
60	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	455993	BE179085		gb:RC0-HT0613-140300-021-d06 HT0613 Homo	3.9
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
65	403956	W28077	Hs.79389	nel (chicken)-like 2	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.9
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	3.9
	430140	AW296771	Hs.221999	ESTs	3.8
	457042	AI382130	Hs.97703	ESTs	3.8
70	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	413071	BE064032		gb:QV3-BT0296-010300-111-b08 BT0296 Homo	3.8
	437354	AA749215	Hs.291886	ESTs	3.8
75	403381				3.8
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	3.8
	430757	AI458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	3.8
80	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	433887	AW204232	Hs.279522	ESTs	3.8
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.8
	404043				3.8

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	431333	AA708488	Hs.120127	Homo sapiens cDNA: FLJ22769 fis, clone K	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
	417663	R07483	Hs.180461	ESTs	3.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
5	436975	AA740723	Hs.212644	ESTs	3.8
	405959				3.8
	400631	AF173937	Hs.109494	secreted protein of unknown function	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
	446158	AI277603	Hs.145990	ESTs, Weakly similar to I38022 hypotheti	3.7
10	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.7
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.7
	436020	AA778177	Hs.121724	ESTs	3.7
	424989	AA985520	Hs.23575	ESTs	3.7
	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.7
15	441416	AI990139	Hs.148609	ESTs	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	3.7
	404453				3.7
	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
20	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
	453530	AW021633		gb:df26c02.y1 Morton Fetal Cochlea Homo	3.7
	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
25	432291	AK001108	Hs.274274	hypothetical protein FLJ10246	3.7
	449623	C00719	Hs.120440	EST	3.7
	419691	W03298	Hs.193521	ESTs	3.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.7
	403271				3.7
30	453123	AI953718	Hs.221849	ESTs	3.7
	400462				3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	443305	AI050693	Hs.133318	ESTs	3.7
	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.6
35	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	3.6
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	3.6
	403296				3.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.6
	436026	AI349764	Hs.217081	ESTs	3.6
40	429864	AA460039	Hs.286	ribosomal protein L4	3.6
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	3.6
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.6
	446304	AW104432	Hs.149761	ESTs	3.6
	441216	BE299830	Hs.192908	ESTs	3.6
45	421494	AI763322	Hs.152104	ESTs	3.6
	404476				3.6
	416327	R99822	Hs.36172	ESTs	3.6
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.6
	417401	AA426026	Hs.187615	ESTs	3.6
50	401200				3.6
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.6
	426306	AA447310	Hs.164059	Homo sapiens cDNA FLJ13338 fis, clone OV	3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	447917	AL048037	Hs.164588	ESTs, Moderately similar to neuronal thr	3.6
55	421328	BE466506	Hs.3981	ESTs	3.6
	447290	AI476732	Hs.263912	ESTs	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	403515				3.6
60	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (fr	3.6
	435554	AF208502	Hs.185708	early B-cell factor	3.6
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	3.6
	410500	R09442		gb:yf26c09.r1 Soares fetal liver spleen	3.6
	439326	W07140	Hs.54721	ESTs	3.6
65	426296	R14454	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.6
	411311	AW836491		gb:PM3-LT0032-281299-002-f02 LT0032 Homo	3.6
	418019	R68911	Hs.176275	ESTs	3.6
	417490	AA203335		gb:zx56g02.r1 Soares_fetal_liver_spleen_	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
70	416575	W02414	Hs.38383	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	450350	T97817	Hs.174880	ESTs	3.5
	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
75	421013	M62397	Hs.1345	mutated in colorectal cancers	3.5
	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRN	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	430533	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	3.5
	457141	AA521410	Hs.41371	ESTs	3.5
80	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	3.5
	440737	AI375167	Hs.132221	hypothetical protein FLJ12401	3.5
	452728	AI915676	Hs.239708	ESTs	3.5
	423266	AA323875	Hs.193574	ESTs	3.5

	413543	AA130228	Hs.324611	ESTs, Moderately similar to ALU8_HUMAN A	3.5
	454447	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
5	415549	F11942		gb:HSC33F061 normalized infant brain cDN	3.5
	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	3.5
	418717	AI334430	Hs.86984	ESTs	3.5
10	400641				3.5
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	3.5
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
	458340	AI457102	Hs.6986	Human glucose transporter pseudogene	3.5
15	412281	AI810054	Hs.14119	ESTs	3.5
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	3.5
	416616	H68270		gb:yr81h09.r1 Soares fetal liver spleen	3.5
	444338	AI937026	Hs.146642	ESTs	3.4
	436946	AW137748	Hs.125956	ESTs	3.4
20	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	3.4
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmi	3.4
	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
25	405970				3.4
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.4
	416100	H18700	Hs.268799	ESTs	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
30	440388	AI693520	Hs.223000	ESTs	3.4
	421072	AI215069	Hs.89113	ESTs	3.4
	424578	AK001973	Hs.150890	hypothetical protein	3.4
	436331	AI239495	Hs.120189	ESTs	3.4
	444063	AI122614		gb:qa96b05.x1 Soares_fetal_heart_NbHH19W	3.4
35	444453	AW379394	Hs.145126	ESTs	3.4
	404196				3.4
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	3.4
	409555	AW410788	Hs.256185	ESTs	3.4
	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	3.4
40	416057	AI927382	Hs.29857	ESTs	3.4
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	3.4
	447738	AI871000	Hs.161330	ESTs	3.4
	430664	AW969834	Hs.303303	ESTs	3.4
	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	3.4
45	415769	H94186	Hs.5912	F-box only protein 7	3.4
	429382	AI791249	Hs.278054	ESTs, Weakly similar to I38022 hypotheti	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	456908	AI953671	Hs.220994	hypothetical protein FLJ14129	3.4
	442826	AI018777	Hs.131241	ESTs	3.4
50	400608				3.4
	436111	AI803082	Hs.157212	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	436577	W84774	Hs.17643	ESTs	3.4
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
55	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.4
	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	3.4
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.4
	409623	AW449185		gb:UI-H-BI3-akg-e-05-0-UI.s1 NCI_CGAP_Su	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
60	420854	AW296927		gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCI_CGAP_Su	3.4
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	432404	AA535246	Hs.50852	ESTs	3.4
	458695	AV660159	Hs.282284	ESTs, Weakly similar to I38022 hypotheti	3.4
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	3.3
65	428766	AA477989	Hs.98800	ESTs	3.3
	439567	AI056618	Hs.134314	ESTs	3.3
	456231	H73183	Hs.129885	ESTs, Weakly similar to 2004399A chromos	3.3
	454318	AW367764	Hs.7857	erythrocyte membrane protein band 4.1-li	3.3
	411966	AA099113	Hs.118609	ESTs	3.3
70	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	3.3
	437037	T63804		gb:yc21e09.r1 Stratagene lung (937210) H	3.3
	407664	AW063476	Hs.279080	ESTs	3.3
	405780				3.3
	426567	AA381579	Hs.182962	ESTs	3.3
75	400432	AX015609	Hs.287767	Sequence 8 from Patent WO9950285	3.3
	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	429875	AI091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	3.3
80	433785	BE044593	Hs.112704	ESTs	3.3
	437876	AA770151	Hs.126424	ESTs	3.3
	444870	AI200621	Hs.148504	ESTs	3.3
	453324	W26592	Hs.232089	ESTs	3.3

	437963	BE396279		gb:601309785F1 NIH_MGC_44 Homo sapiens c	3.3
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	3.3
	408813	AI580090	Hs.48295	RNA helicase family	3.3
	426692	AK001751	Hs.171835	hypothetical protein FLJ10889	3.3
5	407456	AJ237569		gb:Homo sapiens mRNA for T-box transcrip	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
	453242	T98327	Hs.18343	ESTs	3.3
10	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.3
	412040	D86519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	3.3
	435070	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	3.3
	444443	AI149286	Hs.55099	rab6 GTPase activating protein (GAP and	3.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	3.3
15	454145	AA046872	Hs.62798	ESTs	3.3
	405264				3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	416816	T71168	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	3.3
	435325	AI038388	Hs.119309	ESTs	3.3
20	440164	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.65407	ESTs	3.3
	429106	AA446612		gb:zw85g07.s1 Soares_total_fetus_Nb2HF8_	3.3
	405720				3.3
25	400889				3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	422094	AF129535	Hs.272027	F-box only protein 5	3.3
	425374	AI904013		gb:MR-BT041-220199-104 BT041 Homo sapien	3.3
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
30	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	457604	AI004397	Hs.334552	Homo sapiens cDNA FLJ14930 fis, clone PL	3.3
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.3
35	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	3.3
	458885	AA411303	Hs.30022	ESTs, Weakly similar to NAH6_HUMAN SODIU	3.3
	429608	U49250	Hs.210862	T-box, brain, 1	3.2
	437454	AL390159	Hs.269812	Homo sapiens mRNA; cDNA DKFZp761M0415 (f	3.2
	430503	AA533574	Hs.152274	ESTs	3.2
40	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	3.2
	421698	T89677	Hs.324323	ESTs	3.2
	412321	AW936913		gb:RC1-DT0029-030200-012-f08 DT0029 Homo	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
45	441705	AI087052	Hs.55993	ESTs	3.2
	403619				3.2
	435608	AW183971	Hs.250896	ESTs	3.2
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.2
	401132				3.2
50	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (Ik	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.2
	419936	AI792788		gb:ol91d05.y5 NCI_CGAP_Kid5 Homo sapiens	3.2
55	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	406592				3.2
	446530	AV658909	Hs.282642	ESTs	3.2
	454466	AA984138	Hs.155101	ATP synthase, H+ transporting, mitochond	3.2
	401449				3.2
60	431196	AW974436	Hs.154929	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	3.2
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.2
	427335	AA448542	Hs.251677	G antigen 7B	3.2
65	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	3.2
	425156	AA351364		gb:EST59099 Infant brain Homo sapiens cD	3.2
	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens	3.2
70	426660	NM_002719	Hs.171734	protein phosphatase 2, regulatory subuni	3.2
	438315	R56795	Hs.82419	ESTs	3.2
	425523	AB007948	Hs.158244	KIAA0479 protein	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	425636	AK001243	Hs.158370	hypothetical protein FLJ10381	3.2
75	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	447375	AI376660	Hs.257822	ESTs	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
80	410536	N39533		gb:yv27d04.s1 Soares fetal liver spleen	3.2
	448495	AW136516	Hs.208515	ESTs	3.2
	405634				3.2
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoisoadenylate	3.2

421581	U89331	Hs.105932	short stature homeobox	3.1
440633	AI140686	Hs.263320	ESTs	3.1
453264	AA034137	Hs.271955	ESTs	3.1
411656	AW855576		gb:CM4-CT0278-221099-027-d01 CT0278 Homo	3.1
419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	3.1
426591	AA431127	Hs.98685	ESTs	3.1
446966	C01448	Hs.300511	ESTs	3.1
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.1
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.1
423657	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	3.1
400816				3.1
410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
400315	U46120	Hs.193392	Human expressed unknown mRNA	3.1
411965	BE467339	Hs.280115	ESTs	3.1
416316	H58721	Hs.271628	ESTs	3.1
400613				3.1
414819	BE177320	Hs.156148	hypothetical protein FLJ13231	3.1
434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.1
418693	AI750878	Hs.87409	thrombospondin 1	3.1
416258	N45661	Hs.90011	adenylosuccinate synthase	3.1
405093				3.1
415273	Z39840	Hs.22229	ESTs	3.1
450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
422654	AA314316	Hs.163725	ESTs	3.1
414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	3.1
400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.1
402790				3.1
438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	3.1
447524	D80449	Hs.45177	ESTs	3.1
448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
415979	H16427	Hs.271501	ESTs, Weakly similar to I54374 gene NF2	3.1
434479	AI138213	Hs.162035	olfactory receptor, family 52, subfamily	3.1
426724	AA383623	Hs.293616	ESTs	3.1
418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	3.1
405608				3.1
406506				3.1
421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	3.1
452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	3.1
404288				3.1
429878	AA460188	Hs.127263	ESTs	3.1
439834	AI754576	Hs.124523	ESTs	3.1
454564	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo	3.1
450491	BE045604	Hs.202301	ESTs	3.1
409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.1
400579				3.1
402953				3.1
404285				3.1
426890	AA393167	Hs.41294	ESTs	3.1
457770	BE065030	Hs.124179	ESTs	3.1
435477	BE218708	Hs.117270	hypothetical protein FLJ14345	3.1
436391	AJ227892	Hs.146274	ESTs	3.1
456083	U46922	Hs.77252	fragile histidine triad gene	3.1
416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.1
430101	AF110002	Hs.233363	guanylate cyclase activator 1C	3.1
449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
452605	AW968557	Hs.90012	hypothetical protein FLJ23441	3.1
456323	AW752389	Hs.87296	Homo sapiens cDNA FLJ20269 fis, clone HE	3.1
429828	AB019494	Hs.225767	IDN3 protein	3.1
423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	3.1
452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	3.1
401344				3.1
455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	3.1
455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	3.1
433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.1
423600	AI633559	Hs.310359	ESTs	3.1
427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	3.0
407257	AB006834		gb:Homo sapiens mRNA for HRV Fab N6-VH,	3.0
457041	AA399018	Hs.250835	ESTs	3.0
421482	AL135462	Hs.104715	inversin	3.0
459062	AA059246	Hs.110293	ESTs	3.0
436475	R58806	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.0
417489	AW953341	Hs.22573	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	3.0
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	3.0
443741	AW451759	Hs.145420	ESTs	3.0
405090				3.0
432267	AK000672	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
445409	AI949081	Hs.147862	ESTs	3.0

	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.0
	406364				3.0
	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	3.0
5	427050	AA397789	Hs.161803	ESTs	3.0
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	3.0
	448405	AW207634	Hs.170649	ESTs	3.0
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.0
	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
10	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	3.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.0
	426424	BE081745	Hs.272188	Homo sapiens cDNA FLJ12090 fis, clone HE	3.0
	419505	AA243660	Hs.143061	ESTs	3.0
	403743				3.0
15	415452	F09134	Hs.12839	ESTs	3.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	400227				3.0
20	436219	AK001695	Hs.146589	hypothetical protein FLJ10701	3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.0
	403513				3.0
25	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.0
	440122	AI733011	Hs.127678	ESTs	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.0
	446130	AW271635	Hs.170717	ESTs	3.0
30	420288	AW071225	Hs.245556	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	3.0
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	404513				3.0
35	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	3.0
	407762	AW235638	Hs.29475	ESTs	3.0
	403396				3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	3.0
40	400706				2.9
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.9
	444600	R41398	Hs.6996	ESTs	2.9
	403786				2.9
	430187	AI799909	Hs.158989	ESTs	2.9
45	451700	AI470262	Hs.29553	ESTs	2.9
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.9
	457503	AW970244	Hs.162188	ESTs	2.9
	446251	AW867156	Hs.282589	ESTs, Weakly similar to I38022 hypotheti	2.9
	406327				2.9
50	434671	R34758		gb:yg61g02.r1 Soares infant brain 1NIB H	2.9
	430175	AA468724		gb:ne09a06.s1 NCI_CGAP_Co3 Homo sapiens	2.9
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	2.9
	449459	BE546846	Hs.195048	ESTs	2.9
	435934	R19362	Hs.117869	ESTs	2.9
55	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	414514	BE327365	Hs.280187	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
60	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.9
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	2.9
	456186	W26642		gb:34b8 Human retina cDNA randomly prime	2.9
	412222	AA528283	Hs.292737	ESTs	2.9
	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
65	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.9
	435579	AI332373	Hs.156924	ESTs	2.9
	417027	AA192306	Hs.23926	triadin	2.9
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.9
	445909	BE262656	Hs.32603	hypothetical protein MGC3279 similar to	2.9
70	418343	AA216372	Hs.159501	ESTs	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	403341				2.9
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	453830	AA534296	Hs.20953	ESTs	2.9
75	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
	407676	AW064111	Hs.279823	ESTs	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	457049	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	2.9
80	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441874	AA970389	Hs.128055	ESTs	2.9
	416483	H58311	Hs.165077	ESTs	2.9

	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
	446447	AI300402	Hs.202250	ESTs	2.9
	439953	AA918129	Hs.124638	ESTs	2.9
	400643				2.9
5	436594	AI419982	Hs.156189	ESTs	2.9
	438402	D16902	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.9
	451353	N21043	Hs.42932	ESTs	2.9
	419791	AI579909	Hs.105104	ESTs	2.9
	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
10	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.9
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.9
	457178	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	2.9
	401526				2.9
15	408751	N91553	Hs.258343	ESTs	2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
20	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	421847	NM_014717	Hs.108884	KIAA0390 gene product	2.8
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.8
	422225	BE245652	Hs.118281	zinc finger protein 266	2.8
	403011				2.8
25	405170				2.8
	435878	R08330	Hs.20152	ESTs	2.8
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	2.8
	400394	AF040257	Hs.283818	Homo sapiens TNF receptor homolog mRNA,	2.8
	411244	AW833768		gb:QV4-TT0008-130100-077-e06 TT0008 Homo	2.8
30	441817	AW969706	Hs.293332	ESTs	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.8
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.8
	402131				2.8
35	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.8
	438160	AA779332	Hs.122671	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	417877	AI025829	Hs.86320	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
40	451257	AA016255	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.8
	437113	AA744693		gb:ny26c10.s1 NCI_CGAP_GCB1 Homo sapiens	2.8
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
45	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.8
	417827	T79366	Hs.106258	actin binding protein; macrophin (microf	2.8
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glu	2.8
	449676	AW380579	Hs.209657	ESTs	2.8
	454778	AW820199		gb:QV2-ST0296-190100-029-a07 ST0296 Homo	2.8
50	451203	AW070604	Hs.46517	ESTs	2.8
	450180	AW449644	Hs.257182	ESTs	2.8
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.8
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	450003	AA777809	Hs.191995	ESTs	2.8
55	401602				2.8
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.8
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.8
	415652	T79213	Hs.272073	ESTs	2.8
	404076				2.8
60	409416	AW388359	Hs.10667	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
	426960	AA393713		gb:zl71h04.r1 Soares_testis_NHT Homo sap	2.8
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.8
	448597	BE613250	Hs.98265	KIAA1877 protein	2.8
65	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	2.8
	433077	AA314262	Hs.301917	YDD19 protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	447410	AI470235	Hs.172698	EST	2.8
	414652	AI620599	Hs.72068	ESTs	2.8
70	430454	AW469011	Hs.105635	ESTs	2.8
	412417	AA102268	Hs.158622	ESTs	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
	401098				2.8
75	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	2.8
	403549				2.8
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
80	446677	AI800311	Hs.156291	ESTs	2.8
	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.8
	450895	N66727	Hs.10957	ESTs	2.8
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.8

	449358	AA001229	Hs.131436	ESTs	2.8
	422816	AA323586	Hs.93235	ESTs	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
5	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypotheti	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	458023	AW978161	Hs.268555	5'-3' exoribonuclease 2	2.8
	422260	AA315993	Hs.105484	regenerating gene type IV	2.8
10	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	411762	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
15	406992	S82472		gb:beta -pol=DNA polymerase beta {exon a	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
	445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
20	445017	AI205493	Hs.176860	ESTs	2.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	2.7
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
25	427134	AA398409	Hs.173561	EST	2.7
	435689	AA694284		gb:zi35c02.s1 Soares_fetal_liver_spleen_	2.7
	429282	N27596	Hs.21342	ESTs	2.7
	435731	AA699581	Hs.186811	ESTs	2.7
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
30	421274	BE160327	Hs.104572	ESTs	2.7
	403776				2.7
	409526	BE298751	Hs.55014	hypothetical protein FLJ10206	2.7
	410201	AA126129		gb:zm78c07.r1 Stratagene neuroepithelium	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
35	447884	H29505		gb:ym60d10.r1 Soares infant brain 1NIB H	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.7
	434890	AF161345	Hs.283930	Homo sapiens HSPC082 mRNA, partial cds	2.7
40	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	2.7
	413998	AW103807	Hs.243933	ESTs	2.7
	403677				2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	2.7
45	432591	AA643238	Hs.146144	ESTs	2.7
	446800	AI341635	Hs.156486	ESTs	2.7
	454938	AW846134		gb:QV0-CT0179-091199-049-d02 CT0179 Homo	2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
	445233	AV653034	Hs.297559	ESTs	2.7
50	448756	AI739241	Hs.171480	ESTs	2.7
	418379	AA218940	Hs.137516	fidgetin-like 1	2.7
	435068	H16262	Hs.31415	ESTs	2.7
	406092				2.7
	422036	AA302647	Hs.271891	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.7
55	441541	AA938663	Hs.199828	ESTs	2.7
	451395	AI082419	Hs.114761	ESTs	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7
	423949	AI014546	Hs.130912	ESTs	2.7
60	435420	AI928513	Hs.59203	ESTs	2.7
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	2.7
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.7
	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.7
	454767	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	2.7
65	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	2.7
	402429				2.7
	403760				2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
	435448	H17132	Hs.27085	ESTs	2.7
70	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	2.7
	422171	U50529	Hs.112434	Novel human gene mapping to chomosome 13	2.7
	459023	AW968226	Hs.60798	ESTs	2.7
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypotheti	2.7
	404569				2.7
75	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	449880	AI673006	Hs.231948	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
80	415268	R53935	Hs.287827	ESTs, Highly similar to MDR3_HUMAN MULTI	2.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	2.7
	452512	AW363486	Hs.337635	ESTs	2.7
	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	2.7

	419481	AI879195	Hs.90606	15 kDa selenoprotein	2.7
	454352	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.7
	422831	R02504	Hs.332943	ESTs	2.7
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.7
5	426872	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapie	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.7
	446002	AI346468	Hs.145789	ESTs	2.7
	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.7
10	406664	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	2.7
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	2.7
	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	2.7
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	2.7
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	2.7
15	445225	AI216555	Hs.202398	ESTs	2.7
	427175	H06924	Hs.23782	hypothetical protein FLJ12847	2.7
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.7
	438135	AI253025	Hs.190426	ESTs	2.7
	405981				2.7
20	406005				2.7
	430762	AI343652	Hs.105667	ESTs	2.7
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.7
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.7
	434684	AA737282	Hs.190911	ESTs	2.7
25	445660	AI702668	Hs.201955	ESTs	2.7
	400844				2.6
	415725	BE219771	Hs.237146	hypothetical protein FLJ12752	2.6
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
30	430052	AF102850	Hs.227933	Alg5, S. cerevisiae, homolog of	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	417252	AA195014	Hs.85971	ESTs	2.6
	427167	AI239607	Hs.99196	hypothetical protein MGC11324	2.6
35	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.6
	442240	AI791883	Hs.292719	ESTs	2.6
40	452821	AW471181	Hs.160874	ESTs	2.6
	410238	N94320	Hs.144225	ESTs	2.6
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.6
	440801	AA906366	Hs.190535	ESTs	2.6
	440274	R24595	Hs.7122	scrapie responsive protein 1	2.6
45	411597	AW852925		gb:PM0-CT0248-131099-001-f10 CT0248 Homo	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	425176	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcr	2.6
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	2.6
50	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	426098	NM_014906	Hs.166351	KIAA1072 protein	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
	445550	AI242754	Hs.137306	ESTs	2.6
55	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.6
	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.6
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	2.6
	418282	AA215535	Hs.98133	ESTs	2.6
60	442757	AI739528	Hs.28345	ESTs	2.6
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Ho	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	441209	AA922939	Hs.135742	ESTs	2.6
	458679	AW975460	Hs.143563	ESTs	2.6
65	442279	AW867006	Hs.159970	ESTs	2.6
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.6
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	2.6
	404845				2.6
	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.6
70	438298	H23542	Hs.181788	ESTs	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	457630	AI680803	Hs.112627	ESTs	2.6
	424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	2.6
75	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.6
	413174	AA723564	Hs.191343	ESTs	2.6
	438875	AA827640	Hs.189059	ESTs	2.6
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	2.6
	423257	AW161039	Hs.125878	synapsin III	2.6
80	431086	AI829692	Hs.211561	ESTs	2.6
	409337	H71289	Hs.220535	ESTs	2.6
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	2.6
	410004	AI298027	Hs.5057	carboxypeptidase D	2.6

	455935	BE158687		gb:CM0-HT0395-280100-169-b09 HT0395 Homo	2.6
	403273				2.6
	445955	AA332209	Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	2.6
	425626	AI537536	Hs.173519	ESTs	2.6
5	451531	AA018311	Hs.114762	ESTs	2.6
	428085	AA421081	Hs.12388	ESTs	2.6
	429761	AI276780	Hs.135173	ESTs	2.6
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	2.6
	442666	W74633	Hs.303720	ESTs	2.6
10	413088	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	419107	AW085152	Hs.292987	ESTs	2.6
	435766	R11673	Hs.186498	ESTs	2.6
	452879	AW905328	Hs.180842	ribosomal protein L13	2.6
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.6
15	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	424146	AA705092	Hs.202368	ESTs	2.6
	439950	AW937417	Hs.293561	ESTs	2.6
	410366	AI267589	Hs.302689	hypothetical protein	2.6
	417485	AA203304	Hs.32826	CGI-130 protein	2.6
20	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	2.6
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	2.6
	440397	AA884448	Hs.157239	ESTs	2.6
	451236	AI767406	Hs.207026	ESTs, Weakly similar to B56205 transcrip	2.6
	411819	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.6
25	430357	AW976789	Hs.165607	ESTs	2.6
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	2.6
	427506	AK000134	Hs.179100	hypothetical protein FLJ20127	2.6
	401614				2.6
	404531	Z25884	Hs.121483	chloride channel 1 , skeletal muscle (Th	2.6
30	426698	AA394104	Hs.97489	ESTs	2.6
	440479	AA886461	Hs.208161	ESTs	2.6
	443160	AI467915	Hs.36053	ESTs	2.6
	419323	AI092379	Hs.135275	ESTs	2.5
	442813	AI018435	Hs.270970	ESTs	2.5
35	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.5
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	2.5
	434059	AA649162	Hs.236456	ESTs	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	458589	AV654623	Hs.288141	hypothetical protein MGC3156	2.5
40	459716				2.5
	436340	R42246	Hs.21606	ESTs	2.5
	428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	2.5
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.5
	401078				2.5
45	410644	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.5
	411660	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	425201	AA352111		gb:EST60061 Activated T-cells XX Homo sa	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	439096	AA830185	Hs.269680	ESTs	2.5
50	442627	AI027990	Hs.132303	ESTs	2.5
	457799	AF220188	Hs.236510	uncharacterized hypothalamus protein HTM	2.5
	428799	AI478619	Hs.104677	ESTs	2.5
	450402	BE218027	Hs.89969	ESTs	2.5
	411156	AW819939	Hs.273629	ESTs	2.5
55	431673	AW971302	Hs.293233	ESTs	2.5
	415706	BE182587	Hs.57485	ESTs	2.5
	412882	BE006919	Hs.134106	ESTs	2.5
	441300	R35063	Hs.181536	ESTs	2.5
	413257	BE075035		gb:PM3-BT0584-260300-002-g05 BT0584 Homo	2.5
60	434662	AA641957		gb:ns18d08.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
	455255	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.5
	417137	U46265	Hs.81281	mitochondrial ribosomal protein S21	2.5
	417909	R35614		gb:yg66e08.r1 Soares infant brain 1NIB H	2.5
	458043	AW979009	Hs.326108	ESTs	2.5
65	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	2.5
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	2.5
	455756	BE079307		gb:RC1-BT0623-120200-011-g09 BT0623 Homo	2.5
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	2.5
	444963	AI916973	Hs.213603	ESTs	2.5
70	443526	AW792804	Hs.134002	ESTs	2.5
	454532	AA344685	Hs.58831	regulator of Fas-induced apoptosis	2.5
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	2.5
	442003	AW297497	Hs.201891	ESTs	2.5
	452768	AW069459	Hs.61539	ESTs	2.5
75	411355	AW838479	Hs.22692	ESTs	2.5
	458890	AW865523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.5
	400074				2.5
	405241				2.5
	413096	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	2.5
80	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	422884	AW860975	Hs.13256	ESTs	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	431925	AK000890		gb:Homo sapiens cDNA FLJ10028 fis, clone	2.5

	442653	BE269247		gb:601185486F1 NIH_MGC_8 Homo sapiens cD	2.5
	401882				2.5
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.5
	405336				2.5
5	439492	AF086310	Hs.103159	ESTs	2.5
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.5
	436359	Z83806		gb:H.sapiens mRNA for axonemal dynein he	2.5
	429322	D86984	Hs.199243	KIAA0231 protein	2.5
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
10	437107	AA745598	Hs.291840	ESTs, Weakly similar to I78885 serine/th	2.5
	441953	H11695	Hs.322901	disrupter of silencing 10	2.5
	442777	AW341541	Hs.271153	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
15	457824	R84938		gb:yt65f04.r1 Soares retina N2b4HR Homo	2.5
	428550	AW297880	Hs.98661	ESTs	2.5
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.5
	456359	AI967991	Hs.93574	homeo box D3	2.5
	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.5
20	452528	AA742457	Hs.291479	ESTs	2.5
	408444	AW661839	Hs.253204	ESTs	2.5
	440327	R12581	Hs.191146	ESTs	2.5
	410406	AI969703	Hs.1466	glycerol kinase	2.5
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.5
25	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	2.5
	435427	AA682573	Hs.188982	ESTs, Weakly similar to organic anion tr	2.5
	427791	AA412446	Hs.98138	ESTs	2.5
	403509	AF231919	Hs.18759	KIAA0539 gene product	2.5
	436590	AI393115	Hs.127655	ESTs	2.5
30	455556	AW995423		gb:QV0-BN0042-010400-183-g08 BN0042 Homo	2.5
	405869				2.5
	408274	R17315		gb:yg12g11.r1 Soares infant brain 1NIB H	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
35	436154	AA764950	Hs.119898	ESTs	2.5
	406377				2.5
	437030	AA742577	Hs.303781	EST	2.5
	420815	AA280684	Hs.270584	ESTs	2.5
	418421	R58620	Hs.85050	phospholamban	2.5
40	423638	AI003521	Hs.130310	Homo sapiens mRNA for cyclin B3 isoform	2.5
	415425	F08365		gb:HSCZSA121 normalized infant brain cDN	2.5
	404577				2.5
	403568				2.5
	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.5
45	449899	AI610700	Hs.103280	ESTs	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
	453343	AA905353	Hs.121622	ESTs	2.5
	428726	NM_016625	Hs.191381	hypothetical protein	2.5
	409642	AW450809	Hs.257347	ESTs	2.5
50	426235	AI631964	Hs.34447	ESTs	2.5
	452043	H66231		gb:yt03f02.r1 Soares retina N2b5HR Homo	2.5
	401992				2.5
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.5
	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
55	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:tt49a12.x1 NCI_CGAP_GC6 Homo sapiens	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.4
60	421583	AA293333		gb:zt53c09.r1 Soares ovary tumor NbHOT H	2.4
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.4
	454437	AI248173	Hs.191460	hypothetical protein MGC12936	2.4
	419187	AA234852	Hs.44693	ESTs	2.4
	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	2.4
65	405547				2.4
	454086	AW885909	Hs.6975	PRO1073 protein	2.4
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	2.4
	416277	W78765	Hs.180145	HSPC030 protein	2.4
	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.4
70	406468				2.4
	408617	R61736	Hs.124128	ESTs	2.4
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
75	455328	AW896438		gb:PM1-NN0047-040400-001-d09 NN0047 Homo	2.4
	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	2.4
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.4
	419511	AA429750	Hs.75113	general transcription factor IIIA	2.4
	437980	R50393	Hs.278436	KIAA1474 protein	2.4
80	439999	AA115811	Hs.6838	ras homolog gene family, member E	2.4
	403501				2.4
	446845	AI343645	Hs.156108	ESTs	2.4
	401775				2.4

	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411836	AW901879	Hs.314453	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
5	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	428945	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse t	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	2.4
10	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.4
	458239	BE439877	Hs.283389	ESTs	2.4
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	2.4
	441262	AI809130	Hs.176906	ESTs	2.4
	402076				2.4
15	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.4
	400587				2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	411203	AW872430	Hs.273743	ESTs	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
20	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	424131	AA335714	Hs.199665	ESTs	2.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	2.4
	440385	AA884283	Hs.192136	ESTs	2.4
	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.4
25	447179	AW015633	Hs.157299	ESTs	2.4
	412977	AA125910	Hs.191461	ESTs	2.4
	436958	AA740322	Hs.293539	Homo sapiens mRNA for KIAA1758 protein,	2.4
	401361				2.4
	403891				2.4
30	408419	AW250092	Hs.305953	zinc finger protein 83 (HPF1)	2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	458570	AW971698	Hs.12627	TJ6 protein	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
35	459344	AW499533	Hs.257976	ESTs	2.4
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.4
	412114	AW893891	Hs.240833	ESTs, Weakly similar to I38022 hypotheti	2.4
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	2.4
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	2.4
40	428268	AA424957	Hs.294132	ESTs	2.4
	450947	AI745400	Hs.204662	ESTs	2.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.4
	438142	T90309	Hs.269651	ESTs	2.4
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	2.4
45	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	401645				2.4
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.4
50	453393	AW956392	Hs.110376	ESTs	2.4
	436054	AI076262	Hs.119813	ESTs	2.4
	425433	AA357471		gb:EST66274 LNCAP cells I Homo sapiens c	2.4
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	420639	AI683116	Hs.25328	ESTs, Moderately similar to ALU7_HUMAN A	2.4
55	453369	BE551550	Hs.232630	ESTs	2.4
	405017				2.4
	405385				2.4
	435633	AI248152	Hs.270047	ESTs	2.4
	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
60	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	2.4
	434544	C05875	Hs.91575	ESTs	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	455219	AW879403		gb:PM0-OT0019-150300-002-d01 OT0019 Homo	2.4
	458734	AI554946	Hs.158794	ESTs	2.4
65	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	2.4
	444313	AI140494	Hs.197955	KIAA0704 protein	2.4
	440448	AA885428	Hs.125646	ESTs	2.4
	441498	AI379248	Hs.58742	ESTs	2.4
	438205	AA780365	Hs.122161	ESTs	2.4
70	402615				2.4
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.4
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
75	449007	AI620433	Hs.193201	EST, Weakly similar to NIP2_HUMAN BCL2/A	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	2.4
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	2.4
	458914	BE327696	Hs.280922	ESTs	2.4
80	435061	AI651474	Hs.163944	ESTs	2.4
	416458	AA180511		gb:zp53f03.r1 Stratagene NT2 neuronal pr	2.4
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	2.4

	403003				2.4
	405347				2.4
	406091				2.4
	428402	AW237531	Hs.326876	Homo sapiens SOX6 mRNA, complete cds	2.4
5	438762	AW844412	Hs.65450	reticulon 4	2.4
	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
	443921	AI091310	Hs.134848	ESTs	2.4
10	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	2.4
	417154	AI674701	Hs.21388	ESTs	2.4
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068	2.4
	405230				2.4
	405935				2.4
15	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	419233	AA458873	Hs.178306	ESTs	2.3
	414277	BE269910		gb:601186291F1 NIH_MGC_8 Homo sapiens cD	2.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.3
20	453736	AL118674	Hs.34871	zinc finger homeobox 1B	2.3
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.3
	434239	AF119910	Hs.283047	hypothetical protein PRO2964	2.3
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi	2.3
	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.3
25	445688	AI248205	Hs.153244	ESTs	2.3
	451656	BE327088	Hs.212752	ESTs	2.3
	423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,	2.3
	413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo	2.3
	436149	AI754308	Hs.159452	ESTs	2.3
30	405629				2.3
	432702	AW973953	Hs.293744	ESTs	2.3
	433377	AI752713	Hs.43845	ESTs	2.3
	444711	AI188739	Hs.148488	ESTs	2.3
	445621	AI733818	Hs.145549	ESTs	2.3
35	456432	AW966931	Hs.179662	nucleosome assembly protein 1-like 1	2.3
	449236	AJ403126	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H	2.3
	459024	AA020799	Hs.262869	plasminogen-like	2.3
	441037	AA913360	Hs.126468	ESTs	2.3
	431577	T34523	Hs.302040	Homo sapiens DNA sequence from PAC 434O1	2.3
40	438782	AA828380	Hs.126733	ESTs	2.3
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	429044	AI261490	Hs.145527	ESTs	2.3
	431655	AW971119		gb:EST383206 MAGE resequences, MAGL Homo	2.3
45	439642	W81441	Hs.153967	ESTs	2.3
	441721	AI288259	Hs.127652	ESTs	2.3
	443482	AW188093	Hs.250385	ESTs	2.3
	403416	AI744626	Hs.151385	KIAA0564 protein	2.3
	416443	N69469	Hs.194225	ESTs	2.3
50	419714	AA758751	Hs.98216	ESTs	2.3
	415511	AI732617	Hs.182362	ESTs	2.3
	412344	AW938364	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.3
	449264	AI637649	Hs.196105	ESTs	2.3
	451664	AA889081	Hs.153952	5' nucleotidase (CD73)	2.3
55	441269	AW015206	Hs.178784	ESTs	2.3
	402333				2.3
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	2.3
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.3
	404367				2.3
60	403696				2.3
	441622	AW450957	Hs.224864	ESTs	2.3
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo	2.3
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
	428548	AA430058	Hs.98649	EST	2.3
65	404059				2.3
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.3
	413640	BE158118		gb:MR2-HT0378-240200-205-d09 HT0378 Homo	2.3
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.3
	435338	AA678071	Hs.194300	ESTs, Weakly similar to I38022 hypotheti	2.3
70	442710	AI015631	Hs.23210	ESTs	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
	451250	AA491275	Hs.236940	hypothetical protein FLJ12542	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	458455	AV648310	Hs.213488	ESTs	2.3
75	458521	AI651039	Hs.148559	ESTs	2.3
	407938	AA905097	Hs.85050	phospholamban	2.3
	439546	AF088056		gb:Homo sapiens full length insert cDNA	2.3
	441274	AW593781	Hs.131357	ESTs	2.3
	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.3
80	409660	AW452065	Hs.258905	ESTs	2.3
	428532	AF157326	Hs.184786	TBP-interacting protein	2.3
	411384	AW842115		gb:RC0-CN0026-090200-031-e11 CN0026 Homo	2.3
	453687	T55674	Hs.283108	hemoglobin, gamma G	2.3

	410140	AL134435	Hs.22269	neurexin 3	2.3
	422443	NM_014707	Hs.116753	histone deacetylase 7B	2.3
	409071	AW316932	Hs.181982	ESTs	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
5	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
	448458	AW614367	Hs.171054	ESTs	2.3
	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.3
	443718	AI083580	Hs.221373	ESTs	2.3
	445568	H00918	Hs.268744	KIAA1796 protein	2.3
10	400582				2.3
	411262	AW834480		gb:MR2-TT0014-151199-011-b07 TT0014 Homo	2.3
	401145				2.3
	407440	AF227135		gb:Homo sapiens candidate taste receptor	2.3
	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
15	459077	N20370	Hs.235883	ESTs	2.3
	448117	H49129	Hs.172982	ESTs	2.3
	453331	AI240665	Hs.8895	ESTs	2.3
	443751	AI285839	Hs.153324	EST	2.3
	402038				2.3
20	402176				2.3
	456605	AI827786	Hs.259044	ESTs	2.3
	432479	AL042844	Hs.275675	katanin p80 (WD40-containing) subunit B	2.3
	402527				2.3
	449272	AW137656	Hs.197645	ESTs	2.3
25	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.3
	455608	BE011437		gb:CM4-BN0220-080500-170-f03 BN0220 Homo	2.3
	458818	AI523857	Hs.232257	ESTs	2.3
	419875	AA853410	Hs.93557	proenkephalin	2.3
	405521				2.3
30	436517	BE080932	Hs.135225	ESTs	2.3
	456801	AW961886	Hs.138263	Homo sapiens clone 24528 mRNA sequence	2.3
	430444	AW296421	Hs.121035	ESTs	2.3
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.3
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.3
35	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	454456	AW850984		gb:IL3-CT0220-150200-068-H08 CT0220 Homo	2.3
	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo	2.3
40	457028	AW449838	Hs.97562	ESTs	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.3
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	2.3
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	2.3
45	421227	R78581	Hs.266308	mosaic serine protease	2.3
	426902	AI125334	Hs.97408	ESTs	2.3
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	447475	AI380797	Hs.158992	ESTs	2.3
	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.3
50	430712	AW044647	Hs.196284	ESTs	2.3
	458103	AW780192	Hs.267596	ESTs	2.3
	420959	AA282119	Hs.88975	ESTs	2.3
	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
	445641	AI245987	Hs.149442	ESTs	2.3
55	449276	AW241510	Hs.252713	ESTs	2.3
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.3
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	459497	AA825742	Hs.87517	ESTs	2.3
	412852	BE004117	Hs.37415	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
60	437539	AA974673	Hs.121419	ESTs	2.3
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Brn52 Homo sapien	2.3
	411994	R67298	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.3
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	2.3
	452463	R36452	Hs.300817	ESTs	2.3
65	404936				2.3
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.3
	440836	AW370882	Hs.222080	ESTs	2.3
	405120				2.3
	400238				2.3
70	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
	445117	AI208754	Hs.147369	ESTs	2.3
75	431162	AW971180		gb:EST383268 MAGE resequences, MAGL Homo	2.2
	437036	AI571514	Hs.133022	ESTs	2.2
	455849	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	2.2
	447624	AI640326	Hs.62713	ESTs	2.2
	439780	AL109688		gb:Homo sapiens mRNA full length insert	2.2
80	405706				2.2
	447732	AI758398	Hs.161318	ESTs	2.2
	440625	BE539853	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.2
	404257				2.2

	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	2.2
	449133	AI631655	Hs.197919	ESTs	2.2
	456555	AW592167	Hs.293299	ESTs	2.2
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodieste	2.2
5	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446096	AI276454		gb:qf71a12.x1 Soares_NhHMPu_S1 Homo sapi	2.2
	448106	AI800470	Hs.171941	ESTs	2.2
10	450232	BE300815	Hs.201326	ESTs	2.2
	436134	AK000618	Hs.123784	ESTs	2.2
	448466	AI522109	Hs.171066	ESTs	2.2
	420678	AW593288	Hs.3530	TLS-associated serine-arginine protein 2	2.2
	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.2
15	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	423611	AB011163	Hs.129908	KIAA0591 protein	2.2
	444050	AW138295	Hs.135024	ESTs	2.2
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	422669	H12402	Hs.119122	ribosomal protein L13a	2.2
20	403388				2.2
	403780				2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	424719	H90452		gb:yv01c03.r1 Soares fetal liver spleen	2.2
	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	2.2
25	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.2
	427119	AW880562	Hs.114574	ESTs	2.2
	400486				2.2
30	448482	AW294078	Hs.171092	ESTs	2.2
	402621				2.2
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	2.2
	424584	H10692	Hs.13310	ESTs	2.2
	445061	AI253094	Hs.145227	ESTs	2.2
35	431065	AA491286	Hs.128792	ESTs	2.2
	411908	L27943	Hs.72924	cytidine deaminase	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
	422677	AL046388	Hs.208206	hypothetical protein FLJ21162	2.2
40	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo	2.2
	400163				2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.2
	410556	R32158		gb:yh67a07.s1 Soares placenta Nb2HP Homo	2.2
45	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	2.2
	439482	W70045	Hs.58089	ESTs	2.2
	447877	AI435184	Hs.164252	ESTs	2.2
	418297	R91254		gb:yp94e12.s1 Soares fetal liver spleen	2.2
	403534				2.2
50	410594	AW770778	Hs.281238	ESTs	2.2
	414000	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.2
	432762	NM_014099	Hs.278924	PRO1768 protein	2.2
	437606	AA761594	Hs.122440	ESTs	2.2
	438550	AW976002	Hs.258402	ESTs	2.2
55	439626	N22415	Hs.189080	ESTs	2.2
	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens c	2.2
60	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	454204	AW816498		gb:QV0-ST0236-171299-075-b02 ST0236 Homo	2.2
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.2
	432887	AI926047	Hs.162859	ESTs	2.2
	448063	AI459108	Hs.159818	ESTs	2.2
65	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	2.2
	433098	AW190593	Hs.151143	ESTs	2.2
	409781	AW812266	Hs.15220	zinc finger protein 106	2.2
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.2
	423646	H02364		gb:yj35d06.r1 Soares placenta Nb2HP Homo	2.2
70	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
	437334	AL353947	Hs.283780	hypothetical protein DKFZp761N1814	2.2
75	431917	D16181	Hs.2868	peripheral myelin protein 2	2.2
	400843				2.2
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.2
	449560	AA001767	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	408940	M58583	Hs.662	cerebellin 1 precursor	2.2
80	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.2
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.2
	459495	BE544158		gb:601076707F1 NIH_MGC_12 Homo sapiens c	2.2
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	2.2

444547	AV650207	Hs.282437	ESTs, Weakly similar to I38022 hypotheti	2.2
417156	N49476	Hs.166563	replication factor C (activator 1) 1 (14	2.2
416761	H85422	Hs.108556	ESTs	2.2
408867	AA437199	Hs.656	cell division cycle 25C	2.2
406748	AW339106	Hs.217493	annexin A2	2.2
427443	AA402713	Hs.97872	ESTs	2.2
452643	AI796769	Hs.208320	ESTs	2.2
427473	AW274439	Hs.252709	ESTs	2.2
433919	AA746311		gb:oa56d12.r1 NCI_CGAP_GCB1 Homo sapiens	2.2
431058	AW968865		gb:EST380941 MAGE resequences, MAGJ Homo	2.2
428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	2.2
415250	F02614	Hs.27319	ESTs	2.2
440253	AI651329	Hs.160289	ESTs	2.2
434470	AA634818	Hs.298138	ESTs	2.2
418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.2
432463	AA548518	Hs.186733	ESTs	2.2
400861				2.2
407287	AI678812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens	2.2
414817	AW902892	Hs.23782	hypothetical protein FLJ12847	2.2
416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	2.2
449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
412314	AA825247	Hs.250899	heat shock factor binding protein 1	2.2
442952	AI743261	Hs.131860	ESTs	2.2
425187	AW014486	Hs.22509	ESTs	2.2
408221	AA912183	Hs.47447	ESTs	2.2
411480	AW848022		gb:IL3-CT0214-231299-053-A09 CT0214 Homo	2.2
459681				2.2
414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	2.2
442726	AW136066	Hs.19145	ESTs	2.2
450433	AW444538	Hs.231863	ESTs	2.2
437642	AL079309		gb:Homo sapiens mRNA full length insert	2.2
406298				2.2
409723	AW885757	Hs.257862	ESTs	2.2
433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
435090	BE217923	Hs.149595	ESTs	2.2
457187	AA443927	Hs.144360	EST	2.2
446534	AI307356	Hs.175225	ESTs	2.2
403764				2.2
442735	R91949		gb:yq06h06.s1 Soares fetal liver spleen	2.2
455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.2
405965				2.2
408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.2
441679	BE502267	Hs.65996	ESTs	2.2
432781	NM_014133	Hs.278940	PRO0618 protein	2.2
448470	AW026226	Hs.309479	ESTs	2.2
419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.2
443180	R15875	Hs.258576	claudin 12	2.2
422213	AA306385	Hs.133160	ESTs	2.2
423119	AA322201	Hs.131976	ESTs	2.2
450192	AA263143	Hs.24596	RAD51-interacting protein	2.2
428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	2.2
400734				2.2
430499	AW969408	Hs.231991	ESTs	2.2
451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.2
401694				2.2
423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
436640	AA724411	Hs.156065	ESTs	2.2
436802	N34486	Hs.170504	ESTs	2.2
443994	AI094805	Hs.135522	ESTs, Weakly similar to S38038 hypotheti	2.2
445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
446412	AW135313	Hs.150098	ESTs	2.2
448390	AL035414	Hs.21068	hypothetical protein	2.2
449939	T86420	Hs.272139	ESTs	2.2
412700	BE222433	Hs.201262	ESTs, Weakly similar to I38022 hypotheti	2.2
453125	AW779544	Hs.115497	hypothetical protein FLJ22655	2.2
422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.2
452441	BE222078	Hs.113069	ESTs	2.2
402395				2.2
459659				2.2
428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.2
438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypotheti	2.2
409446	AI561173	Hs.67688	ESTs	2.2
408764	BE087164	Hs.302415	ESTs	2.2
408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
436992	AA741074	Hs.120750	ESTs	2.2
439634	W79377	Hs.167	microtubule-associated protein 2	2.2
444199	AI128931	Hs.260681	ESTs, Moderately similar to ALUF_HUMAN I	2.2
446009	AI989885	Hs.231926	ESTs	2.2
435510	BE143837		gb:MR0-HT0164-151299-012-b08 HT0164 Homo	2.1

	403691				2.1
	458333	AI000792	Hs.108209	ESTs	2.1
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	2.1
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.1
5	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protei	2.1
	406941	X58140		(NONE)	2.1
	445712	AI458246	Hs.167451	ESTs	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
10	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.1
	437073	AI885608	Hs.94122	ESTs	2.1
	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.1
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.1
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.1
15	405233				2.1
	446512	H30351	Hs.207982	ESTs	2.1
	403188				2.1
	404443				2.1
	433645	AI821746	Hs.190258	ESTs, Moderately similar to ALU6_HUMAN A	2.1
20	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	2.1
	433479	AW511459	Hs.249972	ESTs	2.1
	455482	AW948353		gb:RC0-MT0015-130400-031-d07 MT0015 Homo	2.1
	446364	AB006624	Hs.14912	KIAA0286 protein	2.1
	452004	AI827815	Hs.277359	ESTs	2.1
25	405059				2.1
	425457	AW964212		gb:EST376285 MAGE resequences, MAGH Homo	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
30	432774	AA564946	Hs.156280	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	2.1
	445532	BE138944	Hs.146200	ESTs	2.1
	456313	AA225741		gb:nc17b10.s1 NCI_CGAP_Pr1 Homo sapiens	2.1
	412818	NM_003337	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 h	2.1
35	450271	AI693900	Hs.200920	ESTs	2.1
	401521				2.1
	422880	AF228704	Hs.121524	glutathione reductase	2.1
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hcKr	2.1
	449233	BE048401	Hs.196511	ESTs	2.1
40	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	2.1
	457003	S78234	Hs.172405	cell division cycle 27	2.1
	417448	AA203135	Hs.130186	ESTs	2.1
	402103				2.1
	450579	AW136774	Hs.48614	ESTs	2.1
45	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.1
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	2.1
	415333	H24415	Hs.13273	KIAA0592 protein	2.1
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	2.1
	434985	AA658229	Hs.291228	ESTs	2.1
50	414729	BE466928	Hs.281901	ESTs	2.1
	400510				2.1
	420844	AA595522		gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sapiens	2.1
	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	2.1
55	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	459108	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	2.1
	430118	AI377255	Hs.183287	ESTs	2.1
	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.1
60	437981	AA774445	Hs.192095	ESTs, Weakly similar to KIAA1397 protein	2.1
	439957	AI453184	Hs.66357	ESTs	2.1
	423734	H02217		gb:yj38d11.r1 Soares placenta Nb2HP Homo	2.1
	450721	AI732271	Hs.25567	ESTs	2.1
	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	2.1
65	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	2.1
	432919	AL079800		gb:DKFZp434O2330_r1 434 (synonym: hles3)	2.1
	434791	AA649235	Hs.116457	ESTs, Weakly similar to NIP3_HUMAN BCL2/	2.1
	445273	AI218441	Hs.153846	ESTs	2.1
	400514				2.1
70	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	439391	AW975638	Hs.293490	ESTs, Weakly similar to I38022 hypotheti	2.1
	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.1
75	429430	AI381837	Hs.155335	ESTs	2.1
	449689	AF228421	Hs.23889	DKFZP564A032 protein	2.1
	430909	AF034632	Hs.248126	G protein-coupled receptor 38	2.1
	453116	AI276680	Hs.146086	ESTs	2.1
	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	2.1
80	423019	AI640185	Hs.283626	ESTs	2.1
	414007	AI733895	Hs.103813	ESTs	2.1
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	2.1
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	2.1

	421279	AW564878	Hs.106645	ESTs	2.1
	443167	AI202009	Hs.132087	ESTs	2.1
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.1
	448078	AI460117	Hs.170464	ESTs, Highly similar to A53933 myosin I	2.1
5	436858	BE545498		gb:601070344F1 NIH_MGC_12 Homo sapiens c	2.1
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.1
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.1
	407401	AF029325		gb:Homo sapiens laminin beta-4 chain pre	2.1
	426336	AA375802		gb:EST88135 HSC172 cells II Homo sapiens	2.1
10	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	2.1
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.1
	406504				2.1
	410626	BE407727		gb:601289771F1 NIH_MGC_21 Homo sapiens c	2.1
	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.1
15	416175	H24230	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	442095	AI733162	Hs.128470	ESTs	2.1
	451878	AI821027	Hs.8429	ESTs	2.1
	449178	AI633748	Hs.197597	ESTs	2.1
20	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	2.1
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.1
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.1
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	2.1
	441543	AI733014	Hs.269715	ESTs	2.1
25	403065				2.1
	428811	AA436052	Hs.99487	ESTs	2.1
	451803	BE541174	Hs.252058	ESTs, Moderately similar to PC4259 ferri	2.1
	442906	AW296888	Hs.170939	ESTs	2.1
	409171	R17126		gb:yg09c11.r1 Soares infant brain 1NIB H	2.1
30	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	2.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	2.1
	412039	AW887384		gb:RC0-OT0089-130300-021-d07 OT0089 Homo	2.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.1
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.1
35	455022	AW850845		gb:IL3-CT0220-111199-028-D11 CT0220 Homo	2.1
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	2.1
	422942	AF054839	Hs.122540	tetraspan 2	2.1
	400451				2.1
	406668	T62745	Hs.184411	albumin	2.1
40	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	404834				2.1
	448732	BE614063	Hs.334689	KIAA1838 protein	2.1
	423453	AW450737	Hs.128791	CGI-09 protein	2.1
	421447	AB005216	Hs.104481	Nck, Ash and phospholipase C binding pro	2.1
45	408774	AW270899	Hs.254569	ESTs, Weakly similar to B34087 hypotheti	2.1
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.1
	405732				2.1
	417848	AA206581	Hs.39457	ESTs, Weakly similar to JC5314 CDC28/cdc	2.1
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.1
50	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.1
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.1
	426953	AI769281	Hs.97439	ESTs	2.1
	440454	AI733037	Hs.129990	ESTs	2.1
	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	2.1
55	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	441963	AI733307	Hs.128002	ESTs	2.1
	439498	AA908731	Hs.58297	CLLL8 protein	2.1
	456224	AW292905	Hs.128770	ESTs	2.1
60	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	2.1
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	2.1
	417787	R14948	Hs.23883	ESTs	2.1
	400612				2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
65	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	451067	BE172186		gb:MR0-HT0559-110300-005-h11 HT0559 Homo	2.1
	455032	AI830890	Hs.192422	ESTs	2.1
	417945	R29072		gb:F1-101D 22 week old human fetal liver	2.1
70	438268	AA782163	Hs.293502	ESTs	2.1
	424754	R09692		gb:yf23b12.r1 Soares fetal liver spleen	2.1
	404599				2.1
	459655				2.1
	402455				2.1
75	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	2.1
	421987	AI133161	Hs.286131	CGI-101 protein	2.1
	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.1
	438206	AA780385	Hs.187885	ESTs	2.1
	458451	AW297181	Hs.195922	ESTs	2.1
80	447534	AW953935	Hs.30837	ESTs	2.1
	417687	AI828596	Hs.250691	ESTs	2.1
	412717	W00973	Hs.334728	ESTs	2.1
	405759				2.1

406413				2.1
442081	AA401863	Hs.22380	ESTs	2.1
457938	AI373638	Hs.133900	ESTs	2.1
420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.1
428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1
411421	BE272110	Hs.21177	ESTs	2.1
437825	AA769123	Hs.291947	ESTs	2.1
437083	AW082597	Hs.244862	ESTs	2.1
409466	AA436207	Hs.226666	ESTs, Moderately similar to I54374 gene	2.1
433523	H29882	Hs.162614	ESTs	2.1
446868	AV660737	Hs.135100	ESTs	2.1
445882	AI948717	Hs.225155	ESTs, Weakly similar to A46302 PTB-assoc	2.1
438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
410486	AW235094	Hs.69233	zinc finger protein	2.1
411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
412446	AI768015	Hs.92127	ESTs	2.1
457289	AW573204	Hs.137078	ESTs	2.1
400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	2.0
435959	AW296243	Hs.118375	ESTs	2.0
448188	AW001835	Hs.13323	hypothetical protein FLJ22059	2.0
418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	2.0
420430	AI703192		gb:wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	2.0
445717	AW664658	Hs.149332	ESTs	2.0
451862	H09260	Hs.32333	ESTs	2.0
459686				2.0
441996	BE349537	Hs.38383	ESTs	2.0
412194	AW900282	Hs.115412	hypothetical protein FLJ13881	2.0
444229	AV648613	Hs.282397	ESTs	2.0
441635	AI908538	Hs.133000	ESTs, Weakly similar to S26689 hypotheti	2.0
421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	2.0
414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.0
426209	AA424197	Hs.98947	ESTs, Weakly similar to S33496 trypsin [	2.0
443520	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	2.0
409248	AB033035	Hs.51965	KIAA1209 protein	2.0
444518	AI160278	Hs.146884	ESTs	2.0
422237	M13149	Hs.1498	histidine-rich glycoprotein	2.0
409316	U28251	Hs.53237	ESTs, Highly similar to Z169_HUMAN ZINC	2.0
402725				2.0
413783	AA314337	Hs.301547	ribosomal protein S7	2.0
423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
425008	AW675764	Hs.174248	ESTs	2.0
427271	AW195922	Hs.188758	connexin 59	2.0
444102	AV647953	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.0
445829	AI452457	Hs.145526	ESTs	2.0
452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.0
429540	M85776		gb:EST02297 Fetal brain, Stratagene (cat	2.0
459456	AA486036	Hs.190124	ESTs	2.0
409840	AW502122		gb:UI-HF-BR0p-ajr-c-08-0-UI.r1 NIH_MGC_5	2.0
441025	AA913880	Hs.176379	ESTs	2.0
457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.0
445627	AW818475	Hs.7363	ESTs	2.0
440299	AI871778	Hs.250112	ESTs	2.0
401236	H24185	Hs.92918	hypothetical protein	2.0
429996	N90822	Hs.48969	ESTs	2.0
455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	2.0
411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	2.0
433449	AW772282		gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapien	2.0
454197	BE140966		gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
445297	BE544163	Hs.87128	hypothetical protein FLJ23309	2.0
403977				2.0
458948	AI695359	Hs.280943	ESTs	2.0
418663	AK001100	Hs.41690	desmocollin 3	2.0
411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.0
426536	AI949749	Hs.44441	ESTs	2.0
442765	BE567353	Hs.99480	ESTs	2.0
400859				2.0
405829				2.0
411863	BE075244	Hs.12420	ESTs	2.0
415258	AW752247	Hs.293853	ESTs	2.0
416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN I	2.0
416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	2.0
437733	AI792574	Hs.122876	ESTs	2.0
453118	AW195849	Hs.252757	ESTs	2.0
457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
444292	AI139794	Hs.146569	ESTs	2.0
431360	NM_000427	Hs.251680	loricrin	2.0
407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, m	2.0
412029	AW886238		gb:RC5-OT0078-280300-022-F01 OT0078 Homo	2.0
438522	AA809431	Hs.258886	ESTs	2.0
422634	NM_016010	Hs.118821	CGI-62 protein	2.0

	418790	H95693		gb:yt95d11.s1 Soares_pineal_gland_N3HPG	2.0
	442950	AI500417	Hs.46764	ESTs	2.0
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.0
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
5	402674				2.0
	408733	AW264812	Hs.254290	ESTs	2.0
	408767	AA057279	Hs.211928	ESTs	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
	418205	L21715	Hs.83760	troponin I, skeletal, fast	2.0
10	404604				2.0
	413627	BE182082	Hs.246973	ESTs	2.0
	402341				2.0
	438090	AA777534	Hs.191992	ESTs	2.0
	421303	T06464		gb:EST04353 Fetal brain, Stratagene (cat	2.0
15	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
20	433755	AW085934	Hs.120868	ESTs	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
	435648	H24347	Hs.27524	ESTs	2.0
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
25	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.0
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.0
	447678	BE385257	Hs.336457	Homo sapiens dopamine receptor interacti	2.0
	448150	AI472167	Hs.302739	ESTs	2.0
	453445	AL036532	Hs.91453	ESTs	2.0
30	444420	AI148157	Hs.146766	ESTs	2.0
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	2.0
	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.0
	428231	U17989	Hs.183105	nuclear autoantigen	2.0
	455873	BE152239		gb:QV4-HT0316-091199-028-f12 HT0316 Homo	2.0
35	430970	AI018210	Hs.144083	ESTs	2.0
	412277	BE277592	Hs.73799	guanine nucleotide binding protein (G pr	2.0
	413025	AA605265	Hs.291646	ESTs	2.0
	424083	AF055018	Hs.139137	Homo sapiens clone 24442 mRNA sequence	2.0
	427654	AA410183	Hs.137475	ESTs	2.0
40	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.0
	423942	AF209704	Hs.135723	glycolipid transfer protein	2.0
	430340	AA476777		gb:zw94g11.r1 Soares_total_fetus_Nb2HF8_	2.0
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.0
	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.0
45	400285				2.0
	405966				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
	415105	D60166		gb:HUM089G11B Clontech human fetal brain	2.0
50	434531	AA642007	Hs.116369	ESTs	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447185	AW377092	Hs.99601	hypothetical protein FLJ12553	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
	456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
55	400617	AF151064	Hs.36069	hypothetical protein	2.0
	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	2.0
	401785				2.0
	433417	AA587773	Hs.6859	Homo sapiens, Similar to RIKEN cDNA 5830	2.0
	420777	AA280223	Hs.130865	ESTs	2.0
60	439509	AF086332	Hs.58314	ESTs	2.0
	430203	L36140	Hs.235069	RecQ protein-like (DNA helicase Q1-like)	2.0
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	2.0
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	2.0
	437620	AW976930	Hs.128760	ESTs	2.0
65	407528	X64990		gb:H.sapiens mRNA HTPCRX16 for olfactory	2.0
	402048				2.0
	403623				2.0
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.0
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	2.0
70	422600	BE143586	Hs.87	retinoblastoma-like 1 (p107)	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.0
	433153	AA578512		gb:nh22e11.s1 NCI_CGAP_Pr1 Homo sapiens	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
75	435373	AW665538	Hs.117689	ESTs	2.0
	442988	AI026130	Hs.131683	ESTs	2.0
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.0
	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0

80

Table 31B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
407764	1014849_1	BE006347 BE008320 BE083307 BE083311 AW075968
408274	104999_1	R17315 Z43964 AA053547
408691	1074933_1	AW250525 BE265117
409171	1104879_1	R17126 R38456 H02771
409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
409623	1144047_1	AW449185 AW449665 BE220971
409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
409816	1155396_1	AW500954 AW501111 AW501394
409840	1156071_1	AW502122 AW502125 AW501663 AW501720
410201	118365_1	AA126129 AA126033 AA082561
410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
410500	1206323_1	R09442 AW846115 AW846108 AW751967 AW846083 AW846087 AW846090
410536	1207322_1	N39533 AW753094 AW753093
410556	1208157_1	R32158 AW754055 AW754054 AW754053 AW754045 AW857320
410615	1212203_1	AW772721 AW873372 H89212
410626	1212621_-1	BE407727
410644	1213795_1	AW902125 AW792853 AW837703 AW837710
410672	1214882_1	AW794600 AW794730
410845	1223881_1	AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283
410888	1225955_1	AW861207 AW809508
410901	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
410934	1227240_1	AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157
410999	1228809_1	AW813004 AW812962 AW812961
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411018	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
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411186	1235090_1	AW821257 AW821267 AW821283
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411382	1242594_1	BE067246 BE067241 BE067254 BE067249 AW841960
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411518	1248692_1	AW850246 AW850251 AW850302
411537	1248899_1	BE073250 BE073378 BE073379 AW850533 AW850529
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411738	1255755_1	AW859353 AW859365 AW859362 AW859356 AW859351 AW859354 AW859355 AW859361 AW859348 AW859364 AW859372 AW859352 AW859349 AW859367 AW859360 AW859374 AW859350
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411819	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
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412323	1288770_1	AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173 AW937159 AW937139 AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179 AW937156 AW937140 AW937135 AW937170
412329	1288943_1	AW937445 AW937457 AW937364 AW937374 AW937395
412400	1292900_1	AW948066 AW948106 AW948020 AW948047 AW948011 AW948033 AW948034 AW948041 AW948028 AW948048 AW948046 AW948056 AW948025 AW948053 AW948043 AW948032 AW948037 AW948050 AW948060 AW948059 AW948051 AW948027 AW948038 AW948052 AW948036 AW948031 AW948030 AW948035 AW948039 AW948026 AW948044 AW948049 AW948042 AW948054 AW948055 AW948013 AW948058 AW948045 AW948057 AW948029 AW948003 AW948016 AW948123 AW948008 AW948001 AW948022 AW948014 AW948023 AW948004 AW948000 AW948018

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412999	1343220_1	BE046255 BE046611 BE046716 BE046732 BE046273
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413088	1348732_1	BE064962 BE064979 BE064853 BE064857 BE064856 BE064977 BE064960 BE064860 BE064815 BE064957 BE064804 BE064816 BE064850 BE064806 BE064796 BE064818 BE064975 BE064819 BE064810 BE064668 BE065059
413096	1349078_1	BE065209 BE065364 BE065110 BE065111
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413252	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
413257	1355963_1	BE075035 BE074999 BE075006 BE075005 BE075032 BE075008 BE075037
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413470	1371600_1	N20934 BE141875 BE141877
413488	1373234_1	BE144017 BE185527 BE144023
413499	1373910_1	BE144884 H97942
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413581	1376335_1	BE150618 BE150616 BE150626
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413986	140720_1	Z43567 H24159 AA134240
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414349	1437515_-1	BE512968
414366	1438636_1	BE549143 BE390613 BE277344
414456	1447655_1	H74314 BE299593
414539	1460320_1	BE379046 BE395459
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414605	1465790_-1	BE390440
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415105	1522674_1	D60165 D60893 D60101
415131	1523680_1	D61119 D81508 D81734
415236	1531080_1	R41400 H06659 Z38637 F02023 T16516
415318	1533859_1	T06544 Z44549 F05465 R61128
415425	1536408_1	F08365 Z43395 R54298
415549	1539692_1	F11942 T78047 R13266
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421813	207654_1	BE048255 AA313083 AA298419
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423121	225175_1	AW864848 AA322213 AA322209 AW961624
423532	229362_1	BE090503 BE090490 BE090483 BE090501 BE090500 BE090365 BE090505 BE090509 BE090499 BE090502 BE090504 BE090497 AA327285
423646	230597_1	H02364 AA329065 AW958111 AW961436
423734	231479_1	H02217 AA330235 AW955673
423841	232507_1	AW753967 AA370795 AA331630 AW962550
423867	232732_1	AA331886 AW962659 AW962655 T89841
423871	232749_1	AA331906 AA332484
424719	242889_1	H90452 AA345767 AW964302 H90399
424754	243305_1	R09692 R09414 AA346353
424872	244505_1	AA347923 AA347928 AW961769

425156	247338_1	AA351364 H19138 R12960
425201	247933_1	AA352111 AW962247 AA429695
425374	250946_1	AI904013 AI904015 AA356332
425433	251775_1	AA357471 AA360564 AW962961
425457	252038_1	AW964212 AA357832 AA357831
425541	252945_1	AA359119 AW963014 D79884
425798	256586_1	AA364002 AI522307
426076	260504_1	AW962714 AA369277 AA369278
426336	265003_1	AA375802 AA375642 AW963815
426497	268121_1	AA379913 AA379981 AW963523
426750	271252_1	AA383950 AA383958 AW966432
426800	272088_1	AA385085 AW966617 T87798
426960	273843_1	AA393713 AA400726
428679	294049_1	AA431765 AA432015
428740	294655_1	AA433838 AA450385 AA683244
429106	299886_1	AA446612 AA456438 AA476655
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430175	314040_1	AA468724 AA468772 AA468643 AW969231
430340	316229_1	AA476777 T86049
430535	319643_1	AW968485 AW968670 AA480922 BE350425
430553	319868_1	AW392821 AW392809 AW843258 AW843049 AW603156 BE165656 AW821728
430692	32200_1	X80240 AI064750 AI133594
430698	322100_1	AA492071 AA484229 AW969850
430757	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
430850	324651_1	BE144152 AA937952 AA487799
431058	327401_1	AW968865 AA491199 C17148
431071	327550_1	AA491379 H86020 AW969148
431162	328726_1	AW971180 AA551515 AA493610 AW089533
431169	328799_1	AW971240 AA493843 AA493723
431453	333457_1	AW753917 BE152926 AA505333 BE155673
431655	336189_1	AW971119 AA574265 AA513268
431822	338082_1	AA516049 AW004922
431925	33905_1	AK000890 BE182413 AW890890 AW844179 BE178834
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432363	345469_1	AA534489 AW970240 AW970323
432779	354024_1	AW979241 AA565006 AA847102
432869	355475_1	AW974094 AA569074 AA602574
432919	356290_1	AL079800 AA570294 L25459
433153	359936_1	AA578512 AA595535 BE177533
433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
433449	366532_1	AW772282 AA592974
433919	377243_1	AA746311 AA927492 AA617995
434098	380006_1	AA625499 AA625269 AA625184
434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
434662	390415_1	AA641957 AW749897 AW749866 AW749887 AW749890
434671	390655_1	R34758 AA642317
435079	399783_1	AA664192 H60250 T71388
435138	401159_1	BE314734 AA666393
435463	406582_1	AA682507 AW851124
435510	407286_1	BE143837 AW749652 AA683327
435634	409239_1	T82384 R05307 AA693714
435689	409755_1	AA694284 H68267 H68264
436359	41847_1	Z83806 AJ132091 AJ132090
436720	425676_1	AW975902 AA729344 AI557342
436858	428095_1	BE545498 AA830720 AI873015 AA732679
437037	431828_1	T63804 T63768 AA742849
437113	433234_1	AA744693 AW750059
437642	43997_1	AL079309 AA281819
437963	44635_-1	BE396279
438005	447553_1	BE151746 BE336853 D63271 T94955 AA774994
438993	46765[illegible]_1	AA828995 AA834879 AI926361
439037	46803_1	AF075084 H53157 H53054
439546	47360_1	AF088056 W76297 W72448
439780	47673_1	AL109688 R23665 R26578
442653	54812_1	BE269247 BE270032 BE270800 BE566840
442735	550247_1	R91949 AI016237 BE072329
443764	579650_1	F23283 AI084941 F35774
444063	590989_1	AI122614 AW869134
444910	624951_1	AI201849 BE069007 AW946544
445432	63943_1	AV653771 BE089370
446096	661959_1	AI276454 AI633717 AI275116
446901	697809_1	AI347274 AW844024
447884	740749_1	H29505 R18575 Z43580 T48738 AI435454 BE004683
448477	76475_1	BE612572 AL040190 F08514
449311	804513_1	AI657014 AW594035 AI657036 AI638390
450024	82296_1	AA005129 AA679084 AA694399
451067	85759_1	BE172186 AA059279 AA020815 AA013437
452043	89532_1	H86231 AA021632 H38271
452542	921410_1	AW812256 AW812257 AI906423 AI906422
453211	95527_1	W84829 AA033900 AW573557
453530	97021_1	AW021633 AA036730 AI866854
453823	982526_1	AL137967 BE064160 BE064186

453901	986414_1	BE065902 AW749032 AW003637
454186	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 BE141749 AW177598
454190	1049996_1	AW177821 AW177896 AW177867
454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969 BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975 BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013 BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646 BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671 AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
454204	1050597_1	AW816498 AW808791 AW808515 AW808379 AW808532 AW808605 AW808977 AW808816 AW178676 AW178486 AW808514 AW178483 AW178485 AW809007 AW808524
454314	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
454352	1129667_1	AW389668 AW389657 AW609198 AW389649
454423	1183079_1	AW603985 AW854350
454447	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
454456	1207088_1	AW850984 AW752836 M86124
454482	1215087_1	BE147919 AW794884 BE147847
454560	1223940_1	AW807281 AW807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367
454564	1224407_1	AW807573 AW807566 AW807572
454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821 AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617 AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754 AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674 AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756 AW807835 AW807608 AW807753 AW807601 AW807956
454597	1226059_1	AW809648 AW809704 AW809643 AW809653 AW809709 AW809949 AW809939 AW810010 AW809705 AW809950 AW809822 AW809667 AW810093 AW810076 AW809673 AW810349 AW809895
454633	1227504_1	AW811380 AW811385
454716	1230503_1	AW850684 AW850150
454747	1233006_1	AW818535 AW818588 AW818651
454754	1233580_1	AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265 AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
454767	1234028_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202 AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
454778	1234343_1	AW820199 AW820434 BE174743
454784	1234630_1	AW820626 AW820621 AW820608
454790	1234752_1	AW820852 AW820773 AW821088
454836	1236509_1	AW833711 AW833620 AW833699
454864	1237929_1	AW835775 AW845768 AW845764 AW845773 AW845757 AW845758 AW845780
454938	1245635_1	AW846134 AW846467 AW846468 AW846386 AW846461 AW846211 AW846179 AW846205 AW846320 AW846379 AW846367 AW846561 AW846556
454962	1246750_1	AW847645 AW847791 AW854083 AW853945
455022	1249160_1	AW850845 BE144010 AW855164
455121	1254339_1	BE156459 BE156469 BE156468 AW857447
455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
455219	1261640_1	AW879403 AW867707
455221	1261678_1	AW867751 AW867770 AW867763
455236	1265662_1	AW875972 AW875983 AW875974 AW876000 AW875966 AW876050
455252	1266222_1	AW876627 AW876630 AW876631 AW876625
455255	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
455275	1272255_1	AW977806 AW887923 AW886321
455280	1272607_1	AW886156 AW887926 AW886324 AW886236 AW887906 AW886304
455310	1278158_1	AW893961 AW893998 AW894034 AW894019
455328	1280063_1	AW896438 AW896534 AW896500 AW896540 AW896446
455464	1292643_1	AW983901 AW984485 AW947715
455482	1293183_1	AW948353 AW948351 AW948331 AW948303 AW948336 AW948305 AW948299 AW948346 AW948352
455488	129372_-1	AA102322
455511	1321229_1	BE144762 AW979091
455534	1322942_1	AW991925 AW991919
455540	1323701_1	BE080231 AW993284 AW993293 AW993000
455556	1325658_1	AW995423 AW995373
455571	1331885_1	BE003714 BE003721 BE003720 BE003716
455587	1335046_1	BE007829 BE007815 BE007822 BE007996 BE007835 BE007837 BE007824 BE007836 BE007827
455608	1337389_1	BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406
455675	1349659_1	BE065984 BE065942 BE065955 BE066085
455688	1350606_1	BE067238 BE067235 BE067240 BE067256 BE067263 BE067236 BE067260 BE067253 BE067248 BE067252
455696	1351077_1	BE067870 BE067866 BE165133 BE165334 BE165329 BE165332
455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
455756	1358603_1	BE079307 BE079309
455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
455780	1364580_-1	BE088828
455849	1375441_1	BE146866 BE146865 BE146867
455851	1375451_1	BE146879 BE146914 BE146918
455866	1377119_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055
455873	1379498_1	BE152239 BE152242 BE152230
455880	1380022_1	BE153208 BE153146 BE152981
455935	1384144_1	BE158687 BE158688
455964	1389912_1	BE166924 BE166921 BE166925 BE166915 BE166970 BE166968
455992	1398552_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997

455993	1398665_1	BE179085 BE179084 BE179086 BE179264
456186	1618618_1	W26642 H88394
456313	177240_1	AA225741 AI734056 AI820965 AI732153 AA259201 AA225731
456394	1843275_-2	W28506
456407	184986_1	AW968614 AA243209 AA281411
456476	191761_1	AA256753 AW628680
457242	307984_1	AA457011 AI978850
457824	41515_6	R84938 AL047151 AA310309 AW063200 AI569528 AI307823 N49975
458804	75803_1	AL157625 N72696 BE622492
458890	812733_2	AW865523 AW865128 AW865467 AW865127 AW865466
459160	920051_1	AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
459201	925883_1	AW391177 W45021

TABLE 31C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400451	8113550	Minus	82189-82320
400462	9929659	Minus	197610-197785
400486	8569885	Plus	181108-181605
400510	9796540	Minus	139633-139910,140469-140979
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400579	9887603	Plus	21323-21526
400582	9887609	Plus	88642-88726,89716-89866
400587	9887626	Plus	25435-25588,25668-25747
400608	9887666	Minus	96756-97558
400612	9929646	Minus	151513-151662
400613	9864507	Plus	92278-92472
400641	8117693	Plus	4786-4992
400643	8117693	Plus	12818-13016
400706	7249204	Minus	78299-78686
400734	8118979	Plus	122853-123971
400816	8569993	Plus	161221-162078
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400859	9757499	Minus	91888-92018,98131-98294,99474-99570
400861	9757506	Plus	163855-164016
400889	9958234	Minus	169782-170036
401078	3687273	Plus	105052-105171
401098	9965518	Minus	85632-86174
401132	8705350	Minus	85679-85795
401145	2547238	Plus	17599-17776
401189	9690246	Minus	90815-90929
401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
401344	9926411	Minus	82478-82602,86952-87110
401361	9958052	Plus	153093-154106
401365	9796180	Minus	119572-119672
401449	8574316	Minus	144928-145030
401497	7381770	Plus	92607-92813
401521	7705251	Plus	9127-9234
401526	7770561	Plus	91570-93177
401602	7689963	Plus	101096-101253
401614	7839924	Plus	17350-17735
401645	7657839	Minus	34986-35133
401694	3540172	Minus	64056-64168
401775	9966311	Minus	110228-110340
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401882	8139716	Plus	86466-87077
401887	7229981	Plus	93973-94120
401986	4406829	Minus	31137-31293
401992	4153858	Plus	31452-31649
402038	7684482	Minus	100751-100885
402048	8072512	Plus	43936-44078
402076	8117410	Plus	128316-128627
402103	7249203	Plus	14453-15414
402131	7704961	Minus	33114-33209,33496-33678
402176	7543687	Minus	10-750
402230	9966312	Minus	29782-29932
402333	8844110	Minus	165693-165856
402341	7656696	Plus	22583-23699
402395	9929693	Minus	131016-131998
402429	9796372	Minus	57622-57793,59282-59402,59624-59827
402430	9796372	Minus	62382-62552
402455	9796753	Minus	139640-139779,140568-140660
402527	9800806	Plus	4722-4916,17858-18037,19964-20140,24423-24605,26699-26881

402615	9926801	Plus	131390-132157
402621	9930950	Plus	130806-131036
402674	8077108	Minus	39290-39502
402725	8979991	Plus	107231-107383
402790	4835258	Minus	147744-147861
402867	5596716	Plus	52806-53106,53500-53818
402953	9408724	Minus	122603-122743
403003	5441423	Minus	79403-79560,79712-80021
403011	6693597	Minus	3468-3623
403065	8954197	Minus	71615-71773,73930-74144
403188	9838289	Minus	157618-157755
403271	7230852	Plus	134283-134485
403273	8018055	Plus	133809-134099
403281	8072630	Minus	7521-7728
403296	8096530	Minus	35913-36520
403310	8139936	Minus	183883-184026
403329	8516120	Plus	96450-96598
403341	8569175	Plus	30699-30910
403344	8569726	Plus	70823-70990
403356	8569930	Plus	92839-93036
403381	9438267	Minus	26009-26178
403388	9438331	Plus	112733-113001,114599-114735
403396	9438367	Minus	952-1160
403501	7534005	Minus	108903-110438
403513	7656757	Minus	155310-155436,158402-158535
403515	7656757	Minus	173358-179553
403534	8076917	Minus	46652-47332
403549	8081591	Minus	137150-137362
403568	8101145	Minus	85509-85658
403574	8101156	Plus	5542-6176
403619	8569810	Plus	62501-62653
403623	8569879	Minus	3519-5426
403625	8569879	Plus	6551-7111
403637	8671936	Minus	142647-142771,145531-145762
403667	6850483	Minus	1344-1442,1545-1697
403677	7331517	Minus	55008-55083,62860-63051
403691	7387384	Minus	88280-88463
403696	3135242	Minus	143467-143634
403743	7652003	Minus	136463-136646
403760	7712202	Minus	45910-46260,47563-47824
403764	7717105	Minus	118692-118853
403776	7770611	Minus	1414-1513,1624-1756
403780	8076989	Plus	93160-93409
403786	8083636	Minus	73028-73217
403891	7331467	Minus	191508-193220
403895	7381715	Minus	3502-4002,4070-4308
403977	7657840	Minus	115573-115820
404043	9558573	Plus	29042-29135,46597-46699
404059	3548785	Plus	104326-106788
404076	9931752	Minus	3848-3967
404196	3805917	Minus	67928-68109
404249	8655533	Plus	64270-64633
404257	9367215	Plus	15262-16227
404285	2326514	Plus	32282-32416
404288	2769644	Plus	3512-3691
404367	9965011	Minus	114391-114628
404443	7579073	Minus	87198-87441
404453	7657714	Plus	27768-29179
404476	8080699	Plus	101841-102043
404513	8151941	Minus	112837-113339
404561	9795980	Minus	69039-70100
404569	7249169	Minus	104257-104348,104822-104970
404577	4020145	Plus	17991-18420
404588	6456726	Minus	40059-40210
404599	8705107	Plus	110443-110733
404604	9212537	Minus	72019-72509
404638	9796751	Minus	99433-99528,100035-100161
404767	7882827	Minus	23244-23759
404793	7232206	Minus	61087-61590
404822	3810614	Plus	7541-8132
404834	6911603	Minus	37948-38226
404845	7958980	Minus	47174-47326,52928-53146,53312-53602
404898	7331420	Minus	177015-177328
404936	6850774	Plus	191519-191664
404957	7407927	Plus	147512-148011
405017	6532084	Plus	35551-35690
405059	7656683	Plus	349-822
405090	8072525	Minus	38552-39202
405093	8072575	Plus	95878-96020
405120	8099940	Plus	140176-140340
405170	9966524	Plus	37047-37198
405229	7249019	Plus	51081-51701
405230	7249032	Minus	97493-97682

405233	7249045	Plus	9588-10065
405241	7249178	Minus	69927-70526
405264	7329374	Plus	28556-28684
405287	3928029	Plus	89802-89999
405302	2078453	Minus	121688-121840
405303	2078453	Minus	130607-130802
405336	6094635	Plus	33267-33563
405347	2979602	Minus	977-1116
405385	6552772	Plus	48332-48454
405443	7408143	Plus	90716-90887,101420-101577
405455	7656675	Plus	134112-134671
405494	8050952	Minus	70284-70518
405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405547	1054740	Plus	124361-124520,124914-125050
405605	5836195	Minus	117070-117270
405608	5815499	Minus	66822-66925
405629	4508116	Minus	101678-101866
405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
405654	4895155	Minus	53624-53759
405692	4314424	Plus	61379-62562
405706	4165003	Plus	44307-44431,49619-49802
405720	9797144	Plus	13409-13861
405732	7534017	Plus	146981-147316
405759	3288022	Minus	18283-18399
405780	7248203	Minus	48204-48371
405784	7417368	Minus	77798-78000
405829	7109593	Minus	15628-16127
405869	6758731	Minus	89867-90358
405935	6758795	Minus	163112-163652
405959	6758815	Plus	1-642
405965	8247786	Minus	179930-180373
405966	8247788	Minus	51762-51978
405970	8247789	Minus	45795-46295
405981	8247790	Plus	4771-5338
406005	8247801	Minus	39912-40220
406053	6758997	Plus	30921-31532
406073	9119150	Plus	60495-60610
406091	9123919	Minus	197370-197935
406092	9123919	Plus	251370-251797,252168-252882
406298	5686278	Minus	30084-30770
406327	9212407	Plus	168241-168492
406333	9213235	Plus	64689-64798
406364	9256114	Minus	50715-50833
406377	9256135	Plus	126826-126979,129755-129942
406413	9256407	Plus	43858-44003,46993-47136
406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
406470	9795562	Minus	15532-15697
406504	7711360	Minus	107068-107277
406506	7711374	Minus	6843-8077F
406592	4567182	Plus	352560-352963

Table 32A lists about 969 genes upregulated in lung fibrosis relative to normal body tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 33A lists about 800 genes upregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 34A lists about 703 genes upregulated in idiopathic pulmonary fibrosis (IPF) relative to hypersensitivity pneumonitis (HP) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 35A lists about 323 genes upregulated in hypersensitivity pneumonitis (HP) relative to idiopathic pulmonary fibrosis (IPF) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 36A lists about 52 genes upregulated in non-specific interstitial pneumonitis (NSIP) relative to hypersensitivity pneumonitis (HP) or idiopathic pulmonary fibrosis (IPF). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 37A lists about 206 genes downregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 38A lists about 207 genes upregulated in lung fibrosis relative to normal tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesels on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

TABLE 32A: About 969 genes upregulated in lung fibrosis relative to normal body tissues

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.
R2: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	22.45	28.63
406964	M21305		FGENES predicted novel secreted protein	16.10	7.65
431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	15.83	14.86
442275	AW449467	Hs.54795	ESTs	15.74	21.96
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	13.83	34.53
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	12.40	7.38
431089	BE041395		ESTs, Weakly similar to unknown protein	12.38	6.05
421110	AJ250717	Hs.1355	cathepsin E	11.86	6.49
457200	U33749	Hs.197764	thyroid transcription factor 1	11.38	9.79
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	10.89	15.94
443709	AI082692	Hs.134662	ESTs	10.84	8.27
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	10.06	8.92
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.96	5.43
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	9.90	7.87
421798	N74880		N-acylsphingosine amidohydrolase (acid c	9.38	8.35
400269			Eos Control	9.03	6.48
444325	AW152618	Hs.16757	ESTs	8.31	6.76
416402	NM_000715	Hs.1012	complement component 4-binding protein,	8.14	5.51
413048	M93221	Hs.75182	mannose receptor, C type 1	7.70	4.09
432985	T92363	Hs.178703	ESTs	7.56	7.83
443324	R44013	Hs.164225	ESTs	7.06	4.47
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	6.90	2.89
408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88	4.00
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56	4.25
421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46	4.47
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.30	13.57
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	6.28	3.38
441835	AB036432	Hs.184	advanced glycosylation end product-speci	5.99	13.26
446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.88	4.10
415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	5.88	3.35
442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	5.87	5.69
414812	X72755	Hs.77367	monokine induced by gamma interferon	5.84	3.34
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72	5.90
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospha	5.59	6.89
436954	AA740151	Hs.130425	ESTs	5.58	4.72
446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	5.48	5.33
421340	F07783	Hs.1369	decay accelerating factor for complement	5.48	2.69
420656	AA279098	Hs.187636	ESTs	5.45	3.99
432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38	3.65
408380	AF123050	Hs.44532	diubiquitin	5.37	3.11
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	5.30	3.98
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.29	4.00
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	5.28	2.48
442832	AW206560	Hs.253569	ESTs	5.20	3.78
407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	5.11	3.81
433293	AF007835	Hs.32417	hypothetical protein MGC4309	5.11	2.88
424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.07	3.46
428043	T92248	Hs.2240	uteroglobin	5.06	9.46
431745	AW972448	Hs.163425	ESTs	5.04	4.16
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04	3.68
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	5.02	4.26
419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	4.97	3.35
428927	AA441837	Hs.90250	ESTs	4.92	3.15
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.79	3.05
442994	AI026718	Hs.16954	ESTs	4.76	2.65
416030	H15261	Hs.21948	ESTs	4.76	4.26
438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.73	3.24
453142	AA033648	Hs.7473	ESTs	4.66	2.92
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64	4.88
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	4.60	2.60
432810	AA863400		ESTs	4.54	2.42
418259	AA215404		ESTs	4.54	2.54
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	4.48	4.86
424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.46	3.62
423575	C18863	Hs.163443	intron of periostin(OSF-2os)	4.44	3.41
428667	AI375550	Hs.346868	nucleolar protein p40; homolog of yeast	4.42	3.41

429228	AI553633		ESTs	4.32	2.98
432435	BE218886	Hs.282070	ESTs	4.30	2.26
446932	AA961459	Hs.125644	ESTs	4.30	2.81
408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30	2.39
409435	AI810721	Hs.95424	ESTs	4.30	2.60
419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	4.29	2.48
452561	AI692181	Hs.49169	KIAA1634 protein	4.23	2.26
427698	AW972594	Hs.335499	ESTs	4.22	3.49
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	4.22	13.34
446608	N75217	Hs.257846	ESTs	4.20	3.62
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18	3.14
459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16	2.64
445885	AI734009	Hs.127699	KIAA1603 protein	4.16	3.99
430280	AA361258	Hs.237868	interleukin 7 receptor	4.13	2.79
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12	2.19
427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.12	3.02
420556	AA276300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.08	3.13
428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.08	3.48
432731	R31178	Hs.287820	fibronectin 1	4.06	2.66
439398	AA284267	Hs.221504	ESTs	4.06	2.86
409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.05	3.51
412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04	2.44
436120	AI248193	Hs.119860	ESTs	4.04	3.11
407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.03	2.69
421462	AF016495	Hs.104624	aquaporin 9	4.00	2.51
443257	AI334040	Hs.11614	HSPC065 protein	4.00	2.61
421659	NM_014459	Hs.106511	protocadherin 17	4.00	3.00
424273	W40460	Hs.144442	phospholipase A2, group X	3.98	2.30
415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.97	3.36
450656	AA010539	Hs.18912	ESTs	3.96	4.37
429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94	2.44
424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	3.93	3.08
413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.92	3.53
452416	AA026115	Hs.114777	ESTs	3.92	2.90
428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.90	5.06
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.90	2.00
453204	R10799	Hs.191990	ESTs	3.90	2.22
450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.81	3.82
422173	BE385828	Hs.250619	phorbolin-like protein MDS019(CEM15)	3.80	2.23
425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.78	2.86
406672	M26041	Hs.198253	major histocompatibility complex, class	3.78	3.70
457411	AW085961	Hs.130093	iroquois-class homeobox protein IRX2	3.76	2.56
432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.76	2.76
436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74	2.83
414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.72	2.55
428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.71	2.25
458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.70	2.26
419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	3.69	7.71
417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68	2.17
426174	AA547959	Hs.115838	ESTs	3.65	2.93
408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	3.64	2.62
435990	AI015862	Hs.131793	ESTs	3.62	2.27
427621	BE621182	Hs.179862	hypothetical protein FLJ12443	3.62	3.48
425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	3.61	3.18
419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.60	3.05
426116	AA868729	Hs.144694	ESTs	3.60	2.80
419235	AW470411	Hs.288433	neurotrimin	3.58	2.88
424054	AA334511	Hs.26638	membrane-spanning 4-domains, subfamily A	3.56	2.58
422667	H25642		ESTs	3.55	2.44
406673	M34996	Hs.198253	major histocompatibility complex, class	3.54	3.98
414142	AW368397	Hs.334485	hemicentin(fibulin 6)	3.54	3.30
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.54	3.11
430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	3.53	2.38
417318	AW953937	Hs.240845	ESTs	3.52	2.02
456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	3.50	3.21
415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.48	2.35
430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.48	2.13
440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.47	2.93
424711	NM_005795	Hs.152175	calcitonin receptor-like	3.47	2.69
418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.46	2.31
416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	3.46	2.37
448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.45	2.07
447183	AI554733	Hs.173182	ESTs	3.42	2.01
435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40	3.49
425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40	2.42
413714	AI560944	Hs.71428	ESTs	3.38	2.52
407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.36	2.13
436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36	2.41
450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36	2.06
407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.35	2.42
410606	AW418779	Hs.114889	ESTs	3.35	2.39
450726	AW204600		retinoic acid receptor, alpha	3.34	6.35
430573	AA744550	Hs.136345	ESTs	3.33	1.94

421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2(	3.32	2.75
433658	L03678	Hs.156110	immunoglobulin kappa constant	3.31	2.22
454076	AW204712	Hs.61957	ESTs	3.31	1.95
452039	AI922988	Hs.172510	ESTs	3.30	2.95
454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30	2.37
430414	AW365665	Hs.120388	ESTs	3.30	2.48
417958	AA767382	Hs.193417	ESTs	3.30	2.04
423001	AA320014	Hs.208603	ESTs	3.29	2.62
443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28	2.35
424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28	2.05
424238	AA337401	Hs.137635	ESTs	3.28	2.45
429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.27	2.63
448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.26	2.67
426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.26	2.04
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22	2.36
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22	3.87
422109	S73265	Hs.1473	gastrin-releasing peptide	3.20	2.79
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	3.20	2.30
413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18	2.42
408761	AA057264	Hs.238936	ESTs, Weakly similar to (defline not ava	3.18	2.12
438568	R98865	Hs.11135	major histocompatibility complex, class	3.18	3.86
451497	H83294	Hs.284122	Wnt inhibitory factor-1	3.18	2.99
444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.17	2.02
446094	AK001760	Hs.13801	KIAA1685 protein	3.17	2.42
442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	3.17	2.27
406685	M18728		gb:Human nonspecific crossreacting antig	3.17	2.80
430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16	1.95
424943	AU077260	Hs.153924	death-associated protein kinase 1	3.16	2.18
436805	AA731533	Hs.270751	ESTs	3.16	1.95
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.15	3.63
409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14	1.74
448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.13	3.35
420729	AW964897	Hs.290825	ESTs	3.12	2.09
419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12	2.06
416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12	2.58
451820	AW058357	Hs.199248	ESTs	3.10	2.26
440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.10	3.01
448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10	2.32
437866	AA156781		metallothionein 1E (functional)	3.10	1.80
428513	BE220806	Hs.184697	plexin C1	3.10	2.11
438607	AW080237	Hs.252884	ESTs	3.10	2.20
445034	AW293376	Hs.143659	ESTs	3.08	2.81
458332	AI000341		ESTs	3.08	1.87
415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.08	1.87
407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08	1.94
407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.07	2.12
452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	3.07	2.16
425509	AF079363	Hs.158213	sperm associated antigen 6	3.06	2.75
431087	H12723	Hs.290791	ESTs	3.06	2.41
452235	AL039743	Hs.28514	testes development-related NYD-SP21	3.06	2.64
449328	AI962493		ESTs	3.06	2.78
422900	AA641201	Hs.222051	ESTs	3.05	1.87
414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.05	1.99
430250	NM_016929	Hs.283021	chloride intracellular channel 5	3.05	2.49
437527	AI241019	Hs.145644	ESTs	3.04	2.17
432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.04	1.78
420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	3.02	2.43
445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	3.02	1.77
411252	AB018549	Hs.69328	MD-2 protein	3.02	1.95
439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02	2.24
420683	AA830168	Hs.271305	ESTs	3.01	2.14
412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00	2.13
410434	AF051152	Hs.63668	toll-like receptor 2	3.00	2.60
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00	1.94
434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.00	1.81
435800	AI248285	Hs.118348	ESTs	3.00	1.89
420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	3.00	2.08
449057	AB037784	Hs.22941	KIAA1363 protein	3.00	2.18
413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.99	2.46
436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	2.99	2.76
411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.99	2.16
444020	R92962	Hs.35052	ESTs	2.98	2.21
427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.98	2.08
432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	2.98	2.40
457675	AF119917	Hs.306574	Homo sapiens PRO3098 mRNA, complete cds	2.96	2.03
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.96	1.74
429950	AW081608	Hs.105053	ESTs	2.96	2.40
420394	AB023161	Hs.97403	KIAA0944 protein	2.95	2.46
406698	X03068	Hs.73931	major histocompatibility complex, class	2.95	4.13
419038	AW134924	Hs.190325	ESTs	2.94	1.72
449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94	2.93
418293	AI224483	Hs.16063	hypothetical protein FLJ21877	2.94	1.94
400880			NM_000611*:Homo sapiens CD59 antigen p18	2.94	1.74

430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94	2.12
419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.93	2.25
439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobin, fa	2.93	3.72
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.92	1.91
419981	AA897581	Hs.128773	ESTs	2.92	2.18
400419	AF084545		Target	2.92	1.83
435176	AA744875	Hs.189413	ESTs	2.91	2.15
413283	R78669	Hs.23756	hypothetical protein similar to swine ac	2.90	2.25
444339	T96555	Hs.31562	ESTs	2.90	3.16
429272	W25140	Hs.110667	ESTs	2.90	2.43
435047	AA454985	Hs.54973	cadherin-like protein VR20	2.90	2.29
435080	AI831760	Hs.155111	hypothetical protein FLJ14428	2.90	2.40
402474			NM_004079:Homo sapiens cathepsin S (CTSS	2.88	2.47
421554	AW137676	Hs.97775	ESTs	2.88	3.37
422770	AL117544	Hs.120021	DKFZP434I092 protein	2.88	2.00
434658	AI624436	Hs.310286	ESTs	2.88	2.06
440248	AA876138		ESTs	2.86	2.24
442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.86	4.32
430515	AA746503	Hs.283313	ESTs	2.86	2.96
446063	AI720140	Hs.151079	ESTs	2.86	2.47
438177	BE327015		ESTs	2.86	1.70
429083	Y09397	Hs.227817	BCL2-related protein A1	2.85	2.06
417105	X60992	Hs.81226	CD6 antigen	2.85	3.00
433230	AW136134	Hs.220277	ESTs	2.84	1.97
438676	AA813745	Hs.123446	ESTs	2.84	2.62
435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.82	4.33
420252	AW270404	Hs.193161	ESTs	2.82	3.22
415788	AW628686	Hs.78851	KIAA0217 protein	2.82	1.78
428065	AI634046	Hs.157313	ESTs	2.81	2.47
434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.81	2.67
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.78	3.39
435517	AA928626	Hs.130177	ESTs	2.78	2.36
439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78	1.82
434158	T86534	Hs.14372	ESTs	2.78	1.96
428923	BE047698	Hs.188785	ESTs	2.78	2.07
413786	AW613780	Hs.13500	ESTs	2.78	1.97
406387			Target Exon	2.77	4.22
421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.76	3.24
444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.76	2.11
427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	2.76	1.94
417726	AW136437	Hs.24790	KIAA1573 protein	2.76	1.78
435154	AA668764		ESTs	2.76	2.10
429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.76	2.21
423387	AJ012074		vasoactive intestinal peptide receptor 1	2.76	2.36
432060	AW971364	Hs.324775	ESTs	2.75	2.02
434164	AW207019	Hs.148135	serine/threonine kinase 33	2.74	2.48
423706	U95218	Hs.131924	G protein-coupled receptor 65	2.74	1.93
442703	AL044949	Hs.116298	ESTs	2.74	1.89
450247	AF123303	Hs.24713	hypothetical protein	2.74	1.73
430998	AF126847	Hs.204038	indolethylamine N-methyltransferase	2.74	2.85
426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.74	1.88
409196	NM_001874	Hs.334873	carboxypeptidase M	2.73	1.86
422389	AF240635	Hs.115897	protocadherin 12	2.72	2.26
444324	AI301330	Hs.143838	ESTs	2.72	1.74
417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	2.72	2.40
428769	AW207175	Hs.106771	ESTs	2.72	2.19
404277			NM_019111*:Homo sapiens major histocompa	2.72	3.12
409653	AW451693	Hs.220826	ESTs	2.72	2.62
437211	AA382207	Hs.5509	ecotropic viral integration site 2B	2.72	2.25
430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.72	2.09
444381	BE387335	Hs.283713	hypothetical protein BC014245	2.71	2.26
443547	AW271273		hypothetical protein FLJ12666	2.71	1.74
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.70	2.39
402674			Target Exon	2.70	1.95
438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.70	2.23
415075	L27479	Hs.77889	Friedreich ataxia region gene X123	2.69	2.11
444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.69	2.28
428656	AB037798	Hs.188790	KIAA1377 protein	2.68	1.91
418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.68	3.95
443951	F13272		ferritin, light polypeptide	2.68	2.66
427581	NM_014788	Hs.179703	KIAA0129 gene product	2.68	1.74
432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	2.68	1.78
446423	AW139655	Hs.150120	ESTs	2.68	2.29
407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.67	2.07
431779	AW971178	Hs.268571	apolipoprotein C-I	2.67	3.00
458124	AW005548	Hs.124590	ESTs	2.67	3.78
432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.66	1.64
445745	AB007924	Hs.13245	KIAA0455 gene product	2.66	1.64
425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.65	1.92
432231	AA339977	Hs.274127	CLST 11240 protein	2.64	4.23
442200	AW590572	Hs.235768	ESTs	2.64	2.46
426828	NM_000020	Hs.172670	activin A receptor type II-like 1	2.64	2.00
448569	BE382657	Hs.21486	signal transducer and activator of trans	2.63	3.23

425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.63	2.48
411213	AA676939	Hs.69285	neuropilin 1	2.62	1.73
439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.62	2.69
446570	AV659177	Hs.127160	ESTs	2.61	2.44
411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.60	3.39
434792	AA649253	Hs.132458	ESTs	2.60	1.74
426762	R14614	Hs.33846	ESTs	2.60	2.36
425371	D49441	Hs.155981	mesothelin	2.60	6.97
447720	AL038765	Hs.161304	ESTs	2.59	3.06
444623	AI183829	Hs.202111	ESTs	2.59	2.77
433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	2.58	2.01
444542	AI161293	Hs.280380	aminopeptidase	2.58	2.31
439549	AW937885	Hs.137314	ESTs	2.58	2.37
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.58	2.56
417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.56	2.47
433308	AA582718	Hs.291650	ESTs	2.56	2.01
443885	H91806	Hs.15284	ESTs	2.55	1.71
408170	AW204516	Hs.31835	ESTs	2.55	1.59
456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.54	1.63
412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.54	2.98
428791	AA435661	Hs.264750	ESTs	2.53	2.29
435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.53	3.91
447357	AI375922	Hs.159367	ESTs	2.52	2.83
431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.52	1.90
424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	2.52	3.45
408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.52	1.98
438698	AW297855		ESTs, Weakly similar to I38022 hypotheti	2.52	1.98
420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	2.52	2.41
424049	AB014524	Hs.138380	KIAA0624 protein	2.51	2.19
438543	AA810141	Hs.192182	ESTs	2.51	2.06
414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	2.51	2.14
424806	AA382523	Hs.105689	MSTP031 protein	2.51	2.11
438580	AA811262	Hs.299202	ESTs	2.50	1.83
434445	AI349306	Hs.11782	ESTs	2.50	3.13
444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.50	1.76
413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.50	2.00
421281	AI299139	Hs.17517	ESTs	2.50	2.40
441384	AA447849	Hs.288660	retinoic acid induced 3	2.50	2.75
436772	AW975688		metallothionein 1E (functional)	2.49	1.80
433102	AI343966	Hs.158528	ESTs	2.49	2.25
430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.48	2.09
445612	N94126	Hs.12969	hypothetical protein	2.48	2.28
445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	2.48	1.87
433854	AA610649	Hs.333239	ESTs	2.48	2.09
447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.48	2.75
411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.48	2.01
440594	AW445167	Hs.126036	ESTs	2.48	1.57
450295	AI766732	Hs.210628	ESTs	2.48	1.99
431316	AA502663	Hs.145037	ESTs	2.48	1.80
438564	AA381553	Hs.198253	major histocompatibility complex, class	2.48	2.80
439593	BE073597	Hs.124863	ESTs	2.48	1.89
422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	2.47	3.74
453134	AA032211	Hs.118493	ESTs	2.46	2.72
417169	R13550	Hs.21388	ESTs	2.46	1.88
434411	AA632649	Hs.201372	ESTs	2.46	1.95
440381	AA917808	Hs.190495	ESTs	2.46	2.09
448782	AL050295		KIAA0758 protein	2.46	2.69
404240			NM_018950:Homo sapiens major histocompat	2.45	2.83
450843	AI741483	Hs.205383	ESTs	2.44	2.25
434137	AA907734	Hs.124895	ESTs	2.44	2.55
438315	R56795	Hs.82419	ESTs	2.44	1.94
420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44	1.61
439402	W02753	Hs.103002	ESTs	2.44	1.90
445903	AI347487	Hs.132781	class I cytokine receptor	2.44	2.32
437323	AA371145	Hs.194397	leptin receptor	2.44	1.70
433923	AI823453	Hs.146625	ESTs	2.44	1.58
442201	AW516704	Hs.208726	ESTs	2.43	1.68
437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	2.43	3.22
452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.43	2.21
407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	2.43	2.13
406973	M34996	Hs.198253	major histocompatibility complex, class	2.43	2.68
428055	AA420564	Hs.101760	ESTs	2.42	2.05
428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	2.42	2.79
433138	AB029496	Hs.59729	semaphorin sem2	2.42	1.68
415757	AA830854	Hs.187810	ESTs	2.42	2.02
438507	AA809052		ESTs	2.42	2.08
450811	AI739486	Hs.245497	ESTs	2.42	1.97
424027	AW337575	Hs.201591	ESTs	2.42	2.76
423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.41	3.15
435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	2.41	2.08
426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	2.40	1.76
416370	N90470	Hs.203697	CD38 antigen (p45)	2.40	1.97
415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	2.40	1.63

445633	AI453386	Hs.17287	ESTs, Weakly similar to S26689 hypotheti	2.39	1.99
431300	AA502346		gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.39	1.79
407690	R47799	Hs.266957	hypothetical protein FLJ14281	2.39	1.84
418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.39	2.21
425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.38	2.09
451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.38	1.78
437479	R61866	Hs.101277	ESTs	2.38	3.00
445784	AI253155	Hs.146065	ESTs	2.38	1.61
418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	2.38	2.25
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.37	1.55
418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.37	2.41
416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	2.37	1.61
418262	Z38968		ESTs	2.37	2.05
420943	AI718702	Hs.279930	major histocompatibility complex, class	2.37	2.00
442762	AF035119	Hs.8700	deleted in liver cancer 1	2.37	2.05
429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.37	1.67
420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.36	1.88
420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	2.36	2.61
439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	2.36	2.84
427250	R35941	Hs.25418	ESTs	2.36	2.15
452194	AI694413		olfactory receptor, family 2, subfamily	2.36	3.41
411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	2.36	3.05
407242	M18728		gb:Human nonspecific crossreacting antig	2.35	2.34
418875	W19971	Hs.233459	ESTs	2.35	1.95
425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.35	1.85
432608	AI492660	Hs.170935	ESTs	2.35	2.06
408048	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2	2.35	1.91
415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.35	2.34
437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	2.35	2.13
410577	X91911	Hs.64639	glioma pathogenesis-related protein	2.34	1.73
422099	AA156022	Hs.111518	hypothetical protein	2.34	1.80
427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	2.34	2.24
427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.33	2.62
420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.32	2.52
431848	AI378857	Hs.271605	ESTs, Highly similar to AF175283 1 zinc	2.32	2.50
446354	AW449650		ESTs	2.32	2.21
423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.32	4.34
423961	D13666	Hs.136348	periostin(OSF-2os)	2.31	2.19
410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	2.31	2.34
457250	AA811987	Hs.125779	ESTs	2.31	1.66
446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	2.31	2.96
426839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	2.30	2.12
422746	NM_004484	Hs.119651	glypican 3	2.30	2.16
439920	H05430	Hs.288433	neurotrimin	2.30	4.06
414942	C14898	Hs.192986	ESTs	2.30	2.02
419092	J05581	Hs.89603	mucin 1, transmembrane	2.29	3.08
424878	H57111	Hs.221132	ESTs	2.29	1.84
406687	M31126		matrix metalloproteinase 11 (stromelysin	2.29	2.76
411605	AW006831		ESTs	2.29	1.58
416965	N26223	Hs.160436	ESTs	2.29	4.71
428713	AA432067		ESTs, Moderately similar to CYA4 RAT ADE	2.29	1.73
435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	2.28	1.90
420380	AA640891	Hs.102406	ESTs	2.28	2.82
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.28	1.52
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28	2.09
447160	AA330310	Hs.24181	ESTs	2.28	1.71
421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	2.27	1.98
453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	2.27	1.91
452114	N22687	Hs.8236	ESTs	2.27	1.88
417355	D13168	Hs.82002	endothelin receptor type B	2.26	1.63
434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.26	1.84
442262	BE170651	Hs.8700	deleted in liver cancer 1	2.26	1.86
426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.26	1.72
425354	U62027	Hs.155935	complement component 3a receptor 1	2.26	1.70
409190	AU076536	Hs.50984	sarcoma amplified sequence	2.26	1.56
414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.26	2.12
435272	AA906415	Hs.110041	ESTs	2.25	2.15
414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.24	3.58
424623	AW963062	Hs.270737	ESTs	2.24	1.87
424665	AW368576	Hs.139851	caveolin 2	2.24	2.15
422426	W79117	Hs.58559	ESTs	2.22	3.33
413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.22	2.39
427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.22	3.28
447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.22	1.59
446142	AI754693	Hs.145968	ESTs	2.22	1.88
410503	AW975746	Hs.188662	KIAA1702 protein	2.22	1.56
435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.22	2.49
437629	AW574774	Hs.121692	ESTs	2.22	1.70
429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	2.21	1.64
430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20	2.73
447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	2.20	2.58
429496	AA453800	Hs.192793	ESTs	2.20	2.97
425516	BE000707	Hs.29567	ESTs	2.20	1.58

422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.19	1.92
423526	AB011086	Hs.129739	KIAA0514 gene product	2.19	2.85
436485	X59135	Hs.156110	immunoglobulin kappa constant	2.19	2.01
426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.19	2.53
443441	AW291196	Hs.92195	ESTs	2.18	1.73
418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	2.18	2.53
408705	AA312135	Hs.46967	HSPCO34 protein	2.18	1.54
419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.18	1.93
430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GCB1 Homo sapiens	2.18	1.57
418791	AA935633	Hs.194628	ESTs	2.17	2.05
432620	AA777749	Hs.5978	LIM domain only 7	2.17	1.75
424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.17	2.01
406646	M33600	Hs.308026	major histocompatibility complex, class	2.17	3.12
424450	AL137526		dynein intermediate chain 2	2.17	4.14
426410	BE298446	Hs.305890	BCL2-like 1	2.16	2.19
416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.16	1.70
421077	AK000061	Hs.101590	hypothetical protein	2.16	1.60
424563	AA446932	Hs.151428	ret finger protein 2	2.16	1.83
405102			C15001220*:gi|4469558|gb|AAD21311.1| (AF	2.16	1.78
452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	2.15	1.87
416206	AW206248	Hs.111092	hypothetical protein FLJ22332	2.15	1.65
418067	AI127958	Hs.83393	cystatin E/M	2.15	2.40
436372	AW972301	Hs.310286	ESTs	2.15	2.35
418728	AW970937	Hs.293843	ESTs	2.14	2.58
450400	AI694722	Hs.279744	ESTs	2.14	2.06
409031	AA376836		ESTs	2.14	2.14
435143	R12375	Hs.194600	ESTs	2.14	1.69
444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	2.14	2.03
453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	2.14	1.57
418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	2.14	1.68
418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.14	2.04
408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.13	1.72
417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2.13	1.68
418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.13	2.47
452353	C18825	Hs.29191	epithelial membrane protein 2	2.12	2.31
418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.12	2.76
424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	2.12	2.11
437581	N59284	Hs.288010	ESTs	2.12	2.85
410976	R36207	Hs.25092	hypothetical protein MGC10744	2.12	2.04
429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.12	2.00
423069	W15613	Hs.1613	adenosine A2a receptor	2.12	1.72
432860	AW974077	Hs.283349	ESTs	2.12	1.75
449509	AA001615	Hs.84561	ESTs	2.12	1.84
456062	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.11	4.42
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.11	1.65
459680	H96982	Hs.42321	ESTs	2.11	2.20
449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.10	2.12
443071	AL080021	Hs.8986	complement component 1, q subcomponent,	2.10	2.48
443021	AA368546	Hs.8904	Ig superfamily protein	2.10	2.42
437838	AI307229		ESTs	2.10	1.67
429421	AL031658		Human DNA sequence from clone RP1-310O13	2.10	1.91
407202	N58172	Hs.109370	ESTs	2.10	1.68
443669	AI140462	Hs.134587	ESTs	2.10	1.64
411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	2.10	1.71
408410	AA447438	Hs.44697	ATPase, Class V, type 10C	2.10	2.05
436293	AI601188	Hs.120910	ESTs	2.10	2.01
410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	2.10	1.66
427876	AI494291		ESTs	2.10	2.48
456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.09	3.11
434987	AW975114		ESTs	2.09	1.69
433735	AA608955	Hs.109653	ESTs	2.09	1.78
433226	AW503733	Hs.9414	KIAA1488 protein	2.09	1.62
425787	AA363867	Hs.155029	ESTs	2.09	1.85
452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.08	3.41
442369	AI565071		ESTs	2.08	1.60
430478	NM_014349	Hs.241535	apolipoprotein L, 3	2.08	2.39
434421	AI915927	Hs.34771	ESTs	2.08	1.66
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.08	1.72
431728	NM_007351	Hs.268107	multimerin	2.08	1.51
444929	AI685841	Hs.161354	ESTs	2.08	3.14
408873	AL046017		calmodulin 2 (phosphorylase kinase, delt	2.08	2.09
437634	AW293046	Hs.255158	ESTs	2.08	1.66
400277			Eos Control	2.08	1.46
443601	AI078554	Hs.42658	ESTs	2.08	1.87
432212	AW137742		ESTs	2.08	2.84
410763	AF279145	Hs.8966	hypothetical protein FLJ21776	2.07	1.48
406122			Target Exon	2.06	2.75
430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	2.06	1.66
408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-102O5 from Y	2.06	1.70
421057	T58283		Homo sapiens cDNA: FLJ22063 fis, clone H	2.06	1.78
413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.06	2.30
431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	2.06	2.31
449444	AW818436		solute carrier family 16 (monocarboxylic	2.06	1.41

	421464	AA291553	Hs.190086	ESTs	2.06	2.61
	424831	H61453		ESTs	2.06	2.12
	434542	AA769310		hypothetical protein FLJ13164	2.06	1.44
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	2.05	2.61
5	418836	AI655499	Hs.161712	ESTs	2.05	1.73
	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	2.05	1.99
	400750			Target Exon	2.05	1.75
	406851	AA609784		major histocompatibility complex, class	2.05	3.94
	414936	C14774		gb:C14774 Clontech human aorta polyA mRN	2.05	2.41
10	453459	BE047032	Hs.257789	ESTs	2.04	1.86
	443450	N66045	Hs.133529	ESTs	2.04	2.46
	430015	AW768399		ESTs	2.04	1.63
	429399	AA452244	Hs.16727	ESTs	2.04	1.51
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	2.04	1.73
15	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.04	1.46
	421757	Z20897	Hs.296259	paraoxonase 3	2.04	2.13
	441942	AF182645	Hs.8024	IK cytokine, down-regulator of HLA II	2.04	1.82
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.04	1.67
	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	2.04	3.23
20	414154	AW205314	Hs.323060	ESTs	2.03	2.96
	449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	1.59
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.03	2.01
	406645	M57466	Hs.814	major histocompatibility complex, class	2.03	2.49
	414516	AI307802		ESTs, Weakly similar to T43458 hypotheti	2.02	1.56
25	417032	AA192469	Hs.271838	ESTs	2.02	1.48
	414875	H42679	Hs.77522	major histocompatibility complex, class	2.02	2.79
	414522	AW518944	Hs.76325	Immunoglobulin J chain	2.02	1.84
	410511	AA743475	Hs.285655	ESTs	2.02	1.87
	423533	NM_014339	Hs.129751	interleukin 17 receptor	2.02	2.26
30	437259	AI377755	Hs.120695	ESTs	2.02	2.34
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.02	1.86
	426722	U53823	Hs.171952	occludin	2.02	1.57
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.02	1.79
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.02	1.97
35	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	2.02	2.09
	449317	AW293413	Hs.132906	19A24 protein	2.02	1.84
	439556	AI623752	Hs.163603	ESTs	2.02	1.62
	443031	AW134696	Hs.49418	ESTs	2.01	1.58
	444838	AV651680	Hs.208558	ESTs	2.01	1.69
40	453108	AI311457	Hs.99472	ESTs	2.01	1.64
	432967	AA572949	Hs.207566	ESTs	2.01	1.83
	441390	AI692560	Hs.131175	ESTs	2.01	1.63
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.01	1.80
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.01	2.32
45	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.01	1.90
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.01	1.90
	415443	T07353	Hs.7948	ESTs	2.00	1.54
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	2.00	2.74
	404394			ENSP00000241075:TRRAP PROTEIN.	2.00	2.99
50	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	2.00	1.89
	437204	AL110216		ESTs, Weakly similar to I55214 salivary	2.00	1.46
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	2.00	1.37
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	2.00	1.51
	431193	AW749505	Hs.296770	KIAA1719 protein	1.99	2.01
55	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	1.99	2.11
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.98	1.79
	417072	BE243915	Hs.81118	leukotriene A4 hydrolase	1.98	2.47
	429073	AA446167	Hs.47385	ESTs	1.98	1.92
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.98	2.94
60	420838	AW118210	Hs.42321	ESTs	1.98	1.67
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	1.97	2.10
	430702	U56979	Hs.278568	H factor 1 (complement)	1.97	1.84
	456804	AI421645	Hs.139851	caveolin 2	1.97	1.58
	439195	H89360		gb:yw28d08.s1 Morton Fetal Cochlea Homo	1.97	1.93
65	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	1.97	2.28
	413836	W92003	Hs.70614	ESTs	1.97	1.80
	400417	X72475		Target	1.97	1.75
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regi	1.96	1.46
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.96	2.18
70	446135	AW130238	Hs.170318	hypothetical protein FLJ10147	1.96	2.06
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot	1.96	2.21
	414572	AU077174	Hs.288181	cathepsin H	1.96	2.65
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	1.95	1.71
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.95	2.88
75	451609	AL046019	Hs.209276	ESTs	1.94	3.26
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	1.94	2.94
	430887	N66801	Hs.260287	KIAA1841 protein	1.94	1.62
	414700	H63202	Hs.38163	ESTs	1.94	1.72
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	1.94	1.56
80	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	1.93	2.22
	425252	AW391162		calreticulin	1.92	2.14
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	1.92	2.19
	425810	AI923627	Hs.31903	ESTs	1.92	1.76

433618	AA602539	Hs.345494	ESTs	1.92	1.84
424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.92	2.27
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.92	1.76
450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	1.92	1.72
409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	1.91	1.83
426780	BE242284	Hs.172199	adenylate cyclase 7	1.91	1.67
452386	R12499	Hs.20468	ESTs	1.91	2.64
438670	AI275803	Hs.123428	ESTs	1.91	3.12
414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.91	1.82
446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.90	2.06
424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.90	1.85
444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	1.90	1.65
428166	AA423849	Hs.79530	M5-14 protein	1.90	1.70
426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	1.89	3.22
449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.07
436576	AI458213	Hs.77542	ESTs	1.88	2.25
437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.88	2.41
449618	AI076459	Hs.15978	KIAA1272 protein	1.88	1.63
430634	AI860651	Hs.26685	calcyphosine	1.88	3.01
440663	AW452976	Hs.247112	hypothetical protein FLJ10902	1.88	1.65
440099	AL080058	Hs.6909	DKFZP564G202 protein	1.88	1.78
414662	AL036058	Hs.76807	major histocompatibility complex, class	1.88	2.37
444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.87	2.07
414464	AI870175	Hs.13957	ESTs	1.87	2.68
427792	M63928	Hs.180841	tumor necrosis factor receptor superfami	1.87	2.25
415801	R24219	Hs.278443	Fc fragment of IgG, low affinity IIb, re	1.87	2.05
430027	AB023197	Hs.227743	KIAA0980 protein	1.87	1.70
425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.87	2.18
412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	1.86	2.27
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	1.86	2.31
420361	N92054	Hs.194718	zinc finger protein 265	1.86	1.63
413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.86	2.13
422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.85	1.77
442434	AA995787	Hs.129583	ESTs	1.85	2.15
422735	AA169685	Hs.119529	Niemann-Pick disease, type C2 gene	1.85	2.77
444083	AI123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.84	1.73
449679	AI823951	Hs.129700	tolloid-like 1	1.84	1.57
418183	NM_001772	Hs.83731	CD33 antigen (gp67)	1.84	2.02
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.84	1.72
414803	X03100	Hs.914	Human mRNA for SB class II histocompatibi	1.84	2.47
408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	1.84	2.29
455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.84	1.69
410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	1.83	2.12
426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.83	1.59
459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	1.83	1.57
417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	1.83	1.45
425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	1.83	2.18
429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	1.83	1.75
438596	AA829427	Hs.243081	ESTs	1.83	2.83
436486	AA742221	Hs.120633	ESTs	1.82	2.14
433365	AF026944	Hs.293797	ESTs	1.82	2.50
449943	AF104266	Hs.24212	latrophilin	1.82	2.08
426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.82	2.37
421563	NM_006433	Hs.105806	granulysin	1.82	2.48
449161	N53431	Hs.47647	ESTs, Weakly similar to T00057 hypotheti	1.81	2.81
453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.81	2.66
418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.81	2.50
432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.81	2.05
432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	1.80	3.13
428677	AI657119	Hs.120036	troponin I, cardiac	1.80	2.94
409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	1.80	2.28
423081	AF262992	Hs.123159	sperm associated antigen 4	1.80	1.56
425458	H89317	Hs.182889	ESTs	1.80	2.21
425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	1.80	1.41
409208	Y00093		integrin, alpha X (antigen CD11C (p150),	1.80	2.20
430570	AI417881	Hs.292464	ESTs	1.80	1.62
439425	AF086244	Hs.114659	ESTs	1.80	2.37
408688	AI634522	Hs.152925	KIAA1268 protein	1.80	2.13
440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	1.80	1.80
423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	1.79	1.57
406621	X57809	Hs.8997	immunoglobulin lambda locus	1.79	2.18
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.79	1.68
403421			NM_016369*:Homo sapiens claudin 18 (CLDN	1.79	2.47
430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical pro	1.79	2.92
416384	AU076903	Hs.79283	selectin P ligand	1.79	1.87
440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	1.78	1.69
422003	AA361760	Hs.296326	ESTs	1.78	2.05
412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140	1.77	1.82
432987	AI864771	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	1.77	2.03
441602	AI655043	Hs.133456	ESTs	1.77	2.01
458194	AW383618		ESTs, Moderately similar to ALU2_HUMAN A	1.76	2.35
432565	AA553477	Hs.152428	ESTs	1.76	2.63
421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHU1E collagen	1.75	2.59

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408989	AW361666	Hs.49500	KIAA0746 protein	1.75	1.66
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.75	1.54
403903			C5001632*:gi|10645308|gb|AAG21430.1|AC00	1.75	3.20
421461	AW291023		ESTs, Weakly similar to A46010 X-linked	1.74	2.67
430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	1.74	2.52
424377	AF081675	Hs.146322	killer cell lectin-like receptor subfami	1.74	2.15
443884	N20617	Hs.194397	leptin receptor	1.74	1.51
423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	1.74	1.63
448262	AW880830	Hs.186273	ESTs	1.73	2.57
431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.73	1.87
431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.73	2.21
412896	AW804157	Hs.308026	major histocompatibility complex, class	1.72	2.37
407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	1.72	2.16
419407	AW410377	Hs.41502	hypothetical protein FLJ21276	1.72	1.52
442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	1.71	1.55
438606	NM_014859	Hs.6336	KIAA0672 gene product	1.71	1.57
434795	BE620794	Hs.4147	translocating chain-associating membrane	1.71	2.21
426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	1.71	1.46
418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	1.71	2.49
421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	1.71	1.57
423857	N48902	Hs.133481	Homo sapiens mRNA; cDNA DKFZp564O0862 (f	1.71	1.56
408393	AW015318	Hs.23165	ESTs	1.70	1.43
432409	AA806538	Hs.130732	KIAA1575 protein	1.70	1.54
440817	AI341423	Hs.288433	neurotrimin	1.70	2.17
421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.69	2.54
453691	H12235	Hs.226505	ESTs	1.69	2.07
422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	1.68	1.54
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.68	2.29
434951	AF161442	Hs.191591	Homo sapiens HSPC324 mRNA, partial cds	1.68	2.24
444301	AK000136	Hs.10760	asporin (LRR class 1)	1.68	1.44
407775	NM_004914	Hs.38772	RAB36, member RAS oncogene family	1.68	2.03
437119	AI379921	Hs.177043	ESTs	1.68	4.21
426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.68	2.28
453498	BE181412	Hs.23245	hypothetical protein FLJ11767	1.68	2.76
428289	M26301	Hs.2253	complement component 2	1.67	2.40
404854			Target Exon	1.67	1.76
450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	1.67	2.32
410048	W76467	Hs.343874	proline oxidase homolog	1.67	3.03
407857	AI928445	Hs.92254	synaptotagmin-like 2	1.66	1.51
447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.66	2.01
417193	AI922189	Hs.288390	hypothetical protein FLJ22795	1.66	2.05
421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	1.66	2.20
433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, clone A	1.66	2.11
417451	AW007280	Hs.115537	putative dipeptidase	1.65	2.11
443791	N64458	Hs.143345	ESTs	1.65	2.11
440475	AI807671	Hs.24040	potassium channel, subfamily K, member 3	1.65	2.04
431743	AW972642	Hs.293055	ESTs	1.64	2.64
400328	X87344		transporter 2, ATP-binding cassette, sub	1.64	2.43
451876	T63141		gb:yb99a12.s1 Stratagene lung (937210) H	1.64	2.02
417321	N68722	Hs.191368	ESTs	1.64	2.53
439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.64	2.01
418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.63	2.17
432176	AW090386	Hs.112278	arrestin, beta 1	1.63	2.04
450708	AA376654		eukaryotic translation initiation factor	1.62	2.05
429570	BE242256	Hs.2441	KIAA0022 gene product	1.62	1.39
448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.62	1.57
439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	1.62	1.44
452424	AI964028	Hs.48353	ESTs	1.62	2.53
423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.62	1.38
416316	H58721	Hs.271628	ESTs	1.62	1.39
431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	1.62	2.67
452203	X57522		transporter 1, ATP-binding cassette, sub	1.62	2.45
427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a l	1.62	1.51
438089	W05391		nuclear receptor subfamily 1, group I, m	1.61	1.45
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.61	1.52
433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.61	2.40
444009	AI380792	Hs.135104	ESTs	1.60	2.15
436057	AJ004832	Hs.5038	neuropathy target esterase	1.60	2.60
437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.60	2.57
433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	1.60	3.30
410494	M36564	Hs.64016	protein S (alpha)	1.59	1.42
411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	1.59	2.02
446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.59	2.52
419918	X80700	Hs.93728	pre-B-cell leukemia transcription factor	1.59	2.04
428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	1.59	1.98
434308	N51517	Hs.47282	ESTs	1.58	2.29
447341	AF106941	Hs.18142	arrestin, beta 2	1.58	2.09
454315	AW373564	Hs.251928	BANP homolog, SMAR1 homolog	1.58	2.10
423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-	1.57	1.75
433671	AW138797	Hs.132906	19A24 protein	1.57	2.05
412869	AA290712	Hs.82407	CXC chemokine ligand 16	1.57	2.71
436906	H95990	Hs.181244	major histocompatibility complex, class	1.57	2.24
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.57	1.43

406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.57	2.37
406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.56	1.61
423329	AF054910	Hs.127111	tektin 2 (testicular)	1.56	2.51
424909	S78187	Hs.153752	cell division cycle 25B	1.55	2.00
431921	N46466	Hs.58879	ESTs	1.54	3.04
437400	AB011542	Hs.5599	EGF-like-domain, multiple 5	1.54	1.44
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	1.54	3.04
415078	AA311223	Hs.283091	found in inflammatory zone 3	1.53	2.61
417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.53	2.18
401854			Target Exon	1.53	2.08
406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.52	1.52
433815	AI696602	Hs.112757	ESTs	1.52	2.57
431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.52	1.36
453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	1.51	1.43
414763	U97276	Hs.77266	quiescin Q6	1.50	2.07
428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	1.50	1.46
412870	N22788	Hs.82407	CXC chemokine ligand 16	1.50	2.83
407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.50	2.04
432894	AW167668	Hs.279772	brain specific protein	1.50	2.25
457941	AI004525	Hs.14587	ESTs, Weakly similar to AF151859 1 CGI-1	1.49	2.22
442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_HUMAN MUCIN	1.49	2.09
419542	AA366037	Hs.90911	solute carrier family 16 (monocarboxylic	1.49	2.40
433124	U51712	Hs.13775	hypothetical protein SMAP31	1.49	1.39
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.49	1.39
429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.48	1.76
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.48	1.41
429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	1.48	1.44
409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.47	1.31
427872	AA835058		Human DNA sequence from clone RP1-261G23	1.47	2.50
449853	AF006823	Hs.24040	potassium channel, subfamily K, member 3	1.47	2.21
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	1.47	1.50
415149	X12451	Hs.78056	cathepsin L	1.46	1.84
447217	BE465754	Hs.17778	neuropilin 2	1.46	1.40
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.46	2.16
445672	AI907438	Hs.282862	ESTs	1.46	2.01
432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.46	2.10
458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	1.46	1.60
452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.45	1.40
419577	L36531	Hs.91296	integrin, alpha 8	1.45	1.40
439620	AA838727	Hs.124405	ESTs, Weakly similar to A46010 X-linked	1.45	1.57
423804	AW403448	Hs.16725	interferon-stimulated transcription fact	1.45	2.10
424658	NM_002406	Hs.151513	mannosyl (alpha-1,3-)-glycoprotein beta-	1.44	2.00
428494	AA233439	Hs.184634	hypothetical protein FLJ20005	1.44	1.45
431573	AW971070	Hs.291160	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.44	1.40
409524	AW402151	Hs.54673	tumor necrosis factor (ligand) superfami	1.43	2.01
406787	AW090702	Hs.240615	tubulin alpha 1	1.42	1.86
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.42	1.95
406422			Target Exon	1.41	2.02
421341	AJ243212		deleted in malignant brain tumors 1	1.41	1.47
421195	BE464560	Hs.133017	ESTs	1.41	2.42
425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	1.41	2.05
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.41	1.34
451220	AF124251	Hs.26054	novel SH2-containing protein 3	1.40	2.10
409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.40	3.64
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.40	3.24
432133	AB033088	Hs.272567	KIAA1262 protein	1.40	2.78
428833	AI928355		ESTs	1.40	2.02
455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.39	1.55
415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	1.39	2.09
427732	NM_002980	Hs.2199	secretin receptor	1.38	2.44
449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	1.38	1.85
407568	AA740964	Hs.62699	ESTs	1.38	3.13
422573	AW297985	Hs.295726	integrin, alpha V(vitronectin receptor	1.38	1.38
427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.37	1.12
457918	AL359590	Hs.162604	hypothetical protein DKFZp762M186	1.36	2.01
423696	Z92546	Hs.131819	Sushi domain (SCR repeat) containing	1.36	2.54
416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.36	2.04
407244	M10014		fibrinogen, gamma polypeptide	1.36	1.29
451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.35	1.34
406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	1.35	2.47
407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	1.34	1.66
445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	1.34	1.92
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	1.34	1.86
427507	AF240467	Hs.179152	toll-like receptor 7	1.34	2.11
446967	AI699629	Hs.156781	ESTs	1.34	3.75
436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.34	2.18
456637	AW161450	Hs.109201	CGI-86 protein	1.33	1.78
422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.33	1.95
417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.32	2.05
414849	AW372721	Hs.291623	ESTs, Weakly similar to unnamed protein	1.32	2.08
436986	AA740983	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.32	2.06
410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	1.32	2.08
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	1.31	1.29

429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	1.30	1.25
413474	T86312	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.30	1.92
406659	AA663985	Hs.277477	major histocompatibility complex, class	1.30	2.22
451049	AA013353		gb:ze28h10.s1 Soares retina N2b4HR Homo	1.30	2.12
436494	AA720997	Hs.128295	ESTs	1.29	2.30
438374	AA321866	Hs.6193	hypothetical protein FLJ14590	1.28	2.34
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	1.28	2.39
425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.28	1.69
428458	AA428820	Hs.251399	neurogranin (protein kinase C substrate,	1.27	2.00
443180	R15875	Hs.258576	claudin 12	1.26	1.25
421764	AI681535	Hs.148135	serine/threonine kinase 33	1.26	2.01
414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.26	1.21
433283	BE041135	Hs.175622	ESTs	1.24	3.05
426759	AI590401	Hs.21213	ESTs	1.23	1.20
436446	AW016809	Hs.119021	ESTs	1.23	1.20
421467	AA291590	Hs.97252	ESTs	1.22	1.54
431353	AA828032		ESTs	1.22	3.00
427403	AA402107	Hs.257146	ESTs, Moderately similar to I38022 hypot	1.22	1.91
453037	AA045175	Hs.17914	ESTs	1.22	2.40
437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.22	2.26
439941	AI392640	Hs.18272	amino acid transporter system A1	1.22	1.22
451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.21	1.49
400496			ENSP00000224716*:GTP-binding protein SAR	1.20	1.25
409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	1.20	1.44
407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.19	2.06
426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.18	2.02
445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2B (p1	1.17	1.14
439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	1.14	1.16
440555	D31292	Hs.6853	hypothetical protein FLJ22167	1.14	2.19
446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.13	1.12
432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.12	2.43
432798	AA565309	Hs.194015	ESTs	1.10	2.23
411274	NM_002776	Hs.69423	kallikrein 10	1.10	1.09
438856	N40027	Hs.7473	ESTs	1.09	1.52
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.09	1.07
448253	H25899	Hs.201591	ESTs	1.08	2.10
409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.08	2.08
409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.06	1.58
449321	AA001150	Hs.132937	ESTs	1.06	2.06
418693	AI750878	Hs.87409	thrombospondin 1	1.06	1.02
402333			Target Exon	1.03	1.03
421814	L12350	Hs.108623	thrombospondin 2	1.02	1.02
425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	2.36
458158	AW296778	Hs.144734	Human DNA sequence from clone RP3-416F21	1.00	2.73
406517			nel (chicken)-like 2	1.00	2.07
442526	AW277221		ESTs	1.00	2.21
446164	AW273539		hypothetical protein FLJ23577	1.00	2.52
449122	AI631310	Hs.196955	ESTs	1.00	2.23
438038	AI732629		ESTs, Weakly similar to TA2R HUMAN, BETA	1.00	2.04
429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	1.00	2.02
453672	U73531	Hs.34526	G protein-coupled receptor	1.00	2.57
436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	1.00	2.64
438909	AF085839		gb:Homo sapiens full length insert cDNA	1.00	2.23
423609	AA328348	Hs.218289	ESTs	1.00	2.19
419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	2.28
436284	AA708016	Hs.190389	ESTs	1.00	2.22
440932	AI801509	Hs.182080	ESTs	1.00	1.66
403420			Target Exon	1.00	1.86
431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	1.00	2.02
425916	NM_006786	Hs.162200	urotensin 2	1.00	2.11
419721	NM_001650		aquaporin 4	1.00	2.26
421761	AL120297	Hs.108043	Friend leukemia virus integration 1	1.00	1.86
425781	AF001622	Hs.159523	class-I MHC-restricted T cell associated	1.00	1.96
415094	D59513	Hs.330778	ESTs	1.00	2.32
434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	2.26
420727	H75701	Hs.99886	complement component 4-binding protein,	1.00	1.84
430049	AW277085	Hs.99619	ESTs	1.00	1.87
446868	AV660737		ESTs	1.00	1.79
418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	1.00	1.44
436391	AJ227892	Hs.146274	ESTs	1.00	1.30
413059	BE151498		gb:RC0-HT0295-291199-031-E11 HT0295 Homo	1.00	1.42
427739	AW196755	Hs.98105	NYD-SP14 protein	1.00	2.41
452788	AW294571	Hs.136040	ESTs	1.00	2.23

TABLE 32B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826

421798	3042_4	BC017829 AW276646 AI984209 AA663933 AA634104 AA551528 AA634041 AA298038 BG483990 T89297 BF853958 H64685 T90329 T60644 T57747 BF852694 T92529 BG482852 BF883064 BF883066 N74880 AA829796 N90716
400269	2726_1	X65018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 BI821373 BI770406 BI823937 BI820265 BI489632 BG482911 AA617783 AI807697 AW205576 T94427 AA487101 T94513 BI819407 BI822450 BI820618 BI824619 BG542824 BG537862
432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46187 BE929954 AA333976 D63102 BF744491
418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
422667	224778_1	AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848 AA398070 AI383375 AW511490
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
430709	1234627_1	AW969880 AA484613 AA501874 R34356
450726	666520_1	AI732297 AW204600 T95017
442048	750422_1	AW340495 AI984319 AA974603
406685	0_0	M18728
440028	598730_1	AW473675 AI190744 W69997 AW104913 AI221098 W69996 AA885487 AA861491
437866	34267_1	U52054 AL581000 AA156850 AW293839 BI335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960 AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AI866686 AI572124 AA687333 D20160 AA812489 AU185248 AU186004 AA156781 AI536733 BM144850 AI471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BI022546 BI021204
458332	1139685_1	AI000341 AI766341 AW873274
407192	2200202_1	AA602964 AA609200
449328	3030726_1	AI884781 AI652306 AI651694 AI638744 AI962493
432340	1619980_1	AA534222 AA632632 T81234
434194	62680_1	AF119847 AA437261 AA436987 AI132965
436198	28727_1	AK001125 AU120581 AU146612 AW301393
440248	2616908_1	AA876138 AI239602 AI698953
442006	1239046_1	AW975183 AA973583 AI365103 AI699495 AI301787
438177	9337_12	AK024965 AU158033 AA978370 R79120 BE327015 AA779740 R79121
435154	126605_1	AW972063 AA668764 AA804491 AW665588 AA765069
423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138
443547	137089_2	AV645808 AA701657 AW271273 AI796734 AI472316 AI017531 AI061178 BF109096 AA548964 N83805 AA131648 AA156589 BE708349 AW952494 D30877 AV684717 Z24837 F00167 BF576150 T63841 R78995 N87474
444314	1027984_1	AW749625 AW749626 AW749644 AI140497
443951	MH1768_18	AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N40935 W52768 AA854747 AA861945 AA878472 AA778270 W32249 AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520
432639	1237887_1	AW973785 H60163 AA557608
438698	598828_1	AW975851 AI911033 AI540093 AA932284 AW297855 AA829228 AA814442 AW105017
413638	1525406_1	H71252 BE154642 BE154668
436772	1239464_1	AA156151 Z25109 C05177 AW975688 AA731063 N67084
448782	34980_1	AB018301 AL050295 BF513128 AW385080 AL551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768 AI453845 AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099 AA995178 AW050649 AW026140 AI796309 AI584012 BE166666 AI767991 AI309041 AA724059 AI695284 AI245095 T63971 Z40627 BE166681 BG570071 BF921915 BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281 BG540263 BG538901 N95226 AI356752 AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361 N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285
438507	2729_4	BG698329 AI417878 AI080171 AI190332 AI092344 AI357100 AA744522 AA412653 AA977007 BF438628 AA743264 AA365279 AW073197 BI493198 AA169355 BI493197 AI283051 BF436642 AA809052 AI833263
415688	1235745_1	AW971218 AA493942 AA166963
431300	1529181_1	BE159863 AA502345 AU186097 R86267 H71358
418262	5824_2	AK055180 AA490810 AI420925 AI473832 AA127397 AA127409 AW820078 AI214567 AA876961 AA283985 AI904240 D20426 BC015835 N28408 Z42826 AI927925 AW590850 AW195543 AI675823 W84675 AA767204 AW207335 AI051690 AI434786 AI051699 AW139875 BF195790 AI250256 AI767042 AI521899 AA829382 AA526451 AI971192 R08173 N20059 AA215409 Z38968 H13200 H01182 R82482 AW972928 BF242637 H01273 H13567 R82532
452194	90339_1	AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 AI709339
446354	831448_1	AI701583 AI291038 AW449650
406687	0_0	M31126
411605	10026_3	BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA699780 T57386 BF903022 R09933 AA678298
428713	21322_7	AA432067 AW572442
414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
414991	1785136_1	D76831 C17898 D78863
447197	2176805_1	R36075 R36167 AI366546
430915	197844_1	BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
424450	1674_1	NM_023036 AJ295276 AF250288 AL137526 AW517074 AI870459 AI215420
409031	9531_1	BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258

			AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267364 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA326366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302
	418304	1093209_1	BE883520 BI057842 AA215702 AA215703 AA368006 BE006876 BE066555
	449677	79505_1	AA002232 T99209 AA002071
	437838	2512601_1	AI308202 AI307229 AA769348
	429421	117617_1	AW341668 AI201382 AW104364 AA648367 AA897604 AW977914 AA811957 AI352198 AL040620
	410730	114639_1	BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823
	427876	1373914_1	AI494291 AI582807 AA417018 AA608841
	434987	121985_1	AW975114 AI096634 AI767001 AA658364 AW517542
	442369	2691713_1	AA993566 AI521958 AI565071 AI864217
	408873	105337_1	AL046017 AW504804 AA532433 AI634701 AI126421 AW151275 AA620782 AA933047 AI828223 AI624555 AI624489 AV749032 BI495751 AI672286 AA342944 AV746076 AV747586 AA058597 H56073 W87367 R71630 H84499 AI866297 D25918 AV746788 N78995 H63752 H82985 R46600 BE786692 R71128 AA608909 R29728 BG534018
	400277	170_1	Y00281 NM_002950 BC010839 BC007995 BG675232 BM468552 AL555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656 AI371816 AA292474 AA375747 AA308414 BM454544 BI333370 BM049921 BI461428 BI465007 BI223401 BE856245 AW821164 BF914775 BF914761 AU125835 BI222678 BI091137 BF340536 BM462798 BI224452 BG707915 AL569160 AA443815 AW572867 AW363410 BF739268 BG010283 BI013120 BF818845 BF763468 AA305165 AI630370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587 BG166574 BI869342 BE562482 BE539637 AA165089 AL579118 AL553699 BE044054 AW117440 AI520674 BF435417 AW245648 AI952404 T29534 AU153459 AU152168 AW591591 AU146918 AI393187 AA478013 AU148143 AI224471 AI640728 AI871537 AW264752 N93787 AI189357 AV756134 AI471659 AU147466 AA779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 AI799771 F04407 AI285530 AI914643 AW068751 AA513325 AA164627 AA639285 AA569644 T96892 AI923594 BF439180 BI770936 BF032438 AU154884 AA682793 AW072992 AU158815 AI884444 AL048031 AU158922 AU152546 AI695187 AL048033 AI245650 AU148507 AW467451 BE536868 BF913001 BF062707 AL573082 AW067993 AA523354 BE886727 AI890705 AU159092 AI982693 AI817553 AA236729 AI687858 BG163767 AI524675 AI678155 AA127100 AI762661 AU159718 AI469720 AA483627 AW131696 R26868 AI199885 AW875614 AW938694 AW578974 BI763988 BG819168 BE874767 BG978292 BE162948 AL555483 AW189719 T56783 AI018819 AI476552 BI492837 AI824440 BG996262 AA932887 AI380726 R79530 AA622108 AI262575 T56782 R27437 BE784153 AW129549 AI675567 AI866759 BG987935
	432212	629625_1	AW972351 AW182936 AI478370 AA528309 BG997292 AW137742 AI632006 AA775020 AA961625 W86628 BF112014 AI275423 AI680786
	421057	265006_1	BE222349 AA830545 BF224127 H99396 N81017 N81016 AI525205 T58283
	449444	2735_1	U59185 NM_004696 AV734324 AI245349 AA369517 H88760 D79128 AA970406 H01059 H88761 H03446 BG620383 AU135008 AU136895 AU158158 AU155762 R73608 R65751 R23756 N74630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 BF382644 BG429539 BE929862 BF811258
	424831	1272834_1	H61453 AA838765 AI693104 AA721107
	434542	11990_1	AF392454 AK023074 AI884890 AI814455 AW966220 BF736545 AA026021 AA286843 AA251918 BG197710 AA026294 AA337356 BC010422 AK023226 NM_022776 BM459496 AA769310 AI826460 AU153650 AU160375 AW166211 AW292992 BF433538 AI823888 AI684798 AI655985 AW770982 AI400454 AI276257 AA639510 AI689818 AW772604 AA807639 AU130298 AU132028 BF900889 BF904822 AY007102 AU143256 BG621460 AA829630 AI864665 AI084922 AA025234 AI360060 AA766554 AA026295 AA825817 AA251762 BE180751 BM464530 AV715833 AA779447 AI452519 AW418525 AA435643 D25894 AA435651 AA286844 N64369 AI702262 BG288063 BE170545 BM466232 BE299160 AA169573 AL567428 BF217285 BE967276
	406851	0_0	AA609784 R97304
	414936	1782849_1	C14774 C17911 D79033
	430015	713_2	BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
	431843	445334_1	AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656
	414516	60847_1	AK057782 AI146454 BG703115 AI765980 AI948611 AA889263 AA947457 BG547193 H11947 Z38147 F10426 BF447329 H11946 T74968 F06195 BG548563 AI004988 AA148735 AI307802 AI439791 BE041453 AI984904 AA148734 F12823
	459557	859794_1	BG623239 N58315 AI524952
	437204	28243_1	AL110216 AI816283 AI688476 AA928351 AW157672 AI288740 BE468242 AI452476 AI291665 AW192364 BE503635 AW592672 AA857393 AW162770 AI680660 AI879565 AI347717 BF880800 AI266546 AA834381 AI291667 AI264567 Z38449 T03352 AI929432 BE673697 AI124770 AI350389 AA910378 R54042 AV746670 AW089037 AV729218 H28971 R38549 AI692560 BE671562 BE669916 BE672206 BF445152 BF445151 AI914323 AI684406 AA932348 BE670597 AA932080
	439195	21979_1	AF086037 H89360 H89546
	433891	647290_1	AW182329 AA613792 T05304 AW858385
	425252	38271_1	AK056513 AL553942 AL553941 BG924307 BE879339 AA576941 BG054674 BF431361 BE467806 BF445874 BE138798 AA425029 BF084265 BE814324 BM466426 BE819467 AW594593 AA341536 AI823511 BI792998 AW296213 AW800506 AW378236 BE819553 AW341342 BE146513 BE146525 BE146515 AW295699 BE146518 BE146516 BF349828 AL520587 AW803944 BE931092 BF375188 BG676709 BF832746 BG696737 AW391179 AI582980 AW582217 AW814484 BE672215 AW391162 AW814336 AW814302 AW814444 AL520586 AI333134 AI378333 AW243412 BE350482 AI628661 AI925481 AI246159 AW593633 AI273558 AI494388 AA806280 AW005606 BE048135 AW341024 AA969419 AA912778 AA621100 AA479920 AI867584 AI290391 BE348490 BF340755 AI225038 AI867592 BG113588 AI566808 AW196841 BF087184 AA353524 AW957546 BF340833 BF037221 BE146523
	409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
	437751	643238_1	AW978796 AA767373 AW173343 AA836163 N27563 AA905328 R97032

	444083	10908_12	BI836699 AI123195
	455508	1239880_1	AW976165 C04000
	417086	1154_2	AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176595 AA176955 AA194350 BC005933 BC017866 AA196396 Z24810 AA181361 AA193115 AA086465 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 AI620346 BG986374 BE706521 C02691 AL596834 F31902 F26078 AA670099 BF475555 F30818 F37524 AJ346558 F28050 F17933 F31637 C03413 AI092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546
	409208	10117_2	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946
	440638	371165_1	BG009500 AI376551 AA897445 T87714
	458194	506272_1	AI692525 AW005307 AW383618 AI689861 AI342712 AA906899
	421461	128918_1	AA291529 AI629027 AI890447 AA677465 BF001179 AI301102 AW452003 AA704419 AA706883 T68871 AW291023
	430850	296806_1	BE144152 AA487799 BF916865 AA937952
	400328		
	451876	2328579_1	T63141 AI821021 BF370092 BF370127 BF370060 T62998
	450708	12745_1	AK055196 AW952031 AI694545 AI742403 AW874431 AW204731 AI887383 BE220997 AA011287 AA115112 AI306385 AW571707 BF433009 AW197042 AI367086 H23002 H11743 R37085 Z39208 AI002267 H10206 T23948 W74801 R51633 R37677 R59986 H10833 BG012000 R13817 H22794 Z43122 H10257 BG984543 H10875 BG984542 AA318232 BF849799 W76367 AA376654 R18795 AA114979 AA303838 AW139819 AI674165 AI686172 W94102 R67170 H11820 BG015023
	452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
	438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701
	427872	4983_5	BI826340 BI868674 R12615 AW887767 BF439409 AI424995 BG059893 AA417003 AI220270 AA418740 AI190974 Z39070 AA742556 AA835058 AA694436 R20520 AA418795 BG460307 BI560147
	458208	45807_4	AI990640 AI380016 BM273298 BM273060
	421341	1407_1	NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492875 AI796676 AI749838 AA918144 AI814590 AI923531 BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985 AW612888 AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311
	411880	1139083_1	BE088101 T05990 AW872477
	428833	317753_1	AI928355 AI709178 AA436447 AI431274 BF946000
	455797	1511159_1	BE091833 BE091874 BE091871
	407244		
	451049	83923_1	W92422 AA013353
	431353	1241126_1	AW977507 AA503803 AA767137 AA828032 AA828033
	451385	85022_1	AA019761 AA017656 AA017374
	442526	450370_1	AF150283 AW182000 AW277221 AV735848
	446164	41648_2	AK026817 AI559708 AW273539 AW892986
	438038	2523501_1	AI732629 AI732831 AA776249
	438909	4045_1	AF085839 R59254 R69137 AW188788
	431169	1235760_1	AW971240 AA493723 AA493843
	419721	40816_1	AK026728 AL138136 BF059437 AI657037 AL600872 C15206 C14676 AA001003 AL157562 BG706081 H24162 BF841047 H15952 Z45355 AL157565 AV721762 AW953127 AA324171 BF476417 R52508 N54211 R46734 BG485659 BF810747 BE766227 AL538364 R19964 T15657 AW197333 R16235 R40826 BG152309 AV729035 R45066 AA016969 BE504976 BF593783 N51085 R61284 BE702264 AI216994 Z41068 N72577 R37645 AW237014 AW197630 AI359402 AA707906 AL119885 H23480 T16037 AI950756 T62597 T91664 R40195 D60186 H23014 T89715 H05749 H24054 AA001565 H15041 C15205 D59987 R13787 R61283 H23479 H07874 R14070 R52555 R21139 H05856 AA348655 AL120460 T62525 AV725241 AA046875 AI361912 H13341 BG150488 AL119338 Z42792 F05895 H07966 F06492 R59866 D31594 H09436 R35726 BI917845 BG704196 BF735198 AL036526 BG569879 AW195713 R59867 AA016968 H09087 BE841173 AW893631
	446868	15525_1	AK074473 BC017997 BI831060 BF971101 AI886394 AI082824 AV708785 W86073 W07772 AV660737 AI816793 R52250 BG183529 AA633473 AI191256 R44763 R19947 BF571346 W86257
	413059	1488711_1	BE063078 BE151503 BE151498

TABLE 32C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400880	9931121	Plus	29235-29336,36363-36580
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
406387	9256180	Plus	116229-116371,117512-117651
404277	1834458	Minus	91665-91946
402674	8077108	Minus	39290-39502
404240	5002624	Minus	116132-116407,116653-116922
405102	8076881	Minus	120922-121296
406122	9144087	Minus	30940-31386
400750	8119067	Plus	198991-199168,199316-199548
404394	3135305	Minus	37121-37205,37491-37762,41053-41140,4132
403421	9665041	Minus	126609-126773,139986-140205
403903	7710671	Minus	101165-102597
404854	7143420	Plus	14260-14537

401854	7770538	Plus	151483-151637,151902-152008,152146-15231
406422	9256411	Plus	163003-163311
400496	9743564	Plus	41515-41695
402333	8844110	Minus	165693-165856
406517	7711431	Plus	7151-7402
403420	9664969	Plus	159835-159938

TABLE 33A: About 800 genes upregulated in lung fibrosis relative to normal lung

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal lung AIs, where the minimum value for the numerator and denominator was set to 50

Pkey	ExAccn	UnigeneID	Unigene Title	R1
406964	M21305		FGENES predicted novel secreted protein	16.10
431089	BE041395		ESTs, Weakly similar to unknown protein	12.38
421110	AJ250717	Hs.1355	cathepsin E	11.86
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	11.62
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.90
444381	BE387335	Hs.283713	hypothetical protein BC014245	8.58
406850	AI624300	Hs.172928	collagen, type I, alpha 1	8.26
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	8.24
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.72
408380	AF123050	Hs.44532	diubiquitin	7.24
432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	7.15
456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	7.12
453355	AW295374	Hs.31412	myopodin	6.96
408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.83
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.72
407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	6.72
438089	W05391		nuclear receptor subfamily 1, group I, m	6.62
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56
421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46
417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	6.32
439195	H89360		gb:yw28d08.s1 Morton Fetal Cochlea Homo	6.29
444301	AK000136	Hs.10760	asporin (LRR class 1)	6.28
414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	6.13
423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	6.11
430702	U56979	Hs.278568	H factor 1 (complement)	6.10
424878	H57111	Hs.221132	ESTs	6.00
417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	6.00
414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.94
408491	AI088063	Hs.7882	ESTs	5.94
419407	AW410377	Hs.41502	hypothetical protein FLJ21276	5.92
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	5.92
407857	AI928445	Hs.92254	synaptotagmin-like 2	5.90
433230	AW136134	Hs.220277	ESTs	5.86
412719	AW016610	Hs.816	ESTs	5.86
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.82
426759	AI590401	Hs.21213	ESTs	5.72
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72
421814	L12350	Hs.108623	thrombospondin 2	5.71
430887	N66801	Hs.260287	KIAA1841 protein	5.70
453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	5.62
436954	AA740151	Hs.130425	ESTs	5.58
411573	AB029000	Hs.70823	KIAA1077 protein	5.55
432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38
410606	AW418779	Hs.114889	ESTs	5.38
410800	BE280421	Hs.94499	ESTs	5.32
413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	5.28
406687	M31126		matrix metalloproteinase 11 (stromelysin	5.26
417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	5.22
412622	AW664708	Hs.171959	ESTs	5.22
439941	AI392640	Hs.18272	amino acid transporter system A1	5.18
440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	5.15
430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	5.13
425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	5.12
444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	5.11
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04
452239	AW379378		protein tyrosine phosphatase, receptor t	4.97
453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	4.96
443884	N20617	Hs.194397	leptin receptor	4.94
444040	AF204231	Hs.182982	golgin-67	4.94
428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	4.93
440687	AL080222	Hs.7358	hypothetical protein FLJ13110	4.92
420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	4.92
432435	BE218886	Hs.282070	ESTs	4.92

	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	4.90
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	4.90
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.90
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	4.82
5	430027	AB023197	Hs.227743	KIAA0980 protein	4.78
	408393	AW015318	Hs.23165	ESTs	4.76
	449509	AA001615	Hs.84561	ESTs	4.72
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	4.72
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	4.72
10	433226	AW503733	Hs.9414	KIAA1488 protein	4.68
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	4.68
	442994	AI026718	Hs.16954	ESTs	4.66
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.66
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.66
15	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	4.65
	433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	4.64
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	4.64
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.62
20	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	4.62
	450086	AW016343	Hs.233301	ESTs	4.61
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	4.60
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	4.59
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.58
25	418259	AA215404		ESTs	4.54
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.54
	432810	AA863400		ESTs	4.54
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.53
	436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.52
30	412652	AI801777		ESTs	4.52
	438899	AF085833	Hs.135624	ESTs	4.52
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	4.52
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	4.52
	443324	R44013	Hs.164225	ESTs	4.51
35	407690	R47799	Hs.266957	hypothetical protein FLJ14281	4.51
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.51
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	4.50
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	4.50
	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	4.46
40	452561	AI692181	Hs.49169	KIAA1634 protein	4.46
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	4.45
	442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	4.44
	436120	AI248193	Hs.119860	ESTs	4.44
	423575	C18863	Hs.163443	intron of periostin (OSF-2os)	4.44
45	429697	AW296451	Hs.24605	ESTs	4.44
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	4.43
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	4.43
	414452	BE622743	Hs.301064	arfaptin 1	4.42
	428698	AA852773	Hs.334838	KIAA1866 protein	4.42
50	420838	AW118210	Hs.42321	ESTs	4.41
	458584	AF217518	Hs.8360	PTD012 protein	4.40
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	4.40
	400076			Eos Control	4.38
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	4.38
55	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (f	4.36
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.36
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.36
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.34
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.34
60	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4.33
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	4.33
	429228	AI553633		ESTs	4.32
	426458	D83032	Hs.169984	nuclear protein	4.30
	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30
65	432476	T94344	Hs.326263	ESTs	4.29
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.28
	436446	AW016809	Hs.119021	ESTs	4.27
	439556	AI623752	Hs.163603	ESTs	4.26
	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-li	4.26
70	428411	AW291464	Hs.10338	ESTs	4.26
	434936	AI285970	Hs.183817	ESTs	4.23
	413048	M93221	Hs.75182	mannose receptor, C type 1	4.23
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.22
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	4.22
75	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	4.22
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.21
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	4.20
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.20
	423578	AW960454	Hs.222830	ESTs	4.20
80	446608	N75217	Hs.257846	ESTs	4.20
	424238	AA337401	Hs.137635	ESTs	4.19
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	4.18
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.18

	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18
	439593	BE073597	Hs.124863	ESTs	4.17
	442369	AI565071		ESTs	4.16
	445885	AI734009	Hs.127699	KIAA1603 protein	4.16
5	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.16
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	4.15
	407347	AA829847		gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens	4.14
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.13
10	430168	AW968343	Hs.145582	DKFZP434I1735 protein	4.12
	451184	T87943		transcription factor 7-like 2 (T-cell sp	4.12
	426174	AA547959	Hs.115838	ESTs	4.12
	431562	AI884334	Hs.11637	ESTs	4.12
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.12
15	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12
	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	4.12
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	4.10
	444020	R92962	Hs.35052	ESTs	4.10
	439424	AI478667	Hs.118183	hypothetical protein FLJ22833	4.10
20	416987	D86957	Hs.80712	KIAA0202 protein	4.10
	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	4.09
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	4.09
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.08
	431193	AW749505	Hs.296770	KIAA1719 protein	4.08
25	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.08
	433308	AA582718	Hs.291650	ESTs	4.08
	445756	AA290690	Hs.300776	ESTs	4.08
	431745	AW972448	Hs.163425	ESTs	4.08
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	4.07
30	440099	AL080058	Hs.6909	DKFZP564G202 protein	4.06
	439398	AA284267	Hs.221504	ESTs	4.06
	432731	R31178	Hs.287820	fibronectin 1	4.06
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	4.05
	433626	AF078859	Hs.86347	hypothetical protein	4.05
35	428055	AA420564	Hs.101760	ESTs	4.04
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04
	413243	AA769266	Hs.193657	ESTs	4.02
	431214	AA294921	Hs.348024	v-ral simian leukemia viral oncogene hom	4.02
	453753	BE252983	Hs.35086	ubiquitin specific protease 1	4.02
40	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	4.02
	434404	AW445034	Hs.256578	ESTs	4.02
	407604	AW191962		collagen, type VIII, alpha 2	4.02
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.02
	436772	AW975688		metallothionein 1E (functional)	4.00
45	443257	AI334040	Hs.11614	HSPC065 protein	4.00
	450187	AA736788	Hs.78521	KIAA1717 protein	3.98
	433913	AI694106	Hs.72325	ESTs, Weakly similar to I38022 hypotheti	3.98
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	3.98
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	3.98
50	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.98
	426818	AA554827	Hs.292996	DKFZp434A0131 protein	3.98
	440118	AB040893	Hs.6968	KIAA1460 protein	3.98
	413836	W92003	Hs.70614	ESTs	3.97
	442647	AL038436	Hs.31388	ESTs	3.96
55	449188	AW072939	Hs.347187	myotubularin related protein 1	3.96
	450656	AA010539	Hs.18912	ESTs	3.96
	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	3.94
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94
	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	3.94
60	407879	AA045464	Hs.6557	zinc finger protein 161	3.93
	438146	Z36842	Hs.57548	ESTs	3.93
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.93
	429355	AW973253	Hs.292689	ESTs	3.92
	437210	AA311443	Hs.293563	Homo sapiens mRNA; cDNA DKFZp586E2317 (f	3.92
65	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	3.92
	452416	AA026115	Hs.114777	ESTs	3.92
	413873	AI310151	Hs.173524	ESTs	3.91
	400196			Eos Control	3.91
	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.90
70	453204	R10799	Hs.191990	ESTs	3.90
	454076	AW204712	Hs.61957	ESTs	3.90
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.90
	437158	AW090198		KIAA1150 protein	3.90
	443970	AI280341	Hs.166571	ESTs	3.90
75	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	3.90
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.90
	444057	AA316896	Hs.257267	FYVE and coiled-coil domain containing 1	3.89
	411495	AP000693	Hs.70359	KIAA0136 protein	3.88
	438452	AI220911	Hs.288959	hypothetical protein FLJ20920	3.88
80	410297	AA148710		lumican	3.88
	427698	AW972594	Hs.335499	ESTs	3.88
	436769	AA748675		ESTs	3.86
	417819	AI253112	Hs.133540	ESTs	3.86

445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	3.86
425838	NM_014071	Hs.159613	nuclear receptor coactivator RAP250; per	3.86
422173	BE385828	Hs.250619	phorbolin-like protein MDS019 (CEM15)	3.86
428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell	3.85
445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	3.85
432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	3.85
412636	NM_004415		desmoplakin (DPI, DPII)	3.84
436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	3.84
418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	3.84
436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypotheti	3.84
430317	AB020645	Hs.239189	glutaminase	3.84
442806	AW294522	Hs.149991	ESTs	3.84
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.82
430512	AF182294	Hs.241578	U5 snRNA-associated Sm-like protein LSm8	3.82
427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.82
430573	AA744550	Hs.136345	ESTs	3.82
453394	AW960474	Hs.40289	ESTs	3.81
431266	AW149321	Hs.105411	ESTs	3.80
434987	AW975114		ESTs	3.80
452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	3.79
435176	AA744875	Hs.189413	ESTs	3.78
437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	3.77
430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.77
427157	U51166	Hs.173824	thymine-DNA glycosylase	3.76
441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	3.76
417228	AL134324	Hs.7312	ESTs	3.76
416546	AA224827		gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	3.76
450779	AW204145	Hs.156044	ESTs	3.75
412408	D51103	Hs.73851	ATP synthase, H transporting, mitochondr	3.75
443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	3.75
414812	X72755	Hs.77367	monokine induced by gamma interferon	3.75
429494	AA769365	Hs.126058	ESTs	3.75
447118	AB014599	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro	3.75
408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	3.74
419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	3.74
448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	3.74
436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74
421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.73
414863	AA926960		CDC28 protein kinase 1	3.72
416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.72
452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	3.72
444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	3.72
438607	AW080237	Hs.252884	ESTs	3.72
408221	AA912183	Hs.47447	ESTs	3.72
418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.70
419900	AI469960	Hs.170698	ESTs	3.70
446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	3.70
446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	3.70
448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.70
413283	R78669	Hs.23756	hypothetical protein similar to swine ac	3.70
447846	AA324057	Hs.77955	Homo sapiens cDNA: FLJ23527 fis, clone L	3.70
436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	3.70
418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.69
408495	W68796	Hs.237731	ESTs	3.69
424452	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	3.68
448479	H96115	Hs.21293	UDP-N-acteylglucosamine pyrophosphorylas	3.68
431974	AW972689	Hs.200934	ESTs	3.68
416354	NM_000633	Hs.79241	B-cell CLL/lymphoma 2 (BCL2)	3.68
417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68
413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	3.67
416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	3.67
419111	AA234172	Hs.137418	ESTs	3.67
423979	AF229181	Hs.136644	CS box-containing WD protein	3.66
418875	W19971	Hs.233459	ESTs	3.66
451690	AW451469	Hs.209990	ESTs	3.66
423032	AI684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.66
414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.66
428347	AI264161	Hs.183773	golgi autoantigen, golgin subfamily a, 4	3.66
426779	AA384577	Hs.93714	ESTs, Weakly similar to T00365 hypotheti	3.66
435335	AI693150	Hs.137928	ESTs	3.66
410577	X91911	Hs.64639	glioma pathogenesis-related protein	3.66
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	3.65
429105	D87077	Hs.196275	KIAA0240 protein	3.64
407813	AL120247	Hs.40109	KIAA0872 protein	3.64
425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	3.64
451678	AA374181	Hs.26799	DKFZP564D0764 protein	3.64
452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.64
452408	AA306477	Hs.29379	hypothetical protein FLJ10687	3.64
441466	AW673081	Hs.54828	ESTs	3.63
414013	AA766605	Hs.47099	hypothetical protein FLJ21212	3.62
420056	AW043684	Hs.99804	ESTs	3.62
424886	H88584	Hs.96900	hypothetical protein; KIAA1830 protein	3.62
431774	BE348813	Hs.268561	hypothetical protein FLJ10726	3.62

	435990	AI015862	Hs.131793	ESTs	3.62
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	3.62
	414715	AA587891	Hs.904	amylo-1,6-glucosidase, 4-alpha-glucanotr	3.62
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	3.62
5	417008	AA191708	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	3.62
	413823	AI341417	Hs.29406	ESTs	3.61
	435354	AA678267	Hs.117115	ESTs	3.60
	427832	AF038362	Hs.180930	TBP-associated factor 172	3.60
	427846	AW499770	Hs.180948	KIAA0729 protein	3.60
10	426116	AA868729	Hs.144694	ESTs	3.60
	457635	AV660976	Hs.3569	hypothetical protein	3.60
	443998	AI620661	Hs.296276	ESTs	3.60
	417867	AW952547	Hs.194603	ESTs, Moderately similar to I38022 hypot	3.58
	418182	AW016405	Hs.16648	ESTs	3.58
15	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	3.58
	424831	H61453		ESTs	3.58
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.58
	421823	N40850	Hs.28625	ESTs	3.58
	414781	D50917	Hs.77293	KIAA0127 gene product	3.57
20	427393	AB029018	Hs.177635	KIAA1095 protein	3.57
	415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.56
	425465	L18964	Hs.1904	protein kinase C, iota	3.56
	417124	BE122762	Hs.25338	ESTs	3.56
	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	3.56
25	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	3.55
	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.55
	410390	AA876905	Hs.125286	ESTs	3.54
	442073	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase	3.54
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	3.54
30	441499	AW298235	Hs.101689	ESTs	3.54
	453256	AI565587	Hs.32556	KIAA0379 protein	3.54
	414142	AW368397	Hs.334485	hemicentin (fibulin 6)	3.54
	438023	AF204883	Hs.6048	FEM-1 (C.elegans) homolog b	3.54
	412245	AI952669	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.54
35	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.53
	446682	AW205632	Hs.211198	ESTs	3.52
	431392	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	3.52
	433430	AI863735		ESTs	3.52
	420394	AB023161	Hs.97403	KIAA0944 protein	3.52
40	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.52
	443547	AW271273		hypothetical protein FLJ12666	3.52
	420676	AI434780	Hs.4248	vav 2 oncogene	3.51
	410690	AA322979	Hs.130266	ESTs	3.50
	459645	AA074346		ESTs	3.50
45	401403			Target Exon	3.50
	451166	T98171	Hs.185675	ESTs	3.50
	418836	AI655499	Hs.161712	ESTs	3.50
	421462	AF016495	Hs.104624	aquaporin 9	3.50
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	3.50
50	432401	NM_013330	Hs.274479	NME7	3.49
	408392	U28831	Hs.44566	KIAA1641 protein	3.49
	425836	AW955696	Hs.90960	ESTs	3.48
	452327	AK000196	Hs.29052	hypothetical protein FLJ20189	3.48
	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.48
55	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	3.48
	422960	AW890487		cadherin 13, H-cadherin (heart)	3.48
	430570	AI417881	Hs.292464	ESTs	3.48
	406387			Target Exon	3.47
	416585	X54162	Hs.79386	telomodin 1, smooth muscle (LMOD1) (Thy	3.46
60	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.46
	412240	H72176		hypothetical protein FLJ13159	3.46
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.46
	443634	H73972	Hs.134460	ESTs	3.46
	422963	M79141	Hs.13234	ESTs	3.46
65	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.46
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	3.46
	425100	AF051850	Hs.154567	supervillin	3.45
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.45
	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	3.44
70	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	3.44
	447764	NM_003776	Hs.19500	nuclear localization signal deleted in v	3.44
	411251	R19774	Hs.22835	HHGP protein	3.44
	432648	AA557952		gb:nl17c05.s1 NCI_CGAP_HSC1 Homo sapiens	3.44
	428708	NM_014897	Hs.190386	KIAA0924 protein	3.44
75	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	3.43
	451743	AW074266	Hs.23071	ESTs	3.42
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	3.42
	448705	H05072	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	3.42
	414489	AI620677	Hs.73105	ESTs	3.42
80	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.41
	435841	R28522	Hs.186937	ESTs	3.41
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	3.40
	451198	AW964541		hypothetical protein FLJ21127	3.40

	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	3.40
	436023	T81819	Hs.302251	ESTs	3.40
	449656	AA002008	Hs.188633	ESTs	3.40
5	437739	AW579216	Hs.264610	ESTs, Moderately similar to Ibd1 [H.sapi	3.40
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	3.40
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	3.40
	456505	AA504595		ESTs	3.40
	439867	AA847510	Hs.161292	ESTs	3.40
	442113	BE622187		ESTs, Weakly similar to I38022 hypotheti	3.40
10	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40
	421263	AB020638	Hs.103000	KIAA0831 protein	3.40
	410300	AW903988	Hs.62119	hypothetical protein FLJ14800	3.40
	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.39
15	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	3.39
	432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN !!!!	3.38
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	3.38
	428412	AA428240	Hs.126083	ESTs	3.38
	448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.38
20	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.38
	413714	AI560944	Hs.71428	ESTs	3.38
	415663	AW296841	Hs.313332	ESTs	3.38
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	3.37
	421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.37
25	440214	AA247118	Hs.7049	hypothetical protein FLJ11305	3.37
	440980	AL042005	Hs.1117	tripeptidyl peptidase II	3.36
	411975	AI916058	Hs.144583	ESTs	3.36
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36
	414783	AW069569		unactive progesterone receptor, 23 kD	3.36
30	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.36
	411213	AA676939	Hs.69285	neuropilin 1	3.36
	420613	AI873871	Hs.7041	ESTs, Weakly similar to A47582 B-cell gr	3.35
	417534	NM_004998	Hs.82251	myosin IE	3.35
35	431698	AI492369		ESTs	3.35
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.35
	441623	AA315805		desmoglein 2	3.34
	420729	AW964897	Hs.290825	ESTs	3.34
	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	3.34
40	448369	AW268962	Hs.111335	ESTs	3.34
	452820	N46161	Hs.35274	ESTs	3.34
	453271	AA903424	Hs.6786	ESTs	3.34
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.34
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.34
45	443291	AA325633	Hs.136102	KIAA0853 protein	3.33
	418720	AI381687	Hs.39526	ESTs	3.33
	452107	AB020681	Hs.27973	KIAA0874 protein	3.33
	439943	AW083789	Hs.124620	ESTs	3.33
	433282	BE539101		hypothetical protein	3.33
50	410344	AW978436	Hs.62515	KIAA0494 gene product	3.33
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	3.32
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.32
	434210	AA665612		ESTs	3.32
	431923	AI741770	Hs.292690	ESTs, Weakly similar to I38022 hypotheti	3.32
55	453199	AI336266	Hs.32353	mitogen-activated protein kinase kinase	3.32
	419534	AA443691	Hs.90858	Homo sapiens clone 25023 mRNA sequence	3.32
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	3.32
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	3.32
	422092	AB007883	Hs.111373	KIAA0423 protein	3.32
60	412262	W26406		seven in absentia (Drosophila) homolog 1	3.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.32
	446094	AK001760	Hs.13801	KIAA1685 protein	3.32
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.32
	420339	AW968259	Hs.186647	ESTs	3.31
65	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.31
	432331	W37862	Hs.274368	MSTP032 protein	3.31
	433697	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.31
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	3.31
	430950	AA489525		ESTs	3.30
70	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	3.30
	417958	AA767382	Hs.193417	ESTs	3.30
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.30
	419543	AA244170		gb:nc05h02.s1 NCI_CGAP_Pr1 Homo sapiens	3.30
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30
75	452039	AI922988	Hs.172510	ESTs	3.30
	443798	R07848	Hs.188522	ESTs	3.29
	449378	AW664026	Hs.59892	ESTs	3.29
	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	3.28
	420126	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	3.28
80	444291	AI598022	Hs.193989	TAR DNA binding protein	3.28
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	3.28
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28

	425657	T89839	Hs.119471	ESTs	3.28
	406672	M26041	Hs.198253	major histocompatibility complex, class	3.28
	419905	AW248229	Hs.93659	protein disulfide isomerase related prot	3.27
	425332	AA633306	Hs.127279	ESTs	3.27
5	418529	AW005695	Hs.250897	TRK-fused gene	3.27
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.27
	433618	AA602539	Hs.345494	ESTs	3.27
	408630	AA748009	Hs.173328	ESTs	3.26
	415914	AA306033	Hs.78915	GA-binding protein transcription factor,	3.26
10	415102	M31899	Hs.77929	excision repair cross-complementing rode	3.26
	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	3.26
	429493	AL134708	Hs.145998	ESTs	3.26
	445860	AA332145	Hs.13392	tethering factor SEC34	3.26
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	3.26
15	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.26
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	3.26
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.26
	436758	AW977167	Hs.155272	ESTs	3.26
	438011	BE466173	Hs.145696	splicing factor (CC1.3)	3.26
20	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	3.25
	426860	U04953	Hs.172801	isoleucine-tRNA synthetase	3.25
	437830	AB020658	Hs.5867	KIAA0851 protein; suppressor of actin 1	3.25
	453368	W20296	Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HE	3.25
	409939	AA463437	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	3.25
25	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	3.24
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	3.24
	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	3.24
	414405	AI362533		KIAA0306 protein	3.24
	445893	AI610702	Hs.202613	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.24
30	434423	NM_006769	Hs.3844	LIM domain only 4	3.24
	408951	AW407227	Hs.227591	hypothetical protein FLJ11088	3.24
	408949	AF189011	Hs.49163	putative ribonuclease III	3.24
	410337	M83822	Hs.62354	cell division cycle 4-like	3.24
	409010	AI648675		Homo sapiens, Similar to RIKEN cDNA 1700	3.24
35	400419	AF084545		Target	3.24
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.24
	422461	NM_003417	Hs.117077	zinc finger protein 264	3.24
	441604	AI683049	Hs.201282	ESTs	3.24
	411960	R77776	Hs.18103	ESTs	3.23
40	414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	3.23
	430522	N75750	Hs.242271	KIAA0471 gene product	3.23
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23
	405268			ENSP00000223174*:KIAA0783 PROTEIN.	3.23
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.22
45	427196	AW967522	Hs.191593	ESTs	3.22
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	3.22
	417727	AL133623	Hs.82501	similar to mouse Xrn1 / Dhm2 protein	3.22
	410853	H04588	Hs.30469	ESTs	3.22
	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	3.22
50	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22
	427480	BE148769	Hs.334477	hypothetical protein FLJ11328	3.22
	444623	AI183829	Hs.202111	ESTs	3.21
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	3.21
55	435874	AA868688	Hs.93102	ESTs	3.20
	443801	AW206942	Hs.253594	intron of: trichorhinophalangeal syndro	3.20
	434982	AW975084		gb:EST387190 MAGE resequences, MAGN Homo	3.20
	430929	AA489166	Hs.156933	ESTs	3.20
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced transl	3.20
60	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	3.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20
	451119	AA805417	Hs.64753	ESTs	3.20
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	3.20
	432676	AI187366		gb:qf29c01.x1 Soares_testis_NHT Homo sap	3.19
65	428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.19
	422040	AA172106	Hs.110950	Rag C protein	3.18
	437838	AI307229		ESTs	3.18
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (defline not ava	3.18
	420789	AI670057	Hs.199882	ESTs	3.18
70	419135	R61448	Hs.106728	ESTs, Weakly similar to KIAA1353 protein	3.18
	446019	AI362520		histone deacetylase 3	3.18
	430848	AW021726	Hs.345490	gb:df27e02.y1 Morton Fetal Cochlea Homo	3.18
	425375	AA631977	Hs.155995	KIAA0643 protein	3.18
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.18
75	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18
	453111	AB014598	Hs.31720	hephaestin	3.18
	454042	H22570		hypothetical protein FLJ20093	3.18
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.18
	447183	AI554733	Hs.173182	ESTs	3.18
80	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.18
	431831	AW023204	Hs.302743	ESTs	3.18
	420664	AI681270	Hs.99824	BCE-1 protein	3.18
	451582	AI963026	Hs.289958	ESTs, Weakly similar to putative p150 [H	3.17

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	432954	AI076345		ESTs	3.17
	444990	AI912410	Hs.27475	Homo sapiens cDNA FLJ12749 fis, clone NT	3.17
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	3.17
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.17
5	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.17
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.16
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.16
	420623	BE245485	Hs.99437	Homo sapiens mRNA; cDNA DKFZp586G1924 (f	3.16
	451475	T19093	Hs.26450	KIAA0725 protein	3.16
10	452066	AA772149	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p	3.16
	429556	AW139399	Hs.98988	ESTs	3.16
	448514	AB020626	Hs.301866	KIAA0819 protein	3.16
	443732	AI188803	Hs.153944	ESTs	3.16
	436805	AA731533	Hs.270751	ESTs	3.16
15	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	3.16
	417511	AL049176	Hs.82223	chordin-like	3.16
	423595	R82626	Hs.220702	ESTs	3.16
	445837	AI261700	Hs.145544	ESTs	3.16
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	3.16
20	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16
	414183	AW957446	Hs.301711	ESTs	3.16
	433194	AB040883	Hs.83243	KIAA1450 protein	3.16
	453915	AA588721	Hs.286218	ribosomal protein L44	3.15
	407725	BE388094	Hs.21857	ESTs	3.15
25	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.14
	440937	AF202724	Hs.7531	KIAA0810 protein	3.14
	449057	AB037784	Hs.22941	KIAA1363 protein	3.14
	446126	AW085909		pleckstrin homology domain interacting p	3.14
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.14
30	419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	3.14
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	3.14
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	3.14
	437296	AA350994	Hs.20261	KIAA1700	3.14
	441381	H22195	Hs.31874	ESTs	3.14
35	457250	AA811987	Hs.125779	ESTs	3.14
	422900	AA641201	Hs.222051	ESTs	3.14
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.14
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.14
	419355	AA428520	Hs.90061	progesterone binding protein	3.14
40	409509	AL036923	Hs.322710	ESTs	3.14
	417308	H60720	Hs.81892	KIAA0101 gene product	3.14
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14
	429160	AW663083	Hs.144469	ESTs	3.14
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.14
45	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (U	3.14
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.14
	451518	AW340925	Hs.174918	ESTs	3.14
	435702	AI033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.13
	439208	AK000299	Hs.180952	dynactin 4 (p62)	3.13
50	451838	AW005866	Hs.193969	ESTs	3.13
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	3.13
	446945	AI193115	Hs.16611	tumor protein D52-like 1	3.13
	453920	AI133148	Hs.36602	I factor (complement)	3.13
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.13
55	417105	X60992	Hs.81226	CD6 antigen	3.12
	433854	AA610649	Hs.333239	ESTs	3.12
	408089	H59799	Hs.42644	thioredoxin-like	3.12
	453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	3.12
	426167	AF039023	Hs.167496	RAN binding protein 6	3.12
60	452195	AA994712	Hs.116878	ESTs	3.12
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12
	424001	W67883	Hs.137476	paternally expressed 10	3.12
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.12
65	433401	AF039698	Hs.284217	serologically defined colon cancer antig	3.12
	409245	AA361037		tRNA isopentenylpyrophosphate transferas	3.12
	414290	AI568801	Hs.71721	ESTs	3.12
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	3.12
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.11
70	448873	NM_003677	Hs.22393	density-regulated protein	3.11
	428471	X57348	Hs.184510	stratifin	3.11
	436288	AI361722	Hs.192410	ESTs	3.10
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.10
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	3.10
75	453468	W00712	Hs.32990	DKFZP566F084 protein	3.10
	412340	AA101809	Hs.182685	ESTs	3.10
	438716	AA814903	Hs.155113	ESTs	3.10
	419440	AB020689	Hs.90419	KIAA0882 protein	3.10
	433017	Y15067	Hs.279914	zinc finger protein 232	3.10
80	428513	BE220806	Hs.184697	plexin C1	3.10
	437866	AA156781		metallothionein 1E (functional)	3.10
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	3.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10

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435445	AA737345	Hs.294041	ESTs	3.10
420997	AK001214	Hs.100914	hypothetical protein FLJ10352	3.09
449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	3.09
406122			Target Exon	3.09
435272	AA906415	Hs.110041	ESTs	3.09
410726	AI623859	Hs.15936	ESTs	3.09
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.08
407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.08
417538	AW050865	Hs.275711	hypothetical protein MGC2452	3.08
434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	3.08
434733	AI334367	Hs.159337	ESTs	3.08
434421	AI915927	Hs.34771	ESTs	3.08
407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08
424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.08
458332	AI000341		ESTs	3.08
445034	AW293376	Hs.143659	ESTs	3.08
446570	AV659177	Hs.127160	ESTs	3.08
429920	AW473208	Hs.115572	ESTs, Weakly similar to I38022 hypotheti	3.08
459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	3.06
419038	AW134924	Hs.190325	ESTs	3.06
451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	3.06
417386	AL037228	Hs.82043	D123 gene product	3.06
453108	AI311457	Hs.99472	ESTs	3.06
449328	AI952493		ESTs	3.06
428656	AB037798	Hs.188790	KIAA1377 protein	3.06
425509	AF079363	Hs.158213	sperm associated antigen 6	3.06
447957	NM_014821	Hs.20126	KIAA0317 gene product	3.06
417226	AW505054	Hs.4283	ESTs	3.05
452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	3.05
426279	AI648520	Hs.169084	tubby like protein 3	3.05
433814	AA609738	Hs.16525	ESTs	3.05
453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.05
431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	3.04
441789	D52059	Hs.7972	KIAA0871 protein	3.04
456437	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.04
438771	NM_016289	Hs.6406	MO25 protein	3.04
448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.04
416240	NM_001981	Hs.79095	epidermal growth factor receptor pathway	3.04
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	3.04
424776	AI867931	Hs.164595	ESTs	3.03
408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.03
429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	3.03
425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	3.03
431625	AW750627	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.03
451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	3.02
432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.02
408683	R58665	Hs.46847	TRAF and TNF receptor-associated protein	3.02
427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (	3.02
440603	AL121733	Hs.7299	Novel human gene mapping to chromosome 1	3.02
415443	T07353	Hs.7948	ESTs	3.02
439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02
406685	M18728		gb:Human nonspecific crossreacting antig	3.02
446013	AI360167	Hs.152774	ESTs	3.02
433902	AW292820	Hs.144906	ESTs	3.02
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.02
432505	AW274526	Hs.277721	KIAA0049	3.01
440040	BE219431	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.01
433255	AI274270	Hs.96840	KIAA1527 protein	3.01
419726	U50330	Hs.1274	bone morphogenetic protein 1	3.01
417258	N58885		gb:yy60a09.s1 Soares_multiple_sclerosis_	3.00
435600	AI248285	Hs.118348	ESTs	3.00
444838	AV651680	Hs.208558	ESTs	3.00
456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	3.00
408360	AI806090	Hs.44344	hypothetical protein FLJ20534	3.00
427982	NM_016156	Hs.181326	KIAA1073 protein	3.00
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00
410434	AF051152	Hs.63668	toll-like receptor 2	3.00
412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00
425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.98
450247	AF123303	Hs.24713	hypothetical protein	2.98
417865	AW086059	Hs.6529	ESTs, Weakly similar to I78885 serine/th	2.98
415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.98
438543	AA810141	Hs.192182	ESTs	2.98
415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	2.98
429138	AB020657	Hs.197298	NS1-binding protein	2.98
447881	BE620886		GCN1 (general control of amino-acid synt	2.96
425481	AW978162		ESTs	2.96
453315	BE544203	Hs.24831	ESTs	2.96
440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	2.95
433208	AW002834	Hs.24095	ESTs	2.95
442495	AI184717		ESTs	2.94
418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.94
408170	AW204516	Hs.31835	ESTs	2.94

430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94
449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94
407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.94
407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.93
436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OV	2.93
449458	AI805078	Hs.208261	ESTs	2.93
449317	AW293413	Hs.132906	19A24 protein	2.92
411118	N27944	Hs.221476	ESTs, Weakly similar to AF108460 1 ubinu	2.92
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	2.91
416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	2.91
433068	NM_006456	Hs.288215	sialyltransferase	2.90
429272	W25140	Hs.110667	ESTs	2.90
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	2.90
445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.88
426782	R14614	Hs.33846	ESTs	2.88
426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.88
413882	AA132973	Hs.184492	ESTs	2.88
421554	AW137676	Hs.97775	ESTs	2.88
446488	AB037782	Hs.15119	KIAA1361 protein	2.84
421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran	2.84
424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	2.82
419284	AW820869	Hs.215658	ESTs, Moderately similar to ZN91_HUMAN Z	2.82
415788	AW628686	Hs.78851	KIAA0217 protein	2.82
448481	W15264	Hs.74832	ESTs	2.82
410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.80
443441	AW291196	Hs.92195	ESTs	2.80
422725	AA315703	Hs.199993	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.80
431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	2.80
420406	AA741024	Hs.88378	ESTs	2.79
437678	AA829860	Hs.122834	ESTs	2.78
440115	R41808	Hs.144924	ESTs, Weakly similar to B Chain B, Solut	2.78
439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78
446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.77
451273	NM_014811	Hs.26163	KIAA0649 gene product	2.76
435154	AA668764		ESTs	2.76
432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.75
442703	AL044949	Hs.116298	ESTs	2.74
419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74
435861	AF254956	Hs.16608	candidate tumor suppressor protein	2.72
420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	2.70
438441	AW664960	Hs.205319	ESTs	2.70
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.67
432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.66
416239	AL038450	Hs.48948	ESTs	2.62
434792	AA649253	Hs.132458	ESTs	2.60
424852	AI222779	Hs.144848	ESTs	2.58
425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.57
419551	AW582256	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	2.56
450571	AF158240	Hs.60397	ESTs	2.56
442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypotheti	2.56
424148	BE242274	Hs.1741	integrin, beta 7	2.56
445784	AI253155	Hs.146065	ESTs	2.53
408072	BE005566	Hs.16773	Homo sapiens clone TCCCIA00427 mRNA sequ	2.52
434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.52
450295	AI766732	Hs.210628	ESTs	2.48
440381	AA917808	Hs.190495	ESTs	2.46
433923	AI823453	Hs.146625	ESTs	2.44
420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44
429670	L01087	Hs.211593	protein kinase C, theta	2.44
437908	AI082424		ESTs	2.43
438676	AA813745	Hs.123446	ESTs	2.37
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28
444969	AI203334	Hs.160628	ESTs	2.26
446423	AW139655	Hs.150120	ESTs	2.27
435517	AA928626	Hs.130177	ESTs	2.27
425354	U62027	Hs.155935	complement component 3a receptor 1	2.26
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.00
429073	AA446167	Hs.47385	ESTs	1.98
433834	AA620742	Hs.130786	ESTs	1.72
417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.52
414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	1.30
402550			Target Exon	1.09

TABLE 33B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
407192	2200202_1	AA602964 AA609200

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	438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701
	439195	21979_1	AF086037 H89360 H89546
5	432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	406687	0_0	M31126
	444314	1027984_1	AW749625 AW749626 AW749644 AI140497
	452239	10116_4	BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600736 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332
10			AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743
	433586	32908_1	BC011194 AW517087 AA601054 T85512
	418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317
15			BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
	432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017
20			AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46187 BE929954 AA333976 D63102 BF744491
	412652	18858_2	AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780
			AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
25	431843	445334_1	AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656
	442048	750422_1	AW340495 AI984319 AA974603
	429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
30	442369	2691713_1	AA993566 AI521958 AI565071 AI864217
	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	407347	810943_1	T23514 AI655785
	451184	1531_4	Z99366 AV716301 BE222333 AI949687 BF732426 AI494086 AV721430 AW577332 N68315 BE672030 AI084440 AI250908 N50901 AA757364 BF515264 AI186231 BE466036 AW631313 AA993514 N54411 BG057515 AW013895 N77963 AA708723 AI273295 N59093 AA522665 AI871574
35			AA505521 AA812256 AA553841 AW467057 W68650 AI166772 AA988308 AA910057 AI868258 AA918322 AI335847 AA621494 AA904390 AI760007 AU146694 AV758440 BM142562 N66507 AI674563 AW628584 AI263902 BF223368 AI090490 AI452918 N71423 AA062767 T94332 AA016003 BG681608 AA082426 AA029451 N71873 BF437845 T54154 AV741757
	444610	2145292_1	AI174783 R12271 R83569
	407604	43771_1	AK074129 AL138071 AI806793 AI453544 AI084616 BF062435 BE672932 AI828296 BF062464 AI803443 AI264326 AI280956 AI743547 AW295227
40			AW139967 AI972561 AI863570 AW062752 AW062756 AW062753 AW176904 AW062755 AW062750 AW062749 AW176886 AI751694 BG251391 AA043621 W30872 BI524827 N94581 AI084614 AA776976 AI377572 AI751695 AI016576 AW439994 AW194255 AW627763 AA668249 AI079870
			AW022524 AI968540 AI248360 AA702490 AA043262 AA631511 AW176883 AW751767 AW176887 AW062748 AW062745 AW176862 AW176815 AW176814 AW176846 AW176841 AW176871 AW176874 AW176819 AI927437 AW191962 R36548 AA853713 AW196059 AA618567 AW176881
45			AW062754 AW062751 AW062746 AW176888 AW751772 AW176859 AW751765 AW751762 AW176833 AW176873 AW751745 AA694513 AA780815 AW176857 AW176834 AW176839 AW751771 AW176878 AW176843 AW176842 AW751755 AW176847 AW176812 AW176830 AW176849 AW176844 AW176877 AW751757 AW176850 AW176851 AW751758 AW751746 AW176858 AW176853 AW751766 AW176845
			AW176872 AW176840 AW176876 AW176852 AW751754 AW176836 AW176856 AW751773 AW751760 AW751751 AL138070 AA639738 AL602588 AA853712 AA317570 R38469 AW291569
	436772	1239464_1	AA156151 Z25109 C05177 AW975688 AA731063 N67084
50	437158	59575_1	AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847
	410297	2990_1	BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907
55			AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893
			AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303
60			AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI764138 AA083847 N22258 AW440825 AA561570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006
			N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954386
	436769	1239572_1	AW975804 AA748675 AA731006
65	412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827
			AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316
			BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW686475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737
70			AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674
			BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510
			AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276
75			BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845
			AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723
			AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599
			BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE005561 BG959922 BF094833 BF094748 BF094583
80			AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77851 AI927207 AI205263 BF082491 AW021347 AI568095 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181

			H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022662 N29754 C03378 N64767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW660878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487
	418876	121279_1	AA740616 AA654854 AA229923
	434987	121985_1	AW975114 AI096634 AI767001 AA658364 AW517542
	430709	1234627_1	AW969880 AA484613 AA501874 R34356
	418546	242836_1	T59708 AA224827 T59843 BE156903
	414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910544 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
	436198	28727_1	AK001125 AU120581 AU146612 AW301393
	413645	1234345_1	AA130992 AW969537 AA503835
	424831	1272834_1	H61453 AA838765 AI693104 AA721107
	433430	2181751_1	AA961586 AI863735 AA588325
	443547	137089_2	AV645808 AA701657 AW271273 AI796734 AI472316 AI017531 AI061178 BF109096 AA548964 N83805 AA131648 AA156589 BE708349 AW952494 D30877 AV684717 Z24837 F00167 BF576150 T63841 R78995 N87474
	459645	722255_1	AW292984 AA724304 AA074346 AA074368
	422960	11862_2	BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260
	432340	1619980_1	AA534222 AA632632 T81234
	412240	8235_1	BF963346 BI460763 BI599362 AI188089 AY055003 AW959185 AA187681 AI692282 AU153608 BI493898 BI493899 AI797349 BE550679 AI701137 AA744561 AA082682 BE218316 AW511501 BF447881 AI859101 BF059295 AI914038 AI346564 AI685003 AI676076 AI125336 AW469637 T10225 AI831296 R53451 AI453440 AA983739 AW470873 AI348290 BE857670 D55901 Z43908 T34429 F07305 AK074340 AL538118 BG201484 AI334192 T35535 AW176751 BI496132 BI496133 AA469961 H72176 BF326265 AI770016 AI693177 BF223634 BF963661 BF962265 BI034894 AI475851 N69071 AI910707 BE219038 AI918036 BE670589 BM193515 AI338497 AA805525 AA487625 AA830336 AA749368 AW104323 AI628055 AI932332 AI272788 AI536849 AW162414 AW161923 T23854 AA610763 AA912188 AW339028 Z39946 T10224 F03171 AI205478 AI638791 F02580 F01551 AW207551 AA421030 BE246012 BI034937 BI035373 BF939581 H19984 BE867247 H92677 N55988 BF957332 H18615 R16442 BF956229 BF961886 R12698 AA101186 AA365932 R53452 BF062714 BF959364 H41634 AW086187 H19985 BF054881 F02581 H18616 H41527 AW003446 BE243443 H92276 AW954002 BI670132
	432648	129028_1	AA677593 AA618150 AA557952
	451198	18361_1	AK024780 NM_024549 AW440385 AW965502 BF477855 AI149742 BE669424 BE349941 AI376717 AA977493 AW592564 AA884111 AA865463 N51840 BF593777 AA044645 AW512183 BF059034 AI984320 AA733139 AI884563 AI559673 AI421262 AI052068 AI085891 BI963100 AA479883 AI271696 AI539839 AI370924 AI147781 AA535765 BI966896 AA877448 AW152259 AA938992 AA996022 AI800410 AA613303 AA588323 R53623 AW571973 AI203770 BI494224 BI494225 D45504 AA705824 AI625183 AA437118 AA640325 AA235528 AA731411 AA626263 AI560519 AW071114 AW005691 AI055933 AA971813 AA334937 N58441 AA536020 AW874174 AL565960 AW607532 H44647
	456505	15472_2	BC017965 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312
	442113	43919_1	AK074156 AI401548 BE002083 BE002085 BE002084 BG113650 AW580909 AA632959 BG610861 BG436183 BF438017 AI568608 AI095503 AI204208 AW244158 BE622614 N52349 BE042940 AI095858 AA976119 AA835838 AI620854 AA456105 AA971569 AI246289 AI335636 AA994082 AI250060 AI095710 AA605125 AA291672 BE463947 N52870 AA287553 AI149093 AA581802 W31684 AA610159 BF247061 BG258954 BE176866 BE177041 AA332106 BE967020
	440028	598730_1	AW473675 AI190744 W69997 AW104913 AI221098 W69996 AA885487 AA861491
	414783	262554_1	BE972667 AW069569 AI392889 H85161 AI074962 AA423935 BE671254 AA912627 H39845 H69083 AA280259 N67746 AA155722
	431698	6468_7	BM423504 BE075913 AI492369 AI831729 AA807134 AI057292 BF059751 AA918209 BE858647 AW016707 AI675289 AI452916 BF593014 AI480099 AI522283 AI628681 AI470402 BF056360 AW236830 AA514206 BF055812 AI796201 BF055617 BF054827 AI288301 AA705763
	441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BG496559 BF248373 BG494800
	433282	759_1	BC015150 BM471660 BM478941 BI759769 BI094332 BE005819 BE005834 BM023432 BE179013 BE675522 AI680275 AA515794 AA256503 F01634 AF002990 BG288697 AI091615 AW002917 AI631085 AW182664 BE501232 AI922188 BF838783 AI631078 BE464544 AI376986 AW503774 AA424131 AW511849 AA872189 BF084885 AI432024 AI491908 BF197906 AA580599 AI274418 AW269225 AW058288 AI611346 AA236200 C00417 BE669699 AI468149 BM460137 AI685282 AI902714 BG990066 BF894391 T83393 T84298 BF809721 BE925494 AV755948 BF928512 BF894494 BF808642 AA256710 BF894347 BE928708 H06072 AA199607 BI859300 AI983233 AI521122 BE168896 BE302846 X76770 BC000927 NM_032632 BG707103 BG913857 BG613824 BG613257 BM313077 BI561132 BI461426 BE389811 BE391509 BE164646 AA746371 AV750611 BE175813 AA332040 BG200997 BG485576 AL043706 AV716994 BF903156 AW820369 AU132824 BF941136 BE543211 AA521432 AW837568 BF809623 AW614670 AU129338 AW880782 AA371070 BG615427 BI667976 BI598706 BI599341 BE869166 BG502432 NM_020144 AF218840 BI461106 BI562235 BI462594 BI458753 BF195561 BF832738 BE890146 AI678629 AL135238 AU129571 AW500045 AA332478 AW502738 BI561031 BE280153 BF087226 BM480024 AW804395 BE707050 R72668 BF038881 BF895070 BG036594 BE551809 BF326901 BG286526 AW962888 BE544939 AW363399
	434210	54921_1	AK057015 AI026834 BE857936 AA149091 AI742972 AW439172 AI253168 AA255613 BF513175 AI005006 T03406 AW338149 AA836442 AA420530 R88566 AI611672 AA433916 AA442855 BF063008 AA812568 AI889706 AA715313 AA768539 AA767620 AA665471 AA404380 AA665612 BF056442 AA706388 AI650676 AA627448 AI141769 H78227 AW901852 H78221 BE701982 BF689273 AA397464 N33072 R60218 AW968247 H14833 AA768305 AA043348 R56470 BF739832 R51827 AI474963 BG494574 AA149090 BF238154 AI802210 BE000129 BF734513 R41964 H21055 R85253 R17705 R40844 BF790218 BG388356 BF003037 AA703138 AA377346 W24822
	412262	4362_1	AK056051 AI971258 AI681134 AU146134 AI803300 AA917325 AA923663 BF895068 AI304442 AI167464 AI284188 AA054272 AA829262 AI351910 T90930 AI886230 U70056 AU119916 BF446537 BE503207 BE502849 AI698102 AA258553 AV718529 AV719917 BF724133 BI438668 AI804000 BE349103 AI912294 BE645117 AA227954 AA446520 AA879147 AA281770 AW136872 AA807907 AI435989 AI339626 AI383274 AA418512 BE771804 BF894509 AA455093 AI379061 AI150855 BF769906 R17298 AU138740 BF808607 BE674633 AV700132 AA227789 AA253099 AW975199 AA935418 T74315 F12566 AA022923 T89028 AA258606 W26406 BE838620 AV700706 AA101321 R41382 H14479 AA253044 R54810 R42784 R44804 R41278
	430950	594908_1	AI525877 AA489525 AW088177

419543	251903_1	AI018087 AA244170 AA244355
455657	1490185_1	BE065209 BE065364 BE065110 BE065111
414405	112689_1	AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545
409010	10331_1	AL575207 AL551714 BM014781 BG542863 BG771232 AA429722 AI377511 AI770155 AA716665 BG003427 AA810811 AA442760 AA128610 AA059411 AI796263 AI494075 AI572127 AA420992 BF436083 AI648675 AA878813 BI488614 BG700886 AA128609 AV702879 AA731146 AI580336 AI373224 AA919169 AI758175 AA976350 BG701414 BF057794 AW135598 AA062583 BI549631 AI185077 AA933879 AW024454 AA193289 AA045194 BG928396 BE856883 BF435859 AA195423 AW237471 R99289 D61992 BE856637 BF368270 AA194235 N51319 AA383499 N63065 BG548812 BF027898 BG779448
411962	2307710_1	AA099050 AA099526 T47733
434982	121871_1	AW975084 T90204 AA658177
432676	3503_22	AI187366 AA618478 AA558869
437838	2512601_1	AI308202 AI307229 AA769348
446019	658727_1	AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827
454042	30254_1	AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570
432954	2159612_1	AI076345 AI887648 AA572691
446126	610_2	BF946219 BF946218 BF851494 AL536879 AA457150 AI590194 AI582629 AA464515 AA916242 AA337109 AA336509 N46906 AA336322 AA336407 AA337222 AA319240 BI026817 BI027058 AL536880 AI693827 AA651730 AI701013 BM068789 AW339506 AA293021 BF891108 AI458885 AW361203 AW974652 AI761251 AI655763 AA628063 BE047125 AW085916 AI129587 N52070 AW172361 AA052951 AW085909 AI000008 AA962570 AI371342 AI364207 AA464514 AI962506 AI824603 AW376300 AA058439 AW361192 AV656660 N50282 BF820514 BF891008 H40784 BF891112 BE708029 AW043567 AA056762
419145	248375_1	BM456602 AV706711 BF379357 H90994 AA234435 AA558020 BF351723 AA328271 R94815 N99638 BG223375 AW973750 N59599
409245	3199_2	AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830 AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024 BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752 BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845 AI693426 AI652147 AI435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897 AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245 AA884954 AI125702 AI382934 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI763667 AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062 D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848 H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
437866	34267_1	U52054 AL581000 AA156850 AW293839 BI335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960 AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AI866686 AI572124 AA687333 D20160 AA812489 AU185248 AU186004 AA156781 AI536733 BM144850 AI471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BI022546 BI021204
458332	1139685_1	AI000341 AI766341 AW873274
459513	417837_1	AV704062 BE162284 AI032946 BF360636
449328	3030726_1	AI884781 AI652306 AI651694 AI638744 AI962493
406685	0_0	M18728
417258	400835_1	BG116781 BI914326 BI030196 N58885 N63406 AV683374 N58892 BG110501 AA333708 AA359583 AW963123 N95562 N95696 N95587
447881	44623_1	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
425481	334120_2	AL520496 AW978162 AI610475 AI688990 AW470054 AA609426 AI167391 AA815231 AA358241
440638	371165_1	BG009500 AI376551 AA897445 T87714
442495	928718_1	AI184717 AW518883 AF121173
416311	1280744_1	AA179446 AA357794 D81719 D80529 C14833
431926	1237041_1	AW972724 AA877998 AA522631 AU185388
435154	126605_1	AW972063 AA668764 AA804491 AW665688 AA765069
437908	13268_11	AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676

TABLE 33C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401403	7710966	Plus	146180-146294
406387	9256180	Plus	116229-116371,117512-117651
405268	4156151	Minus	24404-24521
406122	9144087	Minus	30940-31386
402550	7652009	Minus	80413-80673

TABLE 34A: About 703 genes upregulated in idiopathic pulmonary fibrosis relative to hypersensitivity pneumonitis or non-specific interstitial pneumonitis

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of IPF AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50
R2: 90th percentile of IPF AIs divided by 90th percentile of NSIP AIs, where the minimum value for the numerator and denominator was set to 50

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
405443			Target Exon	9.66	7.50
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.23	3.66
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.63	3.03
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.84	2.81
406964	M21305		FGENES predicted novel secreted protein	4.73	5.69
425259	AL049230	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.34	4.34
407244	M10014		fibrinogen, gamma polypeptide	4.14	5.88
421823	N40850	Hs.28625	ESTs	4.12	1.80
419875	AA853410	Hs.93557	proenkephalin	3.90	2.01
409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.88	2.90
418310	AA814100	Hs.86693	ESTs	3.66	2.84
442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	3.60	3.13
438315	R56795	Hs.82419	ESTs	3.49	3.70
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.47	1.38
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.46	3.46
434233	AF119903	Hs.138453	hypothetical protein PRO2834	3.28	2.51
408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.26	3.26
447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	3.19	2.12
420185	AL044056	Hs.251385	ESTs	3.18	3.01
420195	N44348		Homo sapiens cDNA FLJ11177 fis, clone PL	3.16	3.16
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.08	3.18
408221	AA912183	Hs.47447	ESTs	3.07	1.98
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.02	2.36
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.98	1.72
422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.87	1.48
422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.80	2.66
445745	AB007924	Hs.13245	KIAA0455 gene product	2.78	1.65
407938	AA905097	Hs.85050	phospholamban	2.78	2.46
423575	C18863	Hs.163443	intron of periostin (OSF-2os)	2.78	1.55
446659	AI335361	Hs.226376	ESTs	2.74	1.56
425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	2.74	1.85
437620	AW976930		ESTs	2.72	2.72
414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.67	2.05
416585	X54162	Hs.79386	leiomodin 1, smooth muscle (LMOD1) (Thy	2.66	1.47
425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.66	2.66
430712	AW044647		ESTs	2.62	2.62
453111	AB014598	Hs.31720	hephaestin	2.61	1.72
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.59	1.27
414290	AI568801	Hs.71721	ESTs	2.59	1.23
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.58	2.58
412639	AW961284	Hs.203838	ESTs	2.58	2.29
423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.57	1.74
429757	AW452355	Hs.256037	ESTs	2.57	1.60
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57	1.00
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.56	1.12
430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.56	1.25
411880	AW872477		gb:hm30i03.x1 NCI_CGAP_Thy4 Homo sapiens	2.54	2.54
401645			C16001440*:gi|12330704|gb|AAG52890.1|AF3	2.53	3.38
401673			C16001416*:gi|12743112|ref|XP_010131.2|	2.47	2.83
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.46	1.18
416316	H58721	Hs.271628	ESTs	2.42	3.44
453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.40	1.69
451149	AL047586		RNA binding motif protein 8B	2.40	1.95
421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.40	1.61
410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	2.40	2.40
429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.39	1.27
405120			C4001445:gi|12697999|dbj|BAB21818.1| (AB	2.38	2.38
432224	AW189460	Hs.208358	ESTs	2.38	2.00
418663	AK001100	Hs.41690	desmocollin 3	2.38	2.38
412622	AW664708	Hs.171959	ESTs	2.37	1.63
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.37	1.52
442767	AI017208	Hs.131149	ESTs	2.36	1.22
401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.35	1.79
411800	N39342	Hs.103042	microtubule-associated protein 1B	2.35	1.18
427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.34	2.34
444009	AI380792	Hs.135104	ESTs	2.34	2.07
435143	R12375	Hs.194600	ESTs	2.33	1.68
402333			Target Exon	2.33	3.15
429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.33	1.10
454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.32	1.30
452242	R50956	Hs.159993	gycosyltransferase	2.32	1.45
418693	AI750878	Hs.87409	thrombospondin 1	2.32	2.32
428411	AW291464	Hs.10338	ESTs	2.32	1.54
459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.31	1.98
428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.31	2.49
427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.31	1.32

422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.30	2.30
456536	AW135986	Hs.257859	ESTs	2.28	2.28
428166	AA423849	Hs.79530	M5-14 protein	2.27	1.88
456936	M81349	Hs.1955	serum amyloid A4, constitutive	2.25	2.16
417728	AW138437	Hs.24790	KIAA1573 protein	2.25	1.37
453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.24	2.42
409159	AW673312	Hs.50848	hypothetical protein FLJ20331	2.24	2.24
404942			splicing factor, arginine/serine-rich 9	2.24	2.64
410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.24	2.46
440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	2.24	1.94
421574	AJ000152	Hs.105924	defensin, beta 2	2.23	1.36
418005	AI186220	Hs.83164	collagen, type XV, alpha 1	2.22	1.37
421948	L42583	Hs.334309	keratin 6A	2.20	2.20
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.19	1.61
417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.18	2.40
431089	BE041395		ESTs, Weakly similar to unknown protein	2.16	2.46
447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	2.16	2.00
455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.16	1.26
414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.16	1.99
403362			NM_001615*:Homo sapiens actin, gamma 2,	2.16	1.61
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.15	2.11
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.15	2.24
402641			C1002296:gi|6677817|ref|NP_033126.1| rep	2.14	2.14
418236	AW994005	Hs.337534	ESTs	2.14	2.14
413059	BE151498		gb:RC0-HT0295-291199-031-E11 HT0295 Homo	2.14	2.14
432437	W07088	Hs.293685	ESTs	2.14	2.14
428398	AI249368	Hs.98558	ESTs	2.14	2.14
428336	AA503115	Hs.183752	microseminoprotein, beta-	2.12	1.43
421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	2.12	1.93
436391	AJ227892	Hs.146274	ESTs	2.12	2.12
417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.11	2.17
407443	AF227138		gb:Homo sapiens candidate taste receptor	2.11	2.36
428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.10	1.29
409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.10	2.10
456614	AV653110	Hs.106650	hypothetical protein FLJ20533	2.10	2.00
440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.10	1.37
450271	AI693900	Hs.200920	ESTs	2.09	2.34
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.09	1.40
458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	2.08	2.00
405600			C12001673:gi|9631264|ref|NP_048045.1| or	2.07	1.97
434654	AI825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	2.07	2.52
439261	AI126020	Hs.145674	basic transcription factor 3	2.05	1.45
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	2.04	2.04
457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.04	2.04
423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	2.02	1.33
412505	AA974491	Hs.21734	ESTs	2.02	2.02
443180	R15875	Hs.258576	claudin 12	2.02	2.02
431605	AW972407	Hs.124370	gb:EST384498 MAGE resequences, MAGL Homo	2.02	2.02
415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	2.02	2.17
452571	W31518	Hs.34665	ESTs	2.02	2.09
405061			Target Exon	2.01	2.52
439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.01	2.41
402327			Target Exon	2.00	2.44
418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.00	2.00
447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.00	2.00
438634	AW340400	Hs.126728	ESTs	1.99	2.43
416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	1.97	1.41
423961	D13666	Hs.136348	periostin(OSF-2os)	1.96	1.48
430397	AI924533	Hs.105607	bicarbonate transporter related protein	1.96	1.31
411010	AW813339		gb:MR3-ST0192-101299-013-c05 ST0192 Homo	1.96	2.73
439628	W81007	Hs.58628	ESTs	1.96	1.28
444301	AK000136	Hs.10760	asporin (LRR class 1)	1.96	1.58
431726	NM_015361	Hs.268053	KIAA0029 protein	1.95	1.72
410418	D31382	Hs.63325	transmembrane protease, serine 4	1.95	1.87
452814	AI092790	Hs.334703	hypothetical protein FLJ14529	1.95	1.06
417562	AW888754	Hs.134126	crystallin, gamma S	1.95	2.14
424480	AA341442	Hs.205299	ESTs	1.94	1.94
404342			C7002192*:gi|7299207|gb|AAF54404.1| (AE0	1.92	1.32
443320	AI051607	Hs.16335	ESTs	1.91	2.18
449780	AA443241		ribosomal protein L44	1.90	1.76
423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	1.89	2.16
434416	AA805903	Hs.59498	cell division cycle 2-like 5 (cholineste	1.89	2.04
457505	AL044659	Hs.43791	ESTs	1.89	2.34
425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pl	1.88	1.26
413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	1.88	1.88
428231	U17989	Hs.183105	nuclear autoantigen	1.88	1.88
428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	1.88	1.88
404429			Target Exon	1.88	2.18
447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	1.88	3.04
406641	AJ235667		gb:Homo sapiens mRNA for immunoglobulin	1.86	2.57
417059	AL037672	Hs.81071	extracellular matrix protein 1	1.86	1.48
454565	BE141231		gb:MR0-HT0075-081199-003-a09 HT0075 Homo	1.86	1.21
415115	AA214228	Hs.127751	hypothetical protein	1.85	1.23

	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	1.85	1.45
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	1.84	1.44
	403344			NM_000341:Homo sapiens solute carrier fa	1.84	1.84
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	1.84	2.33
5	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.84	2.02
	401593			Target Exon	1.83	2.34
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	1.83	2.12
	406461			hypothetical protein, clone 24751	1.83	2.01
	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.83	1.26
10	400609			C10001147:gi|12698926|gb|AAK01739.1|AF33	1.82	2.08
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	1.81	1.14
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.81	1.22
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	1.81	2.10
	426521	AF161445	Hs.170219	hypothetical protein	1.81	2.08
15	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.81	1.64
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	1.80	1.34
	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.80	1.80
	459189	AI909090		gb:IL-BT198-010499-007 BT198 Homo sapien	1.80	1.80
	412429	AV650262	Hs.75765	GRO2 oncogene	1.80	2.55
20	402674			Target Exon	1.80	3.41
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.79	1.57
	454824	AW833646		gb:QV4-TT0008-161199-033-d09 TT0008 Homo	1.78	1.94
	401677			BAI1-associated protein 3	1.78	2.28
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	1.78	1.53
25	430028	BE564110	Hs.227750	Target CAT	1.78	1.59
	445988	BE007663	Hs.13503	inactivation escape 2	1.78	2.10
	452272	AW292249	Hs.252739	hypothetical protein DKFZp434P0316	1.78	2.08
	418205	L21715	Hs.83760	troponin I, skeletal, fast	1.78	2.70
	400425	AY004252	Hs.287385	PR domain containing 12	1.77	2.02
30	400419	AF084545		Target	1.77	2.67
	447169	AI989803	Hs.157289	ESTs	1.77	2.21
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	1.77	2.12
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1.76	2.54
	432808	NM_015985	Hs.278973	angiopoietin-3	1.76	1.76
35	437400	AB011542	Hs.5599	EGF-like-domain, multiple 5	1.75	2.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.75	1.47
	444986	AI204197		ESTs	1.75	2.48
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	1.74	1.69
	413524	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.74	1.74
40	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	1.74	2.26
	405579			C22000151:gi|6806921|ref|NP_004165.1| so	1.74	2.12
	405797			CX001015:gi|11322384|emb|CAC16687.1| (AJ	1.73	2.66
	405159			ENSP00000243337*:CDNA FLJ13984 fis, clon	1.73	2.01
	450569	AW192334	Hs.38218	ESTs	1.73	2.08
45	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.73	1.24
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	1.73	2.52
	454231	AW450669	Hs.45068	hypothetical protein DKFZp434I143	1.73	1.64
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	1.72	1.37
	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.72	1.72
50	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.72	1.34
	451862	H09260	Hs.32333	ESTs	1.71	2.16
	403520			Target Exon	1.71	1.39
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	1.71	2.26
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	1.70	1.70
55	418387	R18085	Hs.22279	gb:yg16b12.r1 Soares infant brain 1NIB H	1.70	1.70
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.70	1.87
	402538			C1001634:gi|12621136|ref|NP_075245.1| Ba	1.69	1.57
	414844	AA296874	Hs.77494	deoxyguanosine kinase	1.69	2.06
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.69	1.63
60	446553	AB021179	Hs.15299	HMBA-inducible	1.68	2.02
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	1.68	2.12
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	1.68	2.03
	433930	AA620338		ESTs	1.68	2.28
	404151			Target Exon	1.68	1.80
65	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	1.67	2.18
	430070	AF197927	Hs.231967	ALL1 fused gene from 5q31	1.66	2.16
	400496			ENSP00000224716*:GTP-binding protein SAR	1.66	2.13
	413464	AL121500		ESTs	1.66	2.03
	411188	BE161168		gb:PM0-HT0425-170100-002-a10 HT0425 Homo	1.66	2.12
70	446281	H69416	Hs.14606	hypothetical protein FLJ20271	1.65	2.28
	443282	T47764	Hs.132917	ESTs	1.65	2.04
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.65	1.67
	453355	AW295374	Hs.31412	myopodin	1.65	1.66
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.54
75	437929	T09353	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	1.65	2.04
	410295	AA741357		nidogen (enactin)	1.64	2.30
	437767	AA830103	Hs.293331	ESTs	1.64	1.26
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	1.64	3.38
	450795	AW173371	Hs.60435	ESTs	1.64	1.64
80	421847	NM_014717	Hs.108884	KIAA0390 gene product	1.64	2.75
	403010			C21000152:gi|6226483|sp|Q52118|YMO3_ERWS	1.64	2.03
	406387			Target Exon	1.64	1.78
	440423	AW293995	Hs.192277	ESTs	1.63	2.05

	444381	BE387335	Hs.283713	hypothetical protein BC014245	1.63	2.07
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.63	1.65
	442424	AI342715	Hs.129569	ESTs, Moderately similar to B34087 hypot	1.62	2.40
	402885			Target Exon	1.62	1.18
5	408786	AA773187	Hs.294027	ESTs	1.62	1.59
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	1.62	1.63
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart,	1.62	2.10
	406838	AA827569	Hs.153	ribosomal protein L7	1.61	1.41
	441600	AA939347	Hs.127223	Homo sapiens cysteine knot protein (ZSIG	1.61	2.32
10	420693	NM_001972	Hs.99863	elastase 2, neutrophil	1.60	2.37
	412649	NM_002206	Hs.74369	integrin, alpha 7	1.60	1.23
	432331	W37862	Hs.274368	MSTP032 protein	1.60	1.23
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.60	1.69
	400279			NM_004581*:Homo sapiens Rab geranylgeran	1.60	1.56
15	437865	AI472305	Hs.19565	ESTs	1.60	2.42
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	1.60	1.29
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	1.60	2.11
	410684	AA088500	Hs.170298	ESTs	1.59	1.46
	433149	BE257672	Hs.42949	hypothetical protein HES6	1.59	2.22
20	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	1.59	1.41
	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.59	1.26
	427654	AA410183	Hs.137475	ESTs	1.59	2.83
	411662	D60541	Hs.285519	Homo sapiens cDNA FLJ11904 fis, clone HE	1.59	2.18
	440383	AA884208	Hs.30484	ESTs	1.58	2.19
25	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.58	1.58
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.58	1.47
	407857	AI928445	Hs.92254	synaptotagmin-like 2	1.58	1.51
	411573	AB029000	Hs.70823	KIAA1077 protein	1.57	1.29
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	1.57	1.17
30	428471	X57348	Hs.184510	stratifin	1.57	1.55
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	1.57	1.19
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.57	2.12
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.57	1.05
	430469	AW603667	Hs.288742	Homo sapiens cDNA: FLJ22712 fis, clone H	1.56	1.56
35	445511	AA846512		Homo sapiens cDNA FLJ14459 fis, clone HE	1.55	2.08
	404501			nucleoside phosphorylase	1.55	2.54
	429107	AI470451	Hs.99075	ESTs	1.55	2.05
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.55	1.45
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.54	2.61
40	458091	AF150286		gb:AF150286 Human mRNA from cd34 stem ce	1.54	1.54
	439280	AI125436	Hs.123654	ESTs	1.54	2.06
	428096	AW291771	Hs.42239	Homo sapiens, clone IMAGE:3868989, mRNA,	1.53	1.55
	414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.53	1.39
	451712	AA019290	Hs.110489	ESTs	1.53	1.99
45	402487			Target Exon	1.53	2.02
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.53	1.29
	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	1.53	1.21
	410253	T51823		ESTs	1.52	2.03
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	1.52	1.37
50	432985	T92363	Hs.178703	ESTs	1.51	1.48
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.51	1.15
	429259	AA420450	Hs.292911	Plakophilin	1.51	1.31
	429289	AI400746	Hs.62187	phosphatidylinositol glycan, class K	1.51	1.19
	441457	AW996651	Hs.43838	ESTs	1.51	2.08
55	433365	AF026944	Hs.293797	ESTs	1.51	2.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.51	1.21
	424386	BE146577	Hs.285132	ESTs	1.50	1.53
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	1.50	1.29
	442391	AW450544	Hs.220751	ESTs	1.50	1.65
60	414341	D80004	Hs.75909	KIAA0182 protein	1.50	2.10
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	1.50	2.16
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	1.50
	443878	AW292499	Hs.139709	hypothetical protein FLJ12572	1.50	1.37
	430152	AB001325	Hs.234642	aquaporin 3	1.50	1.43
65	447752	M73700	Hs.105938	lactotransferrin	1.49	0.91
	404455			opioid receptor, kappa 1	1.49	1.36
	424106	AA412442	Hs.98132	ESTs	1.49	1.30
	433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fis, clone HE	1.49	2.02
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.48	1.50
70	456256	AB000450	Hs.82771	vaccinia related kinase 2	1.48	1.42
	439310	AF086120	Hs.102793	ESTs	1.48	1.48
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	1.48	1.15
	437981	AA774445	Hs.145365	ESTs, Weakly similar to KIAA1397 protein	1.48	2.36
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.47	1.21
75	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.47	1.25
	453864	AW021407	Hs.21068	hypothetical protein	1.47	2.18
	401067			ENSP00000252105*:CDNA FLJ12240 fis, clon	1.47	1.81
	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens c	1.47	1.99
	402324			C19001982:gi|3043638|dbj|BAA25483.1| (AB	1.47	2.03
80	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	1.47	1.29
	457734	BE394365	Hs.38750	hypothetical protein FLJ11526	1.47	2.26
	402013			Target Exon	1.46	2.42
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	1.46	2.09

430920	U96402	Hs.248132	goosecoid-like	1.46	2.46
409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	1.46	2.02
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.46	1.43
427719	AI393122	Hs.134726	ESTs	1.46	1.46
433430	AI863735		ESTs	1.46	1.15
423790	BE152393		gb:CM2-HT0323-171199-033-a08 HT0323 Homo	1.46	2.36
444083	AI123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.45	2.29
433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	1.45	1.50
420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	1.45	1.17
456664	AW963354	Hs.334409	metallothionein 1G	1.45	2.20
438158	AI796556	Hs.187884	ESTs	1.45	1.18
409883	AW452419	Hs.296098	ESTs	1.45	2.00
452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.45	1.27
413048	M93221	Hs.75182	mannose receptor, C type 1	1.45	1.36
457462	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	1.45	2.08
452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	1.44	1.28
401116			Target Exon	1.44	2.19
419618	AA528295		gb:nh26e06.s1 NCI_CGAP_Pr3 Homo sapiens	1.44	2.30
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	1.44	2.03
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.43	1.48
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.43	1.51
418742	AW451197	Hs.113418	ESTs	1.43	1.24
418335	R63267	Hs.28399	ESTs	1.43	1.14
408404	AW192518		gb:xl45h08.x1 NCI_CGAP_Pan1 Homo sapiens	1.43	2.08
448175	BE296174	Hs.225160	hypothetical protein FLJ13102	1.43	2.29
431846	BE019924	Hs.271580	uroplakin 1B	1.43	2.12
459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	1.43	2.00
449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	1.43	1.33
442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (	1.43	1.10
454843	AW834536	Hs.258549	gb:MR2-TT0014-241199-012-f06 TT0014 Homo	1.43	1.55
410281	AF076612	Hs.166186	Homo sapiens clone 23928 mRNA sequence	1.43	1.38
402998			NM_002463*:Homo sapiens myxovirus (influ	1.42	2.16
443709	AI082692	Hs.134662	ESTs	1.42	2.22
435259	AA152106	Hs.4859	cyclin L ania-6a	1.42	2.01
454407	AW578420	Hs.118843	gb:RC1-CT0249-120100-022-b04 CT0249 Homo	1.42	1.76
453359	AA448787	Hs.24872	ESTs	1.42	1.33
434126	AI138589	Hs.118205	ESTs	1.41	2.06
417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.41	1.46
442316	Z75331	Hs.8217	stromal antigen 2	1.41	2.20
438330	AW450572	Hs.257316	ESTs	1.41	2.20
410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	1.41	2.02
455885	BE153524		gb:PM0-HT0339-241199-002-C03 HT0339 Homo	1.41	1.33
405550			C7001981*:gi|565157|gb|AAB31881.1| T-cel	1.41	1.24
451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.41	1.99
424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	1.40	2.64
431022	AA490815	Hs.208351	ESTs	1.40	1.26
439781	AA845538		glial cells missing (Drosophila) homolog	1.40	2.72
429379	NM_014840	Hs.200598	KIAA0537 gene product	1.40	1.05
435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprote	1.40	1.26
430702	U56979	Hs.278568	H factor 1 (complement)	1.39	1.18
451331	AK002039		Homo sapiens cDNA FLJ11177 fis, clone PL	1.39	1.26
459198	AI086347	Hs.151138	ESTs	1.39	1.22
442344	AI022925	Hs.79368	epithelial membrane protein 1	1.39	1.35
402917			ENSP00000202587*:Bicarbonate transporter	1.39	1.44
418211	BE244746	Hs.247474	hypothetical protein FLJ21032	1.39	2.08
437158	AW090198		KIAA1150 protein	1.38	2.07
427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	1.38	1.24
433911	AI923092	Hs.8899	ESTs	1.38	2.15
402504			C1003823*:gi|4826521|emb|CAB42853.1| (AL	1.38	1.38
409465	AW393810	Hs.78054	gb:QV4-TT0008-251099-016-e11 TT0008 Homo	1.37	2.22
449426	T92251	Hs.198882	ESTs	1.37	2.38
405491			Target Exon	1.37	2.74
406685	M18728		gb:Human nonspecific crossreacting antig	1.37	1.34
442410	AW996503	Hs.197680	ESTs	1.37	1.56
407701	AW375009	Hs.164407	ESTs	1.36	2.02
400818			Target Exon	1.36	2.10
406475			C15000508*:gi|2558825|gb|AAC53387.1| (AF	1.36	2.78
426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.36	1.41
414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	1.36	2.20
444195	AB002351	Hs.10587	KIAA0353 protein	1.35	0.94
447918	AI129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	1.35	1.22
421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	1.35	1.40
412992	AI423369	Hs.75111	protease, serine, 11 (IGF binding)	1.35	1.24
401025			NM_004055*:Homo sapiens calpain 5 (CAPN5	1.35	1.30
452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	1.34	2.12
425308	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.34	1.02
402308			Target Exon	1.34	1.21
428415	AA337211	Hs.184222	Down syndrome critical region gene 1	1.34	1.40
407242	M18728		gb:Human nonspecific crossreacting antig	1.34	1.22
410741	Z11695	Hs.324473	mitogen-activated protein kinase 1	1.34	2.05
439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobin, fa	1.34	1.12
431254	NM_006069	Hs.251385	murine retrovirus integration site 1 hom	1.33	1.21
405213			Target Exon	1.33	2.03

447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.33	1.05
421535	AB002359	Hs.105478	phosphoribosylformylglycinamidine syntha	1.33	2.09
453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.33	1.32
443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.33	1.18
430385	AA113437		N-myc downstream-regulated gene 3	1.32	1.48
447731	AA373527	Hs.19385	CGI-58 protein	1.32	2.22
400740			hypothetical protein FLJ14280	1.32	2.01
410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	1.32	1.32
440274	R24595	Hs.7122	scrapie responsive protein 1	1.32	1.32
406867	AA157857	Hs.182265	keratin 19	1.32	1.42
456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.32	2.30
443144	BE246335		hypothetical protein MGC14797	1.32	2.03
432810	AA863400		ESTs	1.32	4.01
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.31	1.24
424075	AI807320	Hs.227630	RE1-silencing transcription factor	1.31	2.17
440099	AL080058	Hs.6909	DKFZP564G202 protein	1.31	1.53
428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	1.31	1.31
438874	H02780		gb:yj41a11.r1 Soares placenta Nb2HP Homo	1.31	2.03
402825			Target Exon	1.31	1.24
422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	1.31	1.45
423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.31	1.19
417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	1.31	1.12
436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	1.30	2.06
407409	AF060168		gb:Homo sapiens AS10 protein mRNA, parti	1.30	2.16
400221			NM_002082*:Homo sapiens G protein-couple	1.30	2.02
437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.30	2.44
450008	H52970	Hs.36688	WAP four-disulfide core domain 1	1.30	1.19
441591	AF055992	Hs.183	Duffy blood group	1.29	1.03
405973			Target Exon	1.29	1.32
424604	AW865388	Hs.151076	KIAA1243 protein	1.29	0.92
410899	AW809716		gb:MR4-ST0124-241199-026-h09 ST0124 Homo	1.29	2.06
405818			CX001073:gi|4176497|emb|CAA20116.1| (AL0	1.29	2.05
402621			Target Exon	1.29	3.06
436469	AK001455	Hs.5198	Down syndrome critical region gene 2	1.28	2.35
431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.28	1.44
453331	AI240665		ESTs	1.28	2.36
439791	H77774	Hs.35755	ESTs	1.28	2.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.28	3.00
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	1.28	1.28
446526	H89616		Homo sapiens cDNA FLJ13357 fis, clone PL	1.28	1.28
455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	1.28	1.28
418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.28	2.10
407711	AI085846	Hs.25522	KIAA1808 protein	1.28	1.23
417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	1.28	1.19
420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	1.27	1.24
418203	X54942	Hs.83758	CDC28 protein kinase 2	1.27	2.08
448515	H68441	Hs.13528	hypothetical protein FLJ14054	1.27	2.05
444418	AL034417	Hs.11169	Gene 33/Mig-6	1.27	1.98
427809	M26380	Hs.180878	lipoprotein lipase	1.27	1.09
414690	BE410103	Hs.12313	hypothetical protein FLJ14566	1.27	1.36
439919	AA970710	Hs.128064	ESTs	1.27	2.28
401311			Target Exon	1.27	2.05
444235	AW207346	Hs.143202	ESTs	1.27	2.00
430858	AF007190		Homo sapiens SIB 297 intestinal mucin (M	1.26	1.23
448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	1.26	2.40
400161			Eos Control	1.26	1.33
444239	R57988	Hs.10706	epithelial protein lost in neoplasm beta	1.26	1.20
438369	T77886	Hs.83428	nuclear factor of kappa light polypeptid	1.26	1.26
441944	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA	1.26	1.12
431142	AA852596	Hs.250641	tropomyosin 4	1.26	1.23
434229	R56378	Hs.181223	hypothetical protein PRO2801	1.26	2.04
406733	AA976565	Hs.297753	vimentin	1.26	1.29
422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	1.25	1.16
424137	AA335769	Hs.16262	ESTs	1.25	1.27
434868	R50032	Hs.159263	collagen, type VI, alpha 2	1.24	1.50
424408	AI754813	Hs.146428	collagen, type V, alpha 1	1.24	1.29
433750	H15448	Hs.31330	Homo sapiens clone HQ0319	1.24	1.27
447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.24	1.13
438357	AI042101	Hs.294107	ESTs	1.24	2.04
409959	BE349470		mucin 6, gastric	1.23	2.22
439897	NM_015310	Hs.6763	KIAA0942 protein	1.23	2.44
421982	AF206019	Hs.110347	REV1 (yeast homolog)-like	1.23	2.14
407207	T03651	Hs.336780	tubulin, beta polypeptide	1.23	1.32
416956	AA810664	Hs.101660	hypothetical protein MGC5391	1.23	2.39
413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hevin)	1.23	1.06
442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	1.23	1.51
452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.23	1.01
414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.22	1.41
452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.22	1.17
421341	AJ243212		deleted in malignant brain tumors 1	1.22	1.09
406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.22	1.52
452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	1.22	2.55
423189	M59371	Hs.171596	EphA2	1.22	1.15

	401899			Target Exon	1.22	1.22
	403579			Target Exon	1.22	2.34
	415954	AA171850	Hs.42251	ESTs	1.22	2.24
5	429171	AI743173	Hs.169095	ESTs, Weakly similar to ARL2_HUMAN ADP-R	1.21	1.14
	444071	AI627808	Hs.110524	ESTs	1.21	2.23
	424344	AF036973	Hs.145477	HCGIV-5 protein	1.21	2.15
	434051	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	1.21	1.25
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.21	1.39
10	404600			Target Exon	1.21	1.29
	429751	M55210	Hs.214982	laminin, gamma 1 (formerly LAMB2)	1.21	1.03
	430392	NM_000627	Hs.241257	latent transforming growth factor beta b	1.21	1.21
	422687	AW068323	Hs.119206	insulin-like growth factor binding prote	1.21	1.23
	424855	AW204725	Hs.25560	ESTs	1.20	1.98
15	418890	AA232134	Hs.190028	ESTs	1.20	1.33
	413232	BE073258	Hs.133988	hypothetical protein FKSG28	1.20	2.18
	414154	AW205314	Hs.323060	ESTs	1.20	1.34
	416784	AA334592	Hs.79914	lumican	1.20	1.27
	410933	C15974		gb:C15974 Clontech human aorta polyA mRN	1.19	2.05
20	415388	AF018081	Hs.78409	collagen, type XVIII, alpha 1	1.19	1.11
	406731	AI559131		gb:tq31g07.x1 NCI_CGAP_Ut1 Homo sapiens	1.19	1.19
	447563	BE536115	Hs.160983	EST	1.19	1.14
	405531			Target Exon	1.19	2.02
	400363	NM_001403		eukaryotic translation elongation factor	1.19	1.21
25	426611	BE178050	Hs.171271	catenin (cadherin-associated protein), b	1.19	1.18
	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	1.18	1.16
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.18	1.20
	413856	D13639	Hs.75586	cyclin D2	1.18	1.20
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	1.18	1.12
30	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	1.18	1.05
	412758	Y07818	Hs.74566	dihydropyrimidinase-like 3(ULIP)	1.18	1.06
	446868	AV660737		ESTs	1.18	1.18
	417613	AV654351	Hs.82306	destrin (actin depolymerizing factor)	1.18	1.17
	405542			Target Exon	1.18	1.98
35	419908	AW971327	Hs.293315	ESTs	1.17	2.02
	434095	AA011117	Hs.3745	milk fat globule-EGF factor 8 protein	1.17	1.19
	407230	AA157857	Hs.182265	keratin 19	1.17	1.35
	448413	AI745379	Hs.42911	ESTs	1.17	2.87
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.17	1.39
40	424572	M19650	Hs.179600	2',3'-cyclic nucleotide 3' phosphodieste	1.17	2.08
	440109	AK001138	Hs.333149	hypothetical protein FLJ10276	1.17	1.06
	405131			C1002509:gi|9933010|ref|NP_064684.1| odo	1.17	2.22
	422354	U20982	Hs.1516	insulin-like growth factor-binding prote	1.17	1.19
	442124	R66412	Hs.129013	Homo sapiens cDNA FLJ14309 fis, clone PL	1.17	1.11
45	400080			Eos Control	1.16	2.53
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	1.16	2.00
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	1.16	1.30
	429207	AA447941	Hs.123423	ESTs	1.16	1.27
	415149	X12451	Hs.78056	cathepsin L	1.16	1.12
50	400231			Eos Control	1.16	1.17
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	1.16	1.16
	422813	AV656571	Hs.121068	transmembrane 4 superfamily member 6	1.16	1.10
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.16	1.15
	422424	AI186431	Hs.296638	prostate differentiation factor	1.16	1.21
55	432745	AI821926		gb:nl78f05.x5 NCI_CGAP_Pr3 Homo sapiens	1.15	2.00
	412477	AA150864		microsomal glutathione S-transferase 1	1.15	1.23
	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	1.15	2.31
	424512	X53002	Hs.149846	integrin, beta 5	1.15	1.15
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	1.15	1.24
60	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.15	1.07
	456076	BE243877		ATPase, Na? transporting, beta 3 polypep	1.15	2.00
	403026			Target Exon	1.15	2.32
	422545	X02761	Hs.287820	fibronectin 1	1.15	1.17
	412719	AW016610	Hs.816	ESTs	1.15	1.05
65	421848	X15880	Hs.108885	collagen, type VI, alpha 1	1.15	1.14
	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	1.15	1.16
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	1.14	1.13
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	1.14	2.07
	430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen	1.14	1.14
70	418806	AA485970	Hs.191718	ESTs	1.14	2.14
	424017	AA333789		gb:EST37925 Embryo, 9 week Homo sapiens	1.14	2.16
	422003	AA361760	Hs.296326	ESTs	1.14	1.17
	437272	AW975957		gb:EST388066 MAGE resequences, MAGN Homo	1.14	2.17
	438367	N79688	Hs.204354	ras homolog gene family, member B	1.14	1.23
75	453152	AK001933	Hs.31945	hypothetical protein FLJ11071	1.13	2.36
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	1.13	1.33
	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	1.13	1.06
	425335	BE394327	Hs.296267	follistatin-like 1	1.13	1.08
	434795	BE620794	Hs.4147	translocating chain-associating membrane	1.13	1.08
80	417426	NM_002291	Hs.82124	laminin, beta 1	1.13	1.11
	452924	AW580939	Hs.97199	complement component C1q receptor	1.13	1.01
	416379	N38857	Hs.34145	ESTs	1.12	1.12
	421464	AA291553	Hs.190086	ESTs	1.12	2.01
	442420	AI024834	Hs.131729	ESTs	1.12	1.15

405369			NM_005569*:Homo sapiens LIM domain kinas	1.12	1.99
421730	AW449808	Hs.334534	glucosamine (N-acetyl)-6-sulfatase (Sanf	1.12	2.08
405932			C15000305:gi|3806122|gb|AAC69198.1| (AF0	1.11	2.01
453542	AW836724		Homo sapiens mRNA expressed only in plac	1.11	2.00
437585	AW976857		ESTs	1.11	2.01
412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.11	1.05
449931	AW875786	Hs.25734	ESTs, Weakly similar to BING1 [H.sapiens	1.11	1.03
407085	Z70759		gb:H.sapiens mitochondrial 16S rRNA gene	1.10	1.12
447191	NM_014521	Hs.17667	SH3-domain binding protein 4	1.10	1.04
406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.10	1.07
432675	AI791855	Hs.105884	ESTs	1.10	2.30
432731	R31178	Hs.287820	fibronectin 1	1.09	2.12
430763	AA485468		DNA fragmentation factor, 45 kD, alpha p	1.09	2.10
438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	1.09	1.04
405156			NM_003213*:Homo sapiens TEA domain famil	1.09	2.19
409031	AA376836		ESTs	1.09	2.22
422608	AW160644	Hs.118695	potassium voltage-gated channel, subfami	1.09	2.26
440704	M69241	Hs.162	insulin-like growth factor binding prote	1.09	1.28
410577	X91911	Hs.64639	glioma pathogenesis-related protein	1.08	2.64
414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.07	1.02
452219	AA024860	Hs.61224	ESTs	1.07	2.08
430108	AA465294		ESTs	1.07	2.11
402174			Target Exon	1.07	2.11
416952	AI767736	Hs.290070	gelsolin (amyloidosis, Finnish type)	1.07	1.00
410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	1.07	1.13
442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.07	2.21
442310	AF033199	Hs.8198	zinc finger protein 204	1.06	2.04
405536			NM_005805:Homo sapiens 26S proteasome-as	1.06	2.20
424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.06	1.06
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.06	1.06
425371	D49441	Hs.155981	mesothelin	1.06	1.27
429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	1.06	2.37
406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.06	1.05
409407	AW967370	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.05	2.00
406109			Target Exon	1.05	2.04
418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.05	2.67
403162			C2000231*:gi|9802031|gb|AAF99597.1|AF239	1.05	2.07
411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	1.05	1.07
407225	J04617		eukaryotic translation elongation factor	1.05	1.02
416955	AW889150	Hs.80595	NM_004552*:Homo sapiens NADH dehydrogena	1.05	1.10
451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	1.04	2.12
410276	AI554545		angiopoietin-2	1.04	1.04
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.04	1.04
406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.03	1.05
406773	AA812424	Hs.76067	heat shock 27kD protein 1	1.03	1.10
452082	N51905	Hs.125133	hypothetical protein FLJ22501	1.03	2.01
419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	1.03	2.24
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	1.02	1.00
408339	R97502	Hs.30443	sentrin/SUMO-specific protease	1.02	2.19
400247			Eos Control	1.02	2.04
430030	BE300094	Hs.227751	lectin, galactoside-binding, soluble, 1	1.01	1.01
442275	AW449467	Hs.54795	ESTs	1.01	1.04
406786	AW161678	Hs.111334	ferritin, light polypeptide	1.01	1.06
439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN !!!!	1.01	2.11
428043	T92248	Hs.2240	uteroglobin	1.00	1.06
406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.02
432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	2.16
450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	1.00	0.99
424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	1.00	1.08
432077	AL134685		gb:DKFZp547M126_r1 547 (synonym: hfbr1)	1.00	2.05
427687	AW003867	Hs.1570	histamine receptor H1	1.00	1.00
435256	AF193766	Hs.13872	cytokine-like protein C17	1.00	1.00
420026	AI831190	Hs.166676	ESTs	1.00	1.00
455128	AW861555	Hs.314372	EST	1.00	1.00
410685	AA497117	Hs.58893	ESTs, Moderately similar to ALU1_HUMAN A	1.00	1.00
401404			Target Exon	1.00	1.00
449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	1.00	1.00
443458	R05385	Hs.143509	hypothetical protein FLJ21924	1.00	1.00
452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	1.00	1.00
418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	1.00	1.00
447947	N33033	Hs.270215	ESTs	1.00	1.00
419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	1.00	1.00
455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	1.00	1.00
440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	1.00	1.00
444963	AI916973	Hs.213603	ESTs	1.00	1.00
410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.00	1.00
442849	R10099	Hs.269805	ESTs	1.00	1.00
420407	AA814732	Hs.145010	lipopolysaccaride-specific response 5-li	1.00	1.00
454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	1.00	1.00
418454	AA315308	Hs.195870	hypothetical protein FLJ14991	1.00	1.00
459045	N69101	Hs.40730	ESTs	1.00	1.00
455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	1.00	1.00
411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	1.00	1.00

429932	AI095005	Hs.21586	ESTs	1.00	1.00
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	1.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	1.00	1.00
431374	BE258532	Hs.251871	CTP synthase	1.00	1.00
443162	T49951	Hs.9029	DKFZP434G032 protein	1.00	1.00
432128	AA127221	Hs.296502	ESTs	0.99	2.33
451838	AW005866	Hs.193969	ESTs	0.98	3.26
438414	AA806794	Hs.131511	ESTs	0.97	3.61
435872	AA701357	Hs.192759	ESTs	0.97	0.96
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.97	1.08
424001	W67883	Hs.137476	paternally expressed 10	0.96	2.25
418869	AW516565		gb:xq01d05.x1 Soares_NHCeC_cervical_tumo	0.96	2.07
458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	0.94	2.18
418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	0.94	1.31
432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	0.94	2.12
432093	H28383		gb:yt52c03.r1 Soares breast 3NbHBst Homo	0.94	2.19
452239	AW379378		protein tyrosine phosphatase, receptor t	0.94	0.79
403167			Target Exon	0.94	2.06
402209			Target Exon	0.92	2.04
453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.92	0.74
424090	X99699	Hs.139262	XIAP associated factor-1	0.91	2.11
432816	N38913	Hs.221575	ESTs	0.91	2.15
451779	AW968616	Hs.296234	ESTs, Weakly similar to T31613 hypotheti	0.91	2.14
406851	AA609784		major histocompatibility complex, class	0.89	1.04
427698	AW972594	Hs.335499	ESTs	0.89	0.90
440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	0.88	2.42
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.87	1.14
426024	Z43405	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	0.87	2.04
400986			NM_024085*:Homo sapiens hypothetical pro	0.87	2.10
430353	AW952337		citrate synthase	0.86	2.28
404975			uncharacterized hypothalamus protein HT0	0.86	2.50
406673	M34996	Hs.198253	major histocompatibility complex, class	0.86	1.94
431323	AW970623		gb:EST382705 MAGE resequences, MAGK Homo	0.80	2.08
404926			Target Exon	0.79	2.01
432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	0.77	0.86
437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	2.10
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	0.76	2.66
406646	M33600	Hs.308026	major histocompatibility complex, class	0.76	1.09
442195	NM_001430		endothelial PAS domain protein 1	0.76	2.00
415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.76	0.78
413916	N49813	Hs.75615	apolipoprotein C-II	0.73	2.06
453716	AA037675	Hs.152675	ESTs	0.73	2.10
437802	AI475995	Hs.122910	ESTs	0.70	2.08
422282	AF019225	Hs.114309	apolipoprotein L	0.68	2.95
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	0.54	2.11
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	0.53	0.53

TABLE 34B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
442006	1239046_1	AW975183 AA973583 AI365103 AI699495 AI301787
420195	28714_1	AK002039 AL117524 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676 AA455877 N66571 AA999864 AU157344 AI817146 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145 AI919421 AI584169 AI250173 AI440227 AA669696 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471 BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645
437620	9575_20	AW976930 AW292808 AW451796 BF514112 AI806378 AI658903 AI769457 AW593455 AI625525 AI538551 AI660509 AA761825 AA973287 AA861483 W73065 AI735361 W60499 W76653 BG959557
430712	301999_1	AW044647 AI670953 AI656180 AA484715 AI659205 BF923472
411880	1139083_1	BE088101 T05990 AW872477
451149	4941_2	AF231512 AW300273 BG779015 AW510935 AI989816 AA137069 AI748876 AW150861 AI862628 AI805872 AI675382 BE855437 AW044703 AI677769 AA886718 AI753144 AA626885 AI018092 AI263010 AW026173 BE221138 AA256268 AW571932 AW276137 AI634216 AW296259 AA977716 AI302589 AA348340 AI720838 AI311733 AA015867 N73713 AL047586 AW840354 AA256196 AW840357 AW840504 T35664 Z36755 AW954421 AA247424 AI056930 T31380 BI910428 H88489 BG675223 AA443427 BE879501 AA478530 R72977 AA298568 BF792417 AA356982 BF922499 BE764808 BE565636 BF903986 BF331881 N42207 BG623760 BG611090 BF735387 BE697757 BE697755 BE718853 N78560 AI984095 AA137140 AA053711 N59865 AI078134 AA643796 T57803 AA018642 N66799 AI004600 BG896323 BF895104 N73684 N73806 N73811 AW900287 AA018641
459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
417563	2243443_1	AA203701 R86895
431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
455797	1511159_1	BE091833 BE091874 BE091871
413059	1488711_1	BE063078 BE151503 BE151498
417430	40161_2	AW872732 AW827432 AA199662 AA610519 R54983
432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
458208	45807_4	AI990640 AI380016 BM273298 BM273060
457741	120741_1	BI017968 BE044740 BI017768 AW827360 BF380597 BI017970 BF746974 BF380582 BF380592 BF908552 BF907924 BF380784 BF380651 BF380634 BE166581 BE161439 BF908606 BI017961 BE044718 AW827623 BF907758 BI017967 AW827621 AA653908 BI017765 BI017955 BI017960 BI017798

411010	1066474_1	AW813381 AW816094 AW813357 AW814469 AW813293 AW816099 AW813295 AW813425 AW813331 AW813325 AW813351 AW813427 AW813339
449780	31099_2	BG721806 BG623574 AA367501 BG436403 BG619828 BG570704 BF086115 BF086118 R78932 BG620860 BG571920 BF997723 AA368244 BG620631 BG621967 BG435818 BG620442 BG621518 H12650 BG573175 H61600 R67494 H01715 D78811 BG435953 BF107266 D79043 R67255 H01310 BG570941 BG570693 R21776 AA327133 R32578 R30775 BG570963 T86946 H61601 W86279 BF991104 R21732 BF990905 BG622861 BE929694 AI090290 BE929277 BE929284 AA367783 AA082581 D78839 H78318 N91085 BE929344 D63217 BE929334 H53536 R80360 H54070 C17064 AW962470 R00900 BG619698 BG623946 H94918 BE929345 AA004267 BF957177 BG620685 BF086421 T87029 C17044 H60972 BG573514 AA131924 D78838 BG003560 C18615 W86323 R09737 R02529 AA367502
406641	0_0	AJ235667 AJ235668 AJ235669 AJ235670
454565	1061836_1	BE141160 BE141231 BE141793 BE141791 BE141167 BE141807 BE141806 BE141805 AW807591 AW807590 AW807586 AW807583 BE141803 AW845918 BE141207 BE141158
455657	1490185_1	BE065209 BE065364 BE065110 BE065111
459189	MH1945_5	AV683451 AK057494 BG718853 BM152866 BG390826 BE709644 AI864727 BI045181 BI459637 AI909102 AI909090 BG722507 BI023834
454824	1073655_1	AW833783 AW833646 AW833525 AW833351 AW833526 AW833825
444986	704733_1	AW268472 AI204197 AW592537
413524	1518859_1	BE145894 BE145837 BM263472
422259	140437_1	BF821471 AW795791 BF844843 BF821371 AA307584 AW795790 BF833724 BE154067 BE064709
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
426603	1299162_1	AA994657 AA382291
456235	1979764_1	AA203637 AA832266 H67452
433930	19851_15	AW873618 AA620338
413464	415532_1	AL527514 AI732432 AA133309 AI225224 AV700997 BF589361 AW291763 AL121500 AA129708
411188	1072487_1	AW821260 BE162466 BE161168
410295	2817_1	BG402852 BG545066 AA150252 AL036760 AA452480 AI033256 W68776 W93372 N31248 AI052219 AI367635 W69374 N88610 R58194 BI524854 BI497111 BF940043 AI129268 AI359798 AI056480 AA121421 AI042150 AW449003 AI418180 AI419420 AI356058 BF832243 AI349330 AI359448 W76647 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268 AI336371 AI989381 AI131425 AI147483 AI311537 AW338638 AI141649 AA709414 AI187177 AA780884 AI333805 AA045312 AI623918 AI349421 W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 AI869152 N93462 N71889 AI537432 R71628 AA303089 AI498550 T60941 AV706417 AW067848 AI150677 AW338118 AI336313 AA826256 AI139518 AA662948 AA902723 AI970175 W68682 AI089380 AI148372 H99951 AW183001 AI270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914 AI862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547 N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 AI249109
400279	2140_1	Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536 AW589886 AI244419 AA749261 AA535435 AW205689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051 AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG828155 BF093014
445511	9560_8	BM471219 BE093160 BG171761 BI254009 AI905474 AA453162 AA829759 AI086559 AA776022 AI377446 BF588018 AA452822 AW614566 AA443880 AA476733 AW970674 AI393291 AA988283 AI905528 AW384956 D78656
458091	452694_1	AF150286 AV739062 AA835857
414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
410253	132134_1	AA774785 AA584875 AA577705 AA683178 AA083204 AW362057 T92332 T51823 T02858 AA083375 T92381
407102	7177_2	AW945170 BF930905 F33652 BG057818 AI368018 AI421465 AI300352 AI378525 AI264177 AI276281 AI245302 AI281050 AI190036 AW451438 AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812 R09701 AA349096 R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970 H42536 H24495 R48875 H42961 H22079 R86018
456054	1263570_1	BF314481 BE313241 BI196333 BE383148
409368	110612_1	AA071059 AA085201 AA085020
433430	2181751_1	AA961586 AI863735 AA588325
423790	886344_1	BE152393 AA330984 BE073904 BF176271
444083	10908_12	BI836699 AI123195
419618	252691_1	BG168298 AA247945 AA528295 AW971284
408404	658475_1	BF308898 BE298629 BE298765 AW192518 BE299614 BE300025 BF307463
459557	859794_1	BG623239 N58315 AI524952
455885	1524553_1	BE153524 BE153576 BE153583
451385	85022_1	AA019761 AA017656 AA017374
439781	2592493_1	AA845538 AA890229
451331	28714_1	AK002039 AL117524 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676 AA455877 N66571 AA999864 AU157344 AI817146 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145 AI919421 AI584169 AI250173 AI440227 AA669696 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471 BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645
437158	59575_1	AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847
406685	0_0	M18728
430385	MH497_8	NM_032013 AB044943 AF308609 BI769254 AI819262 AA845639 AI289073 BE670187 AA207127 T33098 AA633492 BE328324 AI083620 AI204945 AA903471 AI372602 AI049836 AI049737 BF000101 AI686167 BF436896 AI659189 T32971 AA311302 AW733149 AI435981 T03438 AA879206 AI972177 T33083 AA613910 AI971019 AI027140 AA853739 AI620528 AI637519 AI972307 BF054861 AK027665 BF082751 AI598127 T33663 AA204743 BE086660 F12132 T26372 BF765338 AA323106 AA322907 BI037062 BE315235 AV722868 BE254381 T66212 BE566142 T09034 AA406202 BF843940 AI743855 AA113356 BG990683 BE086729 BE535539
443144	16112_3	AB058726 AI651414 BE245990 BE245765 BF439734 AA648422 AA040639 AI340155 AA255928 AA278365 BE766296 AA280771 AL555562 AI474638 AI863068 BI260946 AK027039 BG615852 AI698039 AA252016 AA258886 BE905205 AW501167 BF514117 BI857400 AW297001 AI624923 AA125900 AW272165 AA190967 AA280729 AA035532 AW129692 AA125899 BG528645 BE614599 BE464693 AI560128 AA551511 AI351149 AL555561
432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46137 BE929954 AA333976 D63102 BF744491
438874	52147_1	AF075017 R66779 R22463 H02780
400221	9287_3	NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710
437751	643238_1	AW978796 AA767373 AW173343 AA836163 N27563 AA905328 R97032

410899	1063474_1	BF374577 AW809840 AW809996 AW809798 AW809695 AW809646 AW809738 BF374582 AW809716 AW809826 AW809802 AW809747 AW810152
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
446526	11131_17	AK023419 BE464935 BE221668 AI148885 BI859909 AI374780 AA766892 AI347967 AI582917 AA477117 AA229236 AA652637 AA636109 AU134580 F21298 BF802607 BE769124 AV658891 H89616 AV659853
455577	1475566_1	BE006307 BE006341 BE006311
430858	73704_1	AF007190 AW820705 BE168488 AF007192 BF753303 BG978971 BG978568
400161	2656_2	U44839 NM_004651 BC000350 BI458316 AU117940 BG759024 BG749694 BE799505 BG831537 AI816335 AA325352 AL547005 AW157038 AI859331 AI816186 AU150786 AL043549 AW162880 AU159233 AI143169 T03478 BE727648 AA764725 BE206603 AI369814 AI984369 AW157545 BE221486 H99016 AU159025 AI074496 AI494516 BE245950 AA704385 AA280862 AI479595 AI369776 BE671398 T05538 AA682249 BI677303 BE645335 AI359434 H92868 D52599 D53609 D54715 T06015 BE222174 AI954706 D53218 D53787 R69889 W86896 AI497670 R70771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H56512 D55956 BI044097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600 AI858764 D52367 W22034 BG818979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267 W21941 AA328817
409959	2781_3	AW513804 BE179199 BE179195 BE179198 BE179204 BE162686
421341	1407_1	NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492675 AI796676 AI749636 AA918144 AI814590 AI923531 BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985 AW612888 AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311
434051	73505_1	AF116622 AI114507 AA640834 BF111602 AA377999
410933	1064624_1	C16024 C15974 AW811066 AW811052 AW811020
406731	0_0	AI559131
446868	15525_1	AK074473 BC017997 BI831060 BF971101 AI886394 AI082824 AV708785 W86073 W07772 AV660737 AI816793 R52250 BG183529 AA633473 AI191256 R44763 R19947 BF571346 W86257
400231	MH494_5	BC013310 AF261085 BC004109 AY007133 BC009081 BC001601 NM_002046 M33197 BC020308 J02642 M36164 BE794233 AV721080 BE255459 BG926429 BG389312 BG477333 AI031799 BI763443 BI260432 AA989106 AV728576 BI091380 AA402499 AI200513 AI284734 AI223995 AI289749 BG283291 BM013814 AW438544 BM450203 F35435 F33262 BE890952 AA401181 BG939668 F35525 BI088182 F34674 F33506 BM471326 F34677 AW276712 AA187508 F34866 AA114245 AA522581 N23935 AI076923 AI018505 BE879774 BM465637 AI753078 BG222159 AA595947 BF970917 BI094125 AA719841 BE893087 BG775178 BE793983 BE797071 BF339134 BE409272 BE266456 BE796770 BE745957 BG755835 BE266758 BE259342 BM450181 BG748174 BE299322 BM423587 BM467637 BM452667 BM479516 BM452420 BE273297 BM466364 BM450640 BM478743 BM459094 BM455306 BM472001 BM478247 BM478771 BM480379 BM459071 BM450106 BM467584 BM464548 BM465044 BM450176 BF569359 BM462924 BM455329 BM471815 BI862301 BG331736 H04903 AA374894 BE902964
432745	112643_1	AA658826 AI821926 AI791191 AA635129 AA564492
412477	8669_2	AI220117 AI857837 AI218371 BM091400 AI304964 AI198508 AI400738 AW571549 AW950042 AI089943 AA437280 AU150878 BF197070 AI267984 BF594181 BF196688 AI433152 AI338921 AI620364 AI280197 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 N54787 AI338121 AI281153 N51899 AI087072 AA954788 AW069054 AI346309 BG529929 AI340135 BF083036 AI167365 AW819657 AA935468 AI467868 AW148701 AI383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AI553922 AI560688 AW950043 AI961682 AV706506 R01853 AA126514 N62757 AI536893 AI926052 AI418720 N99964 AI568933 AI915737 AI080691 AI185358 N48996 N68575 H82824 H60037 AI247247 T95664 BF593863 AI749637 AW088541 AA991294 AA887452 AI073726 AA633132 AA629674 AA629649 AA629656 AA576595 AI168758 AA804572 AI085786 AA994396 AA991209 AA948663 AA929054 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110 AI382839 AA194837 AA406284 AI250750 R37035 AI525586 W01244
456076	8455_1	BG210376 BG217800 BE925778 W39114 BG682395 N70644 BE709097 AW275615 BC001469 AL564888 AI088126 AW003852 BF792438 AA161295 AW970131 AI127310 AW029307 AW192534 AA843144 AW606235 BE221641 AW008111 AA224203 AA604507 AW794761 AA134005 AA126850 N99165 AW769391 AW818302 AI269871 BE503027 AW401627 AA486231 AA486417 AA191542 AA028128 AA159991 AI498090 AI241024 BM145449 AA774661 AI626021 C18251 BE185811 AA291517 N38896 N59222 AI245611 AA169207 AI298572 AA169585 AI131139 AA157960 AI439983 AI208276 AA936061 W67305 AW337587 AI357055 W04739 AI214517 AA617789 AW241277 AI880213 AI582789 AI143996 BE814848 N49964 AI936222 AI817819 F09976 AA039349 AW805002 T35117 N94388 AI689530 AW384573 AW384555 AW384539 AW384473 AA129709 AW384466 BG194342 BG204579 BG027536 AL578075 AA399553 AW794949 T88866 AW511211 R26588 R36111 BG170598 BE937009 BG678833 AA862899 H96612 H02273 AA768487 BF211173 N32570 AA088287 R68451 AA297563 H16847 R80665 AA421891 W68402 R28379 R64119 R70109 R77661 R67963 BG701844 H68670 AA169664 AA114111 BE715243 R69317 BE715252 BE713804 BG336586 NM_001679 BC011835 U51478 BM463117 AU119746 BI462090 BI227086 BG706303 BF059073 BG706532 BI544716 AI568735 BE858747 AU122881 AU126210 AI186547 AU134705 BE281323 AI147220 BE263820 AW973937 BG281863 BE858367 BE278941 AI262814 AI001194 AI391616 AI200862 N32564 AI161064 AI089818 BF514359 AI370916 AI341797 BE263168 AI218416 AI131096 AI285310 AI928440 AI066642 AI375442 AW028327 AI217792 AI161020 AI342854 AI221544 AI304700 AI343005 BM148839 AA831536 AW074258 BF940569 AI149876 AI914574 AA298442 AI241343 AA668985 AW272172 AI160537 BG209220 AA028152 AA025989
430202	1233214_1	AW968345 AA468998 T85775
424017	888651_1	AW966107 AA334317 AA333789
437272	176_2	AB075828 BG107783 AW021313 BI492345 AW385707 AW580860 AW296117 BE072066 AW580775 BF679498 AW580828 BE003666 BE003672 AW580851 AW580908 BI037146 AW580894 AW580864 H17858 N50343 N54223 F05579 F07386 F05578 AA773248 AA354359 AA330257 C20685 BE548300 AW968728 AW968554 AA777644 AA706896 AA682517 AA832267 BG165087 N51097 N51567 R95837 BI256603 W89042 R95836 R97364 AW975957 AA747943 AA811289
453542	885_22	BF568186 BF899745 AW836724 BE243668
437585	596988_1	AW976857 AI809001 AA769369 AW102732 AA761235
430763	1400_7	AL576301 AI337389 AI671302 AA978185 BF591738 AI765912
409031	9531_1	BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131 AI167170 AA836627 AA443826 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302
430108	1233254_1	AA928810 AW968393 AA465294 AA811301
410276	641443_1	AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552
400247	2764_1	BC022339 BC009610 BC010537 X79805 NM_006713 U12979 BM467614 BM450743 AU132951 AU137129 BG493425 AV758819 BG708412 BG705885 BG702217 AV716638 BG777009 BI545689 BI552153 BM476712 BG770858 BG527656 BG528277 BG391388 AV716861 BI602926

			BG290073 BI667399 BM451469 BI667173 BI602139 BG532171 BI669216 BI544727 BG721852 AV716503 AV701327 BM090738 BI492000 AI308856 BI544904 AL599813 AV715829 AV716505 AV714587 AV717902 BF668072 AV716385 BI461927 BM090954 AV717826 BG503676 AV647719 BG501392 BG428433 BE895629 BM313117 AW021050 BG435032 BM152910 AA313503 AA872377 BG574714 AV712054 AV732696 AA252476 AV712759 AL599643 BE790872 BG654930 W73337 AW675377 AV760376 AV725139 AV716379 AA887165 BE830003 AW023796 AL599291 AI902948 BG944042 F00781 AA352483 BG217897 N33888 AW581924 BG654730 D31410 AA353088 D31288 AA295029 H95170 BE935104 AU139980 BG772963 BG776470 BG532512 BG105449 BI545421 AV715456 AW386083 BG699714 AL535832 AL514940 BG190861 BG210593 AW999254 H95138 AA353863 BE764809 N50375 BE091363 BG701255 BI860846 BI832485 BG168150 BG028647 BE546301 BG900321 BI909737 BG702363 BG614141 BG611137 BG700121 BF031492 N85802 AV715940 N51590 BG993478 BE172016 AW893622
	439403	4937_10	AK056692 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145
	450724	40161_1	BF060834 BI019048 AW862002 AK056737 AA429538 AW063311 AW440655 AW231970 AA428584 AA995028 AW854593 AA984131 AA552874 AA564758 AA528743 BG927275 BE045117 AW975234 AA664937 BF749390 BG928948 AA984546 BE009153 AV732487 BE078167 AW872716 AW063245 AA578441 AI820704 AI732283 R55428 BF999154 BF880485
	432077	452948_1	AL134685 AW972760 AA525319 AA526644 AA525342 AA526632 AA525296 AV739423 AW972755
	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
	455047	1092329_1	AW852530 AW852526 AW852527 AL597969
	410934	1064652_1	AW811114 AW811095 AW811094 AW811124 AW811157 AW811054 AW811087
	454600	1063489_1	AW810001 BF374633 AW809694 AW809672 BF374748 BF374562 AW810209 AW810092 AW809786 AW810428 AW810429 AW809884 BF374650 BF374641 BF374764 BF374744 AW810552 BF374678 BF374653 BF374579 AW810168 AW810170 BF374611 BF374676 BF374667 AW810353 BF374682 AW810154 BF374688 BF374565 BF374757 BF374637 BF374743 BF374719 AW809664 BF374643 BF374680 BF374714 BF374708 BF374716 AW810432 BF374691 BF358066 AW810006 AW810345 AW809960
	455500	1228737_1	AW963582 BE064192 BE064169 BE152580 AW963587
	411745	43036_8	AV704306 BF368780 AW857826 AW859896
	418869	12789_14	AA229762 AA230035
	432093	1237011_1	AW972670 AA525808 H28359 H28383
	452239	10116_4	BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600736 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332 AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743
	406851	0_0	AA609784 R97304
	430353	10288_1	BC010106 AL560552 AU133296 AU133086 BE268567 BE268523 BI544879 BE398161 BG473088 BI544445 BE258021 BE296339 BE255040 BE263020 BG706790 AL598627 AW952337 BG758113 AW512753 BE267666 BE253415 BI225718 BE268350 BE258245 BI224965 AW772605 BG723903 BE397282 BI196341 BG702880 AI878949 AL600437 AA416759 BE259917 AI031582 BF512142 AI088248 BE560328 AI802623 AI288613 AL597585 AW768553 AI816352 BF732831 BI225687 AA833686 AA722593 AA807750 AW068064 AA405187 AI923236 N51593 AL527710 BG282576 AL525927 AL525971 BI869547 AI064725 R91856 H46814 H20112 W01682 AW848870 AW848585 AW376662 AW848985 AW848937 AW848862 AW848581 AW848512 AW848176 AW752623 AW752618 AW376822 AW376821 AW376684 AW376623 AW376622 BE706047 AW752602 AW752691 AW752674 AW752652 AA379167 AW752610 AW752584 AW752613 AW752660 AW848709 AW848576 AW849155 AW848981 AW848980 AW848979 AW848978 AW848973 AW848916 AW848713 AW848708 AW848642 AW848641 AW848639 AW848573 AW848493 AW848492 AW848489 AW848488 AW848487 AW848353 AW848352 AW848220 AW752698 AW752697 AW752682 AW752681 AW752680 AW752679 AW752664 AW752651 AW752638 AW752637 AW752636 AW752628 AW752626 AW752624 AW752619 AW752596 AW752608 AL582019 BE875587 AL529175 AW965868 BG686208 AA259073 BE696973 AA459543 AA358314 W40564 BF926427 AW849000 AW848718 AW848515 AW848507 AW848444 AW848440 AW848232 AW848222 AW752657 AW376786 AW376781 AW376615 AW376614 BI752581 AA534520 AI748906 AA047799 AI014753 AL514460 AL581982 BG743146 W24171 H20102 H11227 AW752607 AW006596 AW130378 BE716519 AW752661 AW848289 BF349557 AW752612 AW752632 AW848910 NM_004077 AF047042 AL560606 BI765896 BI196831 BI855656 BE906674 BG749937 BE535486 BE019810 AA313713 AA992542 AA332541 AA682985 AA356125 BE140478 BG750945 BI457548 BG025661 BF326302 AA325019 BG980676 AA337465 AA321974 BG949285 BG427585 R23979 BG611485 BE560678 W16977 N50379 BG824101 BG471750 BI463171 W04691 AU099360 BG471590 BM011999 BE262945 BE559801 BF756438 BE881957 BE314546 BG911831 BG150811 BG112017 AA157518 T92368 AW752620
	431323	1235269_1	AW970623 AA502839 AA502819
	442195	15007_1	U81984 NM_001430 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403

TABLE 34C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405443	7408143	Plus	90716-90887,101420-101577
401645	7657839	Minus	34986-35133
401673	7689903	Minus	122587-122705,122765-123047
405120	8099940	Plus	140176-140340
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
402333	8844110	Minus	165693-165856
404942	7382153	Plus	92095-92252
403362	8571772	Plus	64099-64260
402641	9958129	Minus	122596-125136
405600	5923640	Plus	26662-27225
405061	7656744	Minus	132492-132932
402327	7656695	Minus	108675-108770,109801-109910
404342	9838093	Plus	115854-116033
404429	7407979	Plus	31352-31498
403344	8569726	Plus	70823-70990
401593	7230957	Plus	10368-10572,11293-12356
406461	9756020	Minus	158842-159136
400609	9887671	Minus	92037-92247
402674	8077108	Minus	39290-39502
401677	9965537	Minus	62856-63086,63603-63884
405579	6456174	Plus	100996-101542
405797	1934909	Minus	5599-5681,5821-6104

405159	9966252	Plus	79659-79804	
403520	7684483	Minus	97621-98084	
402538	9801137	Minus	96314-96539	
404151	7534014	Minus	69038-69399	
400496	9743564	Plus	41515-41695	
403010	3132346	Plus	78385-79052	
406387	9256180	Plus	116229-116371,117512-117651	
402885	9926751	Plus	71919-72049	
404501	7229859	Minus	37270-37526	
402487	9797538	Plus	75677-75843	
404455	7677926	Minus	26927-27611	
401067	5764724	Minus	153366-153509	
402324	7630361	Plus	26052-26803	
402013	7407997	Plus	174540-174634,175449-175568	
401116	9966559	Plus	123579-124447	
402998	2996643	Minus	17175-17373	
405550	1552494	Plus	91720-92115	
402917	7406502	Minus	1034-1177,3143-3266	
402504	9797871	Plus	12366-12614	
405491	5801645	Plus	81857-82045	
400818	8569994	Plus	172644-172765,173085-173200	
406475	9797684	Plus	125417-125563,126052-126180	
401025	8117518	Minus	179287-179483,181044-181166,181844-18203	
402308	7340295	Minus	92080-93638	
405213	6692345	Minus	50267-51151	
400740	7329267	Minus	79920-80510,80576-80746	
402825	6165330	Minus	78572-78807	
405973	8247789	Plus	103859-104254	
405818	4071056	Plus	29055-29196	
402621	9930950	Plus	130806-131036	
401311	9212516	Minus	180124-180754	
401899	7230209	Minus	155620-155815	
403579	8101179	Minus	36167-36365	
404600	8705107	Plus	118354-118444,118649-118792	
405531	9665194	Plus	35602-35803	
405542	9857564	Plus	71331-72183	
405131	8516051	Minus	136764-137594	
403026	7670575	Plus	56521-56840	
405369	2078469	Minus	34183-34357,35686-35751	
405932	7767812	Minus	123525-123713	
405156	9966228	Plus	146733-146860,147899-147961,153127-15325	
402174	8575912	Plus	253499-253674	
405536	9795661	Plus	164091-164162,164397-164516,166720-16679	
406109	9127147	Minus	58328-58485	
403162	9838085	Plus	82652-83613	
401404	7710968	Plus	136474-136646	
403167	9838127	Plus	162599-162935	
402209	8576119	Minus	53315-53472	
400986	8085497	Minus	63140-63319	
404975	3419864	Minus	86096-86605	
404926	7341919	Minus	150411-151484	

TABLE 35A: About 323 genes upregulated in hypersensitivity pneumonitis relative to idiopathic pulmonary fibrosis or non-specific interstitial pneumonitis

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of HP AIs divided by 90th percentile of IPF AIs, where 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.
R2: 90th percentile of HP AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
402550			Target Exon	4.03	4.70
421563	NM_006433	Hs.105806	granulysin	3.37	2.70
424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	3.31	2.42
417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	3.09	1.51
411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	2.99	1.28
416350	AF188625	Hs.189507	phospholipase A2, group IID	2.71	1.43
406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	2.70	1.53
459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	2.70	1.14
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.69	2.99
452194	AI694413		olfactory receptor, family 2, subfamily	2.63	2.67
447709	U97145	Hs.19317	GDNF family receptor alpha 2	2.63	1.52
410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.59	1.00
454671	AW812929	Hs.336908	ESTs	2.50	2.34
441859	AW194364	Hs.94814	interleukin-4 induced gene-1 protein (FI	2.45	1.90
422398	AI476149	Hs.334489	hypothetical protein FLJ21992	2.45	1.36
403244			C2002870*:gi|82698|pir||JQ0985 hydroxypr	2.40	1.53

	415462	R52692	Hs.12698	ESTs	2.40	1.00
	447028	AI973128	Hs.167257	brain link protein-1	2.33	1.64
	412394	AW984150		gb:PM2-HN0008-170300-001-h09 HN0008 Homo	2.32	1.00
	450165	AA007235	Hs.63931	ESTs	2.32	1.32
5	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.30	1.81
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	2.28	1.69
	413682	BE156991		gb:RC3-HT0371-290100-013-e02 HT0371 Homo	2.27	1.59
	441320	AI768724		fibulin 1	2.27	1.87
	456766	R87310	Hs.7740	oxysterol binding protein-like 1	2.27	1.36
10	420340	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide (TiT3 com	2.26	1.98
	459721	AI299050	Hs.143835	gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.25	1.82
	405452			Target Exon	2.25	1.29
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.25	5.80
	401447			Target Exon	2.25	1.55
15	423066	Y18264	Hs.123094	sal (Drosophila)-like 1	2.24	1.51
	441704	AI458766	Hs.192125	ESTs	2.24	1.00
	405097			ENSP00000175238*:A disintegrin and metal	2.24	1.00
	408544	AW293825		ESTs	2.22	1.95
	413454	BE141162		gb:MR0-HT0076-021299-001-d03 HT0076 Homo	2.20	2.26
20	444404	M31525		major histocompatibility complex, class	2.20	1.37
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.19	2.88
	436063	AK000028		ribosomal protein S24	2.19	1.42
	429212	NM_001504	Hs.198252	G protein-coupled receptor 9	2.18	1.22
	400712			Target Exon	2.18	1.00
25	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.17	1.79
	403478			NM_022342:Homo sapiens kinesin protein 9	2.17	1.80
	418747	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 n	2.17	1.76
	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquinone oxidore	2.16	1.44
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.16	2.12
30	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	2.15	2.88
	456057	AA947457	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.15	2.50
	444346	AI142274		ESTs	2.15	2.38
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.14	1.93
	451318	AA029888	Hs.95071	ESTs	2.14	1.16
35	458935	Y16521	Hs.24812	CDP-diacylglycerol synthase (phosphatida	2.13	1.52
	417105	X60992	Hs.81226	CD6 antigen	2.13	2.61
	408219	BE061111	Hs.254211	gb:QV0-BT0041-011199-039-f02 BT0041 Homo	2.13	1.94
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	2.11	2.66
	443711	N67861	Hs.49390	ESTs	2.10	1.00
40	423234	AA323534	Hs.296162	AD037 protein	2.10	1.52
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.09	3.74
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	2.08	1.84
	405827			Target Exon	2.08	1.00
	406909	L20777	Hs.73885	gb:Human MHC class I HLA-G gene (HLA-A33	2.08	2.29
45	437295	AW779318	Hs.88417	ESTs	2.07	1.72
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	2.07	1.00
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.07	2.16
	423901	AA333006		gb:EST37064 Embryo, 8 week I Homo sapien	2.07	1.50
	405075			Target Exon	2.07	1.15
50	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.07	2.67
	406267			Target Exon	2.07	1.30
	423365	AA324992	Hs.257168	ESTs	2.06	1.70
	449970	AI678058	Hs.201227	ESTs	2.06	2.48
	430733	AW975920	Hs.121036	ESTs	2.06	1.00
55	446323	AI288274	Hs.345792	ESTs	2.06	1.00
	402240			Target Exon	2.05	1.94
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.05	1.44
	424463	AW195353	Hs.119903	ESTs	2.04	1.32
	400107			Eos Control	2.04	2.42
60	404811			NM_021096:Homo sapiens calcium channel,	2.03	2.18
	403589			Target Exon	2.03	1.57
	404088			Target Exon	2.03	1.00
	414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.03	2.04
	429073	AA446167	Hs.47385	ESTs	2.03	3.10
65	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	2.02	1.92
	401897			C17001987:gi|7303380|gb|AAF58438.1| (AE0	2.02	1.55
	431094	AW972276	Hs.116195	ESTs	2.02	1.00
	424899	AL119387	Hs.119062	ESTs	2.01	2.41
	419711	C02621	Hs.159282	ESTs	2.01	1.92
70	459019	AA017156	Hs.40719	hypothetical protein KIAA1164	2.01	1.76
	405453			NM_005748*:Homo sapiens YY1-associated f	2.01	1.24
	402516			Target Exon	2.01	1.00
	457365	AA577297	Hs.303249	EST	2.01	2.36
	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfami	2.01	2.62
75	436553	AW407157	Hs.8997	immunoglobulin lambda locus	2.00	1.64
	406266			Target Exon	2.00	2.46
	419409	AW297831	Hs.143792	hypothetical protein MGC2656	2.00	1.60
	435028	AW193035	Hs.187370	ESTs	2.00	1.55
	404696			NM_013443:Homo sapiens CMP-NeuAC:(beta)-	2.00	1.21
80	403533			Target Exon	2.00	1.17
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.00	1.00
	424148	BE242274	Hs.1741	integrin, beta 7	1.99	3.66
	419833	AA251131	Hs.220697	ESTs	1.99	1.69

423196	AK001866	Hs.125139	hypothetical protein FLJ11004	1.99	1.84
426416	AW612744	Hs.169824	killer cell lectin-like receptor subfami	1.98	2.56
449317	AW293413	Hs.132906	19A24 protein	1.98	2.44
424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	1.97	2.51
422109	S73265	Hs.1473	gastrin-releasing peptide	1.97	3.32
424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.96	1.86
406303			C16000922:gi|7499103|pir||T20903 hypothe	1.96	2.16
438676	AA813745	Hs.123446	ESTs	1.95	3.62
404240			NM_018950:Homo sapiens major histocompat	1.95	2.06
404056			Target Exon	1.94	2.60
425508	AA991551	Hs.97013	Homo sapiens, Similar to RIKEN cDNA 2310	1.93	3.24
429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	1.93	2.35
416941	BE000150	Hs.48778	niban protein	1.92	2.24
446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.92	5.44
409153	W03754	Hs.50813	hypothetical protein FLJ20022	1.92	6.08
419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	1.90	5.52
446608	N75217	Hs.257846	ESTs	1.90	4.63
425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.89	1.50
414812	X72755	Hs.77367	monokine induced by gamma interferon	1.89	4.93
422994	AW891802	Hs.296276	ESTs	1.88	3.30
424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.88	2.17
433671	AW138797	Hs.132906	19A24 protein	1.88	1.83
412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	1.86	3.12
447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of	1.86	1.88
432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TIT3	1.84	1.65
419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	1.83	2.46
427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	1.82	2.07
431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	1.82	2.63
436485	X59135	Hs.156110	Immunoglobulin kappa constant	1.82	2.75
432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.81	4.56
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.80	5.10
448569	BE382657	Hs.21486	signal transducer and activator of trans	1.79	1.89
429670	L01087	Hs.211593	protein kinase C, theta	1.78	3.34
412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.78	3.55
413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.78	1.97
406672	M26041	Hs.198253	major histocompatibility complex, class	1.76	2.12
452203	X57522		transporter 1, ATP-binding cassette, sub	1.75	1.55
426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	1.73	2.04
447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	1.73	1.56
414512	AL044336	Hs.6831	golgi phosphoprotein 1	1.73	2.00
426752	X69490	Hs.172004	titin	1.73	2.62
444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	1.72	2.30
452334	D60471	Hs.13390	gb:HUM111D09B Clontech human fetal brain	1.72	2.12
446227	AI281459	Hs.270114	ESTs	1.72	2.48
407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.72	2.72
423799	AW026300	Hs.132906	19A24 protein	1.71	2.40
458332	AI000341		ESTs	1.70	3.71
408380	AF123050	Hs.44532	diubiquitin	1.70	2.71
437644	AA748575	Hs.136748	lectin-like NK cell receptor	1.70	2.58
402736			NM_024852:Homo sapiens hypothetical prot	1.69	2.10
438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.69	1.39
422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	1.68	2.02
426202	BE266484	Hs.82916	chaperonin containing TCP1, subunit 6A (	1.68	2.14
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	1.68	3.30
420440	NM_002407	Hs.97644	mammaglobin 2	1.67	2.42
416967	BE616731	Hs.80645	interferon regulatory factor 1	1.67	1.49
415823	R81864	Hs.205103	ESTs	1.65	2.16
421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	1.65	1.58
427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	1.63	1.94
444929	AI685841	Hs.161354	ESTs	1.63	2.16
439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.63	1.74
418196	AI745649	Hs.26549	KIAA1708 protein	1.62	2.76
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.62	4.42
438568	R98865	Hs.11135	major histocompatibility complex, class	1.62	1.74
430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.62	1.85
433934	AW273261	Hs.216292	ESTs	1.62	2.00
443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	1.61	2.00
450000	AI952797	Hs.10888	hypothetical protein FLJ21709	1.61	1.46
415349	AI766697	Hs.13231	ESTs	1.60	2.00
406656	M16714	Hs.89643	major histocompatibility complex, class	1.60	1.47
456974	M12529	Hs.169401	apolipoprotein E	1.60	1.63
416401	N80139	Hs.268916	ESTs	1.59	1.68
439372	AF088033	Hs.159225	ESTs	1.59	2.04
434666	AF151103	Hs.112259	T cell receptor gamma locus	1.59	4.08
417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	1.58	3.06
417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	1.58	2.37
431903	AB029488	Hs.272100	SMS3 protein	1.57	2.14
413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1.57	2.28
425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	1.56	1.46
412472	AW975398	Hs.293836	ESTs	1.56	2.26
451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	1.56	2.38
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.55	1.67
449835	AW979300	Hs.293813	ESTs	1.55	2.16

	405545			Target Exon	1.55	2.64
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	1.55	3.81
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.54	2.14
	424243	AI949359	Hs.143600	ESTs, Highly similar to cis Golgi-locali	1.53	2.62
5	457500	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	1.53	2.04
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	1.53	2.00
	439039	AI656707	Hs.48713	ESTs	1.53	2.38
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.52	2.65
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.52	2.06
10	415198	AW009480	Hs.943	natural killer cell transcript 4	1.52	1.40
	431594	AI823999		ESTs	1.52	2.12
	432656	NM_000246	Hs.3076	MHC class II transactivator	1.52	2.20
	422426	W79117	Hs.58559	ESTs	1.52	2.22
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	1.51	2.80
15	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	1.50	1.67
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.49	3.12
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.49	1.78
	419166	AA234638	Hs.293584	ESTs	1.49	2.10
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	1.49	1.47
20	435304	H10709	Hs.269524	ESTs	1.48	2.96
	452834	AI638627	Hs.105685	KIAA1688 protein	1.48	2.14
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.48	1.38
	429272	W25140	Hs.110667	ESTs	1.48	3.19
	428379	X06026	Hs.2259	CD3G antigen, gamma polypeptide (TiT3 co	1.48	1.66
25	433231	AB040926	Hs.143552	KIAA1493 protein	1.47	2.16
	408847	AW290997	Hs.30348	ESTs	1.46	2.08
	405441			Target Exon	1.46	2.99
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	1.45	1.56
	459644	AW197203		gb:xm38b01.x1 NCI_CGAP_GC6 Homo sapiens	1.45	2.44
30	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	1.45	1.70
	422934	BE244189	Hs.122492	hypothetical protein	1.44	1.27
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	1.44	3.46
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.44	1.71
	421407	T82331	Hs.182278	ESTs, Weakly similar to CGHU6C collagen	1.43	1.56
35	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	1.43	1.25
	400269			Eos Control	1.43	2.02
	420973	AA743415	Hs.291368	ESTs	1.42	2.06
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	1.42	2.20
	430015	AW768399		ESTs	1.41	2.06
40	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	1.41	1.31
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	1.72
	437479	R61866	Hs.101277	ESTs	1.40	2.52
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	1.40	2.17
	416030	H15261	Hs.21948	ESTs	1.40	2.62
45	419886	AA251562	Hs.146168	ESTs, Weakly similar to AF118023 1 SH3 d	1.40	1.68
	443951	F13272		ferritin, light polypeptide	1.40	1.64
	414875	H42679	Hs.77522	major histocompatibility complex, class	1.40	1.42
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	1.40	1.34
	428782	X12830	Hs.193400	interleukin 6 receptor	1.40	2.30
50	400680			NM_014207:Homo sapiens CD5 antigen (p56-	1.39	1.93
	428289	M26301	Hs.2253	complement component 2	1.39	1.39
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypotheti	1.39	1.42
	406645	M57466	Hs.814	major histocompatibility complex, class	1.39	1.45
	441379	AW175787	Hs.334841	selenium binding protein 1	1.38	1.32
55	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.38	2.04
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.38	1.35
	423526	AB011086	Hs.129739	KIAA0514 gene product	1.37	1.41
	424168	L29277	Hs.321677	signal transducer and activator of trans	1.37	1.33
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.37	1.74
60	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.35	1.38
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.35	1.54
	452353	C18825	Hs.29191	epithelial membrane protein 2	1.34	1.47
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.31	1.77
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	1.31	1.53
65	444633	AF111713	Hs.286218	junctional adhesion molecule 1	1.30	1.37
	430998	AF126847	Hs.204038	indolethylamine N-methyltransferase	1.29	1.49
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.28	1.36
	451864	N20370	Hs.69547	ESTs	1.28	1.42
	421140	AA298741	Hs.102135	signal sequence receptor, delta (transio	1.28	1.31
70	412790	NM_014767	Hs.74583	KIAA0275 gene product	1.28	1.63
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	1.28	1.38
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.28	1.36
	435822	T95594	Hs.187435	ESTs	1.27	1.82
	455863	AA907305	Hs.36475	ESTs	1.27	1.36
75	404277			NM_019111*:Homo sapiens major histocompa	1.27	1.52
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	1.27	1.54
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	1.27	1.53
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.26	1.27
	434747	AA837085		ESTs	1.26	1.60
80	425320	U29344	Hs.83190	fatty acid synthase	1.25	1.35
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.25	1.41
	434544	H98071	Hs.4055	chromosome 21 open reading frame 50	1.25	1.30
	404854			Target Exon	1.25	1.57

406973	M34996	Hs.198253	major histocompatibility complex, class	1.25	1.57
421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHU1E collagen	1.24	1.26
431779	AW971178	Hs.268571	apolipoprotein C-I	1.24	1.39
416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	1.23	2.08
406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.23	1.20
426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.22	1.24
415661	AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.22	1.16
406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.22	1.17
420679	X57152	Hs.99853	fibrillarin	1.22	1.30
443071	AL080021	Hs.8986	complement component 1, q subcomponent,	1.22	1.58
418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfami	1.21	1.33
430250	NM_016929	Hs.283021	chloride intracellular channel 5	1.21	1.60
406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.20	1.20
436906	H95990	Hs.181244	major histocompatibility complex, class	1.19	1.27
422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.19	1.62
408279	AF216965	Hs.44095	Homo sapiens, clone MGC:12617, mRNA, com	1.18	1.25
411372	AI147861	Hs.213289	low density lipoprotein receptor (famili	1.17	1.33
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.16	1.49
406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.16	1.15
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	1.16	1.38
432805	X94630	Hs.3107	CD97 antigen	1.16	1.22
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	1.16	1.41
438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.16	1.36
443623	AA345519	Hs.9641	complement component 1, q subcomponent,	1.15	1.27
429832	AW293301	Hs.288472	ESTs, Weakly similar to UBPF_HUMAN UBIQU	1.15	1.72
438183	BE263252	Hs.6101	hypothetical protein MGC3178	1.15	1.21
432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	1.14	1.21
406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	1.14	1.41
414662	AL036058	Hs.76807	major histocompatibility complex, class	1.12	1.25
452547	AA335295	Hs.74120	adipose specific 2	1.11	1.39
414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.11	1.22
430280	AA361258	Hs.237868	interleukin 7 receptor	1.10	1.73
441384	AA447849	Hs.288660	retinoic acid induced 3	1.09	1.22
424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.09	1.14
419200	AW966405		EST	1.08	1.64
416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.08	1.18
409428	M33680	Hs.54457	CD81 antigen (target of antiproliferativ	1.07	1.12
447023	AA356764	Hs.17109	integral membrane protein 2A	1.07	1.71
421481	AW391972	Hs.104696	KIAA1324 protein	1.07	1.58
406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.07	1.23
412819	T25829	Hs.24048	FK506 binding protein precursor	1.06	1.45
418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.06	1.24
431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.05	1.17
448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.04	1.21
407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.04	9.14
418156	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	1.03	6.65
438089	W05391		nuclear receptor subfamily 1, group I, m	1.03	8.00
429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	1.01	1.25
406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.18
438091	AW373062		nuclear receptor subfamily 1, group I, m	0.99	12.84
407018	U49869		NM_018955:Homo sapiens ubiquitin B (UBB)	0.99	1.07
412896	AW804157	Hs.308026	major histocompatibility complex, class	0.98	1.57
435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	0.97	1.40
426530	U24578	Hs.278625	complement component 4A	0.96	1.28
456898	NM_001928	Hs.155597	D component of complement (adipsin)	0.95	1.29
407241	M34516		gb:Human omega light chain protein 14.1	0.94	1.11
425371	D49441	Hs.155981	mesothelin	0.92	1.45
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	0.91	1.28

TABLE 35B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
411089	5597_6	BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680
452194	90339_1	AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 AI709339
410910	1063929_1	AW810196 AW810555 AW810507 AW810204 AW810619 AW810534
412394	1174616_1	AW947794 AW947793 AW947802 AW947798 AW947792 AW984150 AW984166 AW984167 AW984168 AW984179 AW984134 AW984160 AW984180 AW984194 AW984202 AW984190
413682	1527038_1	BE156943 BE157375 BE156965 BE156949 BE156956
441320	58978_5	AI346734 AI377971 BG193341 BG548376 AA928353 AI768724 BG215700 AA449370 BI462157 BI060283 BG677508 AA318802 BG719160
408544	683260_1	AW293825 AW235391
413454	1515217_1	BE141291 BE141306 BE141288 BE141283 BE141162 BE141168 BE141290 BE141161 BE141165
444404	16136_1	BC013183 AW408658 NM_002119 M31525 M26039 BM456399 BF732381 BM152457 AW407685 BM193161 AW407778 BI819141 AA702254 BF855074 BI761232

436063	5483_1	AK000026 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N26596 AA884747 AA512890 BG436593
444346	47906_14	AI147991 AI142274 AI198553
424281	892055_1	AA338252 AA338213
423901	887384_1	AW962691 AA333006 AA332289
414991	1785136_1	D78831 C17898 D78863
411673	1096744_1	BF330730 BF350539 BE153665 BE065062 BE064650 BE064863 BF330763 BE153820 BE064737 BE155079 BE064651 AW856751 AW856622 BE064691 BE153674 BE153698 BE064730 BE153536
452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA366648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
458332	1139685_1	AI000341 AI766341 AW873274
431594	1236764_1	AI823999 AA970060 AA508176 AW972585 AI873427 AW972389
414372	484211_1	BI093452 AW970865 BG118285 AA559075 AA492132 AW753140 AA213770 AA143654
459644	662385_1	W03900 AW197203 AW753300
400269	2726_1	X65018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 BI621373 BI770406 BI823937 BI820265 BI489632 BG482911 AA617783 AI807697 AW205576 T94427 AA487101 T94513 BI819407 BI822450 BI820618 BI824619 BG542824 BG537862
430015	713_2	BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW026983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
443951	MH1768_18	AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N40935 W52768 AA854747 AA861945 AA878472 AA778270 W32249 AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520
413497	1518002_1	BE177661 H06215 BE144709 BE144829
434747	117643_1	AW976537 AI033582 AA837085 AA745261 AA648395
406782	0_0	AA430373 AA968771
419200	9531_1	BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302
438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581

TABLE 35C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402550	7652009	Minus	80413-80673
403244	7637828	Plus	175792-176144
405452	7656638	Minus	93876-94275

401447	8574299	Minus	65053-65283
405097	8072599	Plus	171191-171360
400712	8118874	Plus	36087-36268
403478	9958258	Plus	116458-116564
405827	7109593	Plus	10279-10972
405075	7770506	Minus	124680-125321
406267	7528342	Minus	2570-2731
402240	7690131	Plus	104382-104527,106136-106372
404811	3702428	Plus	26424-26596,28854-28987
403589	8101229	Plus	5-330
404088	9958257	Plus	184131-184295
401897	8569218	Plus	604-767
405453	7656675	Minus	83710-83980
402516	9798099	Minus	195342-195511
406266	7528342	Minus	2365-2518
404696	9800109	Minus	60037-60144,62675-63081
403533	8076874	Plus	162922-163658
406303	8575868	Plus	173622-173786
404240	5002624	Minus	116132-116407,116653-116922
404056	3548785	Plus	75843-76980,77146-78263
402736	9212044	Minus	66876-67010
405545	1054740	Plus	118677-118807,119091-119296,121626-12182
405441	7408124	Plus	100952-101283
400680	8118752	Plus	118343-118684,120720-121013
404277	1834458	Minus	91665-91946
404854	7143420	Plus	14260-14537

TABLE 36A: About 52 genes upregulated in non-specific interstitial pneumonitis relative to hypersensitivity pneumonitis or idiopathic pulmonary fibrosis

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of NSIP AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50.
R2 90th percentile of NSIP AIs divided by 90th percentile of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
435140	AA668123	Hs.134170	ESTs	2.76	2.76
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57	1.00
435375	AI733610		ESTs	2.55	2.55
420813	X51501	Hs.99949	prolactin-induced protein	2.55	1.35
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.52	0.73
421296	NM_002666	Hs.103253	perilipin	2.50	2.45
419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.43	1.79
408882	H12084	Hs.31110	ESTs, Weakly similar to MAGE-B4 [H.sapie	2.42	1.77
437318	AW362939	Hs.120721	ESTs	2.36	1.61
421823	N40850	Hs.28625	ESTs	2.29	0.56
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.28	0.89
430536	AI809163	Hs.9908	nitrogen fixation cluster-like	2.25	2.80
414009	R67516		ESTs	2.19	1.86
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.19	0.33
430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	2.18	1.24
413722	BE247354	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.14	1.95
433874	AW204429	Hs.155033	ESTs	2.13	1.72
429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.12	0.91
414290	AI568801	Hs.71721	ESTs	2.11	0.81
451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.11	1.01
406785	AA588061		gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens	2.10	1.61
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.08	0.85
444179	W35132	Hs.267442	ESTs	2.08	1.13
430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.05	0.80
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.04	0.79
439134	AA830599		ESTs	2.04	1.89
418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.02	2.02
457311	AI497811	Hs.172753	Homo sapiens chromosome 19, BAC 41195 (C	2.00	1.45
402274			C19000498*:gi|4567179|gb|AAD23607.1|AC00	1.88	2.24
453222	AA033929	Hs.19156	ESTs	1.77	2.00
447261	NM_006691	Hs.17917	extracellular link domain-containing 1	1.73	2.02
427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	1.69	1.69
406714	AI219304	Hs.266959	hemoglobin, gamma G	1.62	2.47
418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	1.59	2.04
404090			Target Exon	1.48	2.03
444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	1.39	2.06
414386	X00442	Hs.75990	haptoglobin	1.09	1.44
439372	AF088033	Hs.159225	ESTs	1.05	2.13
432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.01	2.08
412472	AW975398	Hs.293836	ESTs	1.00	2.26
432894	AW167668	Hs.279772	brain specific protein	0.97	1.19
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.96	2.06
416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	0.95	1.08

424310	AA338648	Hs.50334	testes development-related NYD-SP22	0.93	1.47
422109	S73265	Hs.1473	gastrin-releasing peptide	0.92	3.05
420440	NM_002407	Hs.97644	mammaglobin 2	0.91	2.11
418196	AI745649	Hs.26549	KIAA1708 protein	0.90	2.25
418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	0.89	1.11
419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	0.85	1.74
446608	N75217	Hs.257846	ESTs	0.82	2.10
418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	0.73	1.32
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	0.70	1.76

TABLE 36B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
435375	130020_1	AI733610 AI049989 AA678769
414009	438978_1	BE221268 R67515 AV730582 R67516
406785	0_0	AA588061
439134	2581476_1	AA830599 AA970659 AA883802
418512	12225_6	BM046773 AA224297 T33786 T08951 T09274 T08592 T30936 AA350905
418333	73080_1	AF264624 AW668618 AV731446 R93353 AA584550 AV732728 BF802614 BF434359 AA077092 BI027317 AA199812 AW629027 AA831618 AI124782 AA765804 AA055698 AA677404 AA055366 AA889402 AA765530 BE503126 BE467367 AW139964 W81697 AI887846 W81696 AA447817 AA447667 F13631 BF055573 AW268271 AW088477 BF677839 AL601859 AW502118 AW502624 AA574189 BI020104

TABLE 36C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402274	2935596	Plus	5604-6527
404090	9967460	Minus	100815-100966

TABLE 37A: About 205 genes downregulated in lung fibrosis relative to normal lung

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of normal lung AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigeneID	Unigene Title	R1
454229	AW957744	Hs.278469	lacrimal proline rich protein	11.67
432128	AA127221	Hs.296502	ESTs	9.86
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	7.69
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.32
420958	AA309431	Hs.66	interleukin 1 receptor-like 1	7.13
402608			Homo sapiens defensin, alpha 1, myeloid-	6.67
406714	AI219304	Hs.266959	hemoglobin, gamma G	5.40
406673	M34996	Hs.198253	major histocompatibility complex, class	5.22
416539	Y07909	Hs.79368	epithelial membrane protein 1	5.04
418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	4.77
409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	4.74
450847	NM_003155	Hs.25590	stanniocalcin 1	4.46
404518			CD83 antigen (activated B lymphocytes, i	4.36
413951	AW051200	Hs.75640	natriuretic peptide precursor A	4.32
407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	4.25
456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.23
429509	AW614420	Hs.204354	ras homolog gene family, member B	4.14
445769	AI741471	Hs.23666	ESTs	4.10
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.06
425571	AJ007292	Hs.158306	ephrin-A2	3.92
423168	R34385	Hs.124940	GTP-binding protein	3.80
401234			mitogen-activated protein kinase 8 inter	3.78
402181			Target Exon	3.77
403479			NM_007064:Homo sapiens serine/threonine	3.68
435424	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL	3.68
402911			NM_021158*:Homo sapiens protein kinase d	3.66
442195	NM_001430		endothelial PAS domain protein 1	3.65
400089			Eos Control	3.60

	413948	C05145	Hs.75636	myosin light chain 2a	3.56
	438564	AA381553	Hs.198253	major histocompatibility complex, class	3.54
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.54
	431319	AA873350	Hs.302232	ESTs	3.52
5	434292	AF124368	Hs.306551	Homo sapiens IMAGE Consortium ID 839832,	3.48
	401540			NM_002675:Homo sapiens promyelocytic leu	3.46
	426477	AA379464	Hs.154073	gb:EST92386 Skin tumor I Homo sapiens cD	3.43
	402328			Target Exon	3.42
	401590			Target Exon	3.42
10	403645			NM_024513*:Homo sapiens FYVE and coiled-	3.37
	403376			Target Exon	3.36
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.35
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.28
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.27
15	401126			NM_006856*:Homo sapiens activating trans	3.27
	408243	Y00787	Hs.624	interleukin 8	3.23
	412429	AV650262	Hs.75765	GRO2 oncogene	3.22
	426420	BE383808	Hs.322430	NDRG family, member 4	3.21
	449338	H73444	Hs.394	adrenomedullin	3.19
20	401904			Target Exon	3.16
	401919			NM_012448*:Homo sapiens signal transduce	3.14
	406443			ENSP00000236574*:Hypothetical 21.8 kDa p	3.14
	458232	BE217872	Hs.279537	ESTs	3.12
	406016			Target Exon	3.12
25	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	3.11
	451831	NM_001674	Hs.460	activating transcription factor 3	3.08
	450562	AW136468	Hs.202199	ESTs	3.07
	405938			Target Exon	3.04
	451029	AA852097	Hs.25829	ras-related protein	3.02
30	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	2.98
	439839	AA889354		ESTs	2.98
	439891	AL389940	Hs.109968	ESTs	2.96
	418935	T28499	Hs.89485	carbonic anhydrase IV	2.95
	418853	NM_005236	Hs.89296	excision repair cross-complementing rode	2.95
35	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.94
	410326	AI368909	Hs.47650	ESTs	2.88
	407244	M10014		fibrinogen, gamma polypeptide	2.85
	459721	AI299050	Hs.143835	gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.84
	416212	R40290	Hs.124685	ESTs	2.84
40	428686	AA431801	Hs.98764	ESTs, Weakly similar to A29861 actin gam	2.83
	437508	AI204354	Hs.121347	ESTs	2.82
	437990	AI686579	Hs.121784	ESTs	2.82
	443709	AI082692	Hs.134662	ESTs	2.81
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	2.80
45	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	2.79
	404231			Target Exon	2.78
	434305	AI018280	Hs.130189	ESTs	2.77
	445493	AI915771		metallothionein 1E (functional)	2.76
	418056	AA524886		gb:nh34f02.s1 NCI_CGAP_Pr3 Homo sapiens	2.76
50	404102			Target Exon	2.75
	440206	AI762232	Hs.46794	ESTs	2.75
	403031			cathepsin D (lysosomal aspartyl protease	2.75
	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	2.74
	459330	C16931		gb:C16931 Clontech human aorta polyA mRN	2.74
55	456967	AW004056	Hs.168357	T-box 2	2.74
	427602	AI375258	Hs.98005	ESTs	2.74
	431367	Z20964	Hs.323817	DKFZP547E1010 protein	2.72
	406059			Target Exon	2.71
	420575	BE263301	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	2.71
60	457275	AA463422	Hs.209431	ESTs	2.71
	432559	AW452948	Hs.257631	ESTs	2.71
	402483			NM_020389:Homo sapiens putative capacita	2.70
	416069	R37101	Hs.20982	ESTs	2.70
	445445	AF238870	Hs.275706	Homo sapiens clone GLSH-3 similar to gli	2.69
65	436232	AA707006	Hs.187863	ESTs	2.68
	418773	T39748	Hs.325474	Target CAT	2.67
	434038	AA622104		ESTs	2.67
	405448			Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.66
	404439			ENSP00000067222*:Mitochondrial 28S ribos	2.65
70	435724	N39308	Hs.117898	ESTs	2.65
	404026			Target Exon	2.65
	400881			NM_025080:Homo sapiens hypothetical prot	2.64
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	2.62
	405429			Target Exon	2.62
75	402642			C1002296:gi|6677817|ref|NP_033126.1| rep	2.61
	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	2.61
	449293	AA001088	Hs.29739	ESTs, Weakly similar to C34323 GTP-bindi	2.61
	416157	NM_003243	Hs.342874	transforming growth factor, beta recepto	2.60
	446122	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.59
80	433291	AF007191		gb:Homo sapiens SIB 276 intestinal mucin	2.59
	426795	AI810474	Hs.196945	ESTs	2.58
	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	2.58
	430768	AB030207	Hs.247888	guanine nucleotide binding protein 13, g	2.58

	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.57
	442681	AI809182	Hs.130907	ESTs	2.57
	408652	R43409	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	2.56
	402217			C19001662*:gi|6753872|ref|NP_034345.1| i	2.56
5	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.56
	455674	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	2.56
	457831	AA706937	Hs.120802	ESTs, Moderately similar to A26641 Na?ex	2.56
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.55
	458648	AW444551	Hs.35380	x 001 protein	2.55
10	456663	BE251104	Hs.113052	RNA cyclase homolog	2.54
	440178	AW502463	Hs.196521	ESTs	2.53
	457139	AI557280	Hs.184270	capping protein (actin filament) muscle	2.52
	405857			Target Exon	2.51
	410204	AJ243425	Hs.326035	early growth response 1	2.50
15	412851	AI826502	Hs.97269	ESTs	2.49
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	2.49
	409209	AA460160	Hs.73217	ESTs	2.49
	447173	AW449385	Hs.157294	ESTs	2.48
	440034	AI908639	Hs.246781	ESTs	2.44
20	418168	R85350	Hs.101368	ESTs	2.43
	417295	AW993524	Hs.43148	epithelial membrane protein 1	2.43
	406305			transcriptional adaptor 3 (ADA3, yeast h	2.42
	427886	AA417083	Hs.104789	ESTs	2.42
	436409	AJ238982	Hs.183656	VNN3 protein	2.42
25	413861	BE175424		gb:RC4-HT0578-170300-012-d01 HT0578 Homo	2.40
	403605			C3000142*:gi|4503015|ref|NP_003900.1| co	2.37
	402594			C1002603*:gi|9887091|gb|AAG01738.1|AF248	2.37
	402803			NM_001397:Homo sapiens endothelin conver	2.37
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.36
30	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	2.36
	442630	AW572938	Hs.130580	ESTs	2.35
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	2.33
	405156			NM_003213*:Homo sapiens TEA domain famil	2.31
	448162	AL039531	Hs.323363	hypothetical protein FLJ22169	2.31
35	403591			Target Exon	2.31
	406193			Target Exon	2.30
	420813	X51501	Hs.99949	prolactin-induced protein	2.30
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	2.28
	400703			C11001794*:gi|10946612|ref|NP_067286.1|	2.27
40	415026	AA159356	Hs.72308	ESTs	2.25
	400334	Y13187		Homo sapiens dmd gene, intron 11	2.18
	445878	AI262974	Hs.145587	ESTs	2.18
	404975			uncharacterized hypothalamus protein HT0	2.18
	436370	R01220	Hs.185679	ESTs	2.17
45	400513			Target Exon	2.16
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.15
	415405	R59141		gb:yg96d11.r1 Soares infant brain 1NIB H	2.15
	407612	U26403	Hs.37142	ephrin-A5	2.12
	409837	AW501504		gb:UI-HF-BP0p-ajd-h-04-0-UI.r1 NIH_MGC_5	2.08
50	458637	AV657446		gb:AV657446 GLC Homo sapiens cDNA clone	2.07
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	2.00
	418922	AW956580	Hs.42699	ESTs	1.98
	402404			NM_024967*:Homo sapiens hypothetical pro	1.98
	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	1.98
55	413731	BE243845	Hs.75511	connective tissue growth factor	1.96
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.96
	428193	NM_004235		Kruppel-like factor 4 (gut)	1.93
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.92
	439453	BE264974	Hs.5566	thyroid hormone receptor interactor 13	1.92
60	433883	AI925688	Hs.222312	ESTs	1.91
	406564			msh (Drosophila) homeo box homolog 2	1.91
	403581			Target Exon	1.90
	403716			Target Exon	1.90
	404758			Target Exon	1.90
65	439500	W73158	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	1.89
	448793	AI864581		ESTs	1.84
	435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	1.83
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.82
	402051			Target Exon	1.81
70	409859	AW501926		gb:UI-HF-BR0p-ajp-f-08-0-UI.r1 NIH_MGC_5	1.78
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.78
	405063			Target Exon	1.78
	405163			C5000561*:gi|7513700|pir||T14151 Inv pro	1.75
	402386			Target Exon	1.73
75	406755	N80129	Hs.199263	metallothionein 1L	1.73
	409811	AW500896		gb:UI-HF-BP0p-air-a-03-0-UI.r1 NIH_MGC_5	1.70
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.70
	400489			Target Exon	1.70
	428704	AA432007	Hs.192090	ESTs	1.69
80	429307	AU076592	Hs.198951	jun B proto-oncogene	1.67
	400116			Eos Control	1.65
	404795			Target Exon	1.65
	408053	AW139474	Hs.246862	ESTs	1.65

	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	1.63
	428800	M57627	Hs.193717	interleukin 10	1.63
	451676	R84770	Hs.33538	ESTs, Weakly similar to oxygen-regulated	1.62
	402394			Target Exon	1.61
5	404818			Target Exon	1.60
	436364	X06096		gb:Human macrophage alpha1-antitrypsin c	1.55
	420369	U96769	Hs.97220	chondroadherin	1.54
	405590			CX001497*:gi|4557543|ref|NP_001384.1| ex	1.54
	402448			Target Exon	1.53
10	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.51
	409020	AA062549	Hs.21162	retbindin	1.51
	405443			Target Exon	1.12

TABLE 37B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409385	110758_1	T65940 T64515 AA071267 AA071334
442195	15007_1	U81984 NM_001430 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403
439839	2594580_1	AI023587 AA889354 AA846791
445493	423456_1	AV711317 AI809938 AI808768 AI240593 AI915771
418056	286199_1	AW971347 AA524886 AA211537 BF903005 BF357120
413164	1492512_1	BE068758 BE068745 BE068689 BE068778 BE068529 BE068683 BE068445 BE068392 BE068719 BE068473 BE068521 BE068628 BE068422 BE068618 BE068354 BE068390 BE068414 BE068433 BE068369 BE068384 BE068661 BE068324 BE068301 BE068436 BE068754 BE068329 BE068672 BE068494 BE068596 BE068332 BE068347 BE068588 BE068328 BE068493 BE068740 BE068685 BE068759 BE068307 BE068429 BE068303 BE068693 BE068374 BE068295 BE068625 BE068302 BE068663 BE068675 BE068579 BE068311 BE068674 BE068547 BE068602 BE068605 BE068352 BE068306 BE068401 BE068537 BE068552 BE068450 BE068723 BE068393 BE068671 BE068748 BE068317 BE068447 BE068568 BE068632 BE068357 BE068330 BE068498 BE068631 BE068540 BE068410 BE068626 BE068591 BE068522 BE068676 BE068499 BE068361 BE068598 BE068350 BE068299 BE068580 BE068567 BE068692 BE068321 BE068327 BE068739 BE068526 BE068538 BE068765 BE068340 BE068733 BE068293 BE068565 BE068480 BE068476 BE068761 BE068712 BE068706 BE068549 BE068419 BE068383 BE068434 BE068418 BE068525 BE068543 BE068752 BE068550 BE068623 BE068470
459330	105725_1	BG563152 BF846777 BF849354 BF849359 BF846636 BF849201 BF849356 C16931 AA056717 AW864542 AW882724 AA056567
434038	630986_1	AI910738 AW139227 AA932891 AA622104
433291	73706_1	AF007191 AW820706 BG978594 BF872238
423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138
455674	1490762_1	BE065941 BE065997 BE066003 BE066070 BE066098
413861	1561647_1	BF352282 BE175424 BE175418 BE175383
409368	110612_1	AA071059 AA085201 AA085020
415405	1872126_1	W18191 R59141 R54142 R12130 F11362 Z42794 F08242 F07925 H21084 R54090 R59142
409837	915621_1	AW501504 AW501656 AW503048 AW502449 AW502098
458637	395206_1	AV657752 AV657446
428193	430_1	AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AI290876 AI014784 AI393429 AI266211 AW074303 AA620711 BF197792 AW008766 D25944 AI687397 AA621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201 AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031 AI365073 AI024576 AA298805 H04001 H45668 BG682146 AL552388 BI462361 BG547513 BG896863 BI256661
448793	3006936_1	AI936948 AI864581 AI570641
409859	916430_1	AW501926 AW502566 AW501927
409811	58948_2	AK057581 AW500962 AW500896 AW501105
400116	5269_1	D42041 NM_014610 AJ000332 BI758702 BG720650 AU141129 AU130711 AU141380 AU132402 BM048556 AU127520 BE259984 AU128952 BE614151 AL601516 BM146777 AU128103 BM194094 BE937951 BE696396 AK026997 AK026567 BF969293 BE798100 BI086881 BG166248 BE877845 BG385414 AW886747 BF093789 AW390159 BF820311 AA421676 AW880845 AW404827 BF726465 BE161190 BE254102 AW406002 BE161223 AI912055 BF930228 AW374357 AW794531 BE720524 BE933982 BE933658 BE933694 BE933978 BE933654 BE933583 BE166557 BE933874 BE933641 BE933859 BE933626 BE933866 BE933633 BE933864 BE933631 BE933867 BE933634 BE933857 BE933624 BE933883 BE933650 BE720491 AA420426 BE720410 BE720458 BE720444 BE720411 AW368748 BF874616 BE933498 BE835979 BF926667 AW849921 AW850026 AW850022 AW849977 AW849900 BG250251 W87689 AI192625 AI692824 AA426263 AI090315 AI309537 AA877437 AA478438 AI538868 AW276162 AI279916 AA600318 AI188836 AW662284 AI262619 AA293457 BF347442 AA421677 AA658063 AA565510 AA937060 AI142684 AA788940 AA827426 AU152614 AI342784 AU148738 AA219664 AA047835 H99450 AA018563 AI073634 BM475120 BG875251 BG248778 U46372 AA383858 AU140356 BG821891 BF935049 BI760656 BI054103 BF982309 BE872215 BI257291 AU158469 AU160599 AU152469 AU152375 AU152059 AU148575 N32267 AU149554 AI627459 AI719840 AW779017 AI291493 AW304181 AW470055 AI086491 AI311387 AI634232 AI151241 AI288848 AW050588 AW589580 AI241353 AI880219 AA039309 AA026517 AA016238 AA013444 H86822 R87530 AA058462 N27082 Z39679 BE544309 W52619 AA018076 AI813668 AW189907 AI418104 AU159878 AU150087 R21754 AA015932 H67274 AU153097 AI961344 AA018208 W32429 R45344 R77453 BM470129 AU130415 BI227374 BE298179 AW844963 AW844983 AI904066 AA379006 BF850571 AA355641 BG747156 AL547262 AW367941 BE560004 BI116061 BG899031 BE560318 BF174177 BI051456 BE001967 BE386446 BF969326 BF808765 BF684480 BG421617 AI940607 AW875483 BE789632 BF808711 BI192691 AW904249 BI911430 BE265407 BE730343 BE397808 BI226516
414580	623093_1	BG333973 BE385437 BE408833 BE387650
436364	1414_37	X05826 X06096 BG468890 AW951851 W23562 T28392 H56742 H58030 T69205

TABLE 37C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402608	9910096	Plus	37495-37669
404518	8151988	Plus	84494-84603
401234	9929642	Plus	120173-120337
402181	8575912	Plus	449746-450040
403479	7329292	Minus	148369-148533,150678-150809
402911	7263904	Plus	142689-142979
401540	8072433	Plus	106838-107310
402328	4464283	Minus	13758-13922,14558-14752
401590	9966320	Minus	33547-33649
403645	8699714	Minus	4433-4582
403376	9369545	Minus	108698-108830
401126	8699701	Minus	68290-68487
401904	8671966	Plus	60959-61603,62670-62890,63778-63838
401919	9502466	Plus	67536-67666
406443	9280765	Plus	85951-87327
406016	8272661	Plus	41341-41940
405938	6758795	Minus	166671-167411
404231	8218035	Minus	61077-61322
404102	7229900	Plus	97685-98018
403031	7768597	Minus	1308-1416
406059	9103984	Minus	13856-14004
402483	7574980	Minus	65578-66119
405448	7582529	Plus	136347-136532
404439	7139680	Plus	55316-55585
404026	7582549	Minus	79674-79968
400881	2842777	Minus	91446-91603,92123-92265
405429	7321905	Minus	51577-51723
402642	9958129	Minus	125599-125756
402217	9795981	Minus	21521-21757
405857	6758728	Plus	26564-26819
406305	8575869	Plus	108239-108386,112216-112378,115388-11557
403605	6862654	Plus	91614-91718
402594	7705170	Plus	103082-103414
402803	3287156	Minus	55923-56033
405156	9966228	Plus	146733-146860,147899-147961,153127-15325
403591	8101229	Plus	4201-4833
406193	7289992	Plus	30183-30662
400703	8118859	Plus	63657-63857,64802-64905
404975	3419864	Minus	86096-86605
400513	9796593	Plus	74613-74823
402404	3970932	Plus	53154-53280
406564	7711604	Minus	52788-53013
403581	8101182	Plus	6794-7396
403716	7239669	Plus	86899-87122
404758	7706327	Minus	130204-130806
402051	8082020	Minus	19346-19480,20041-20119
405063	7658414	Minus	111047-111666
405163	9966267	Minus	161171-161299
402386	9799769	Plus	22069-22303
400489	8954013	Plus	131475-131652
404795	4826439	Plus	147501-147780
402394	9929690	Plus	33308-33482
404818	2769655	Plus	33671-33839
405590	6960456	Plus	90492-90818
402448	9796640	Plus	112942-113069,114303-114521
405443	7408143	Plus	90716-90887,101420-101577

TABLE 38A: About 207 genes upregulated in lung fibrosis relative to normal tissues

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of lung fibrosis AIs divided by 70th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigeneID	Unigene Title	R1
437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.28
407891	AA486620	Hs.41135	endomucin-2	4.14
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.07
410219	T98226	Hs.171952	occludin	3.96
434666	AF151103	Hs.112259	T cell receptor gamma locus	3.88
425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	3.87
406617			Target Exon	3.76
420568	F09247	Hs.247735	protocadherin alpha 10	3.70
425873	NM_013390	Hs.160417	transmembrane protein 2	3.69

	438797	C16161	Hs.283040	hypothetical protein PRO2543	3.68
	410315	AI638871	Hs.152519	Homo sapiens cDNA: FLJ22524 fis, clone H	3.65
	446714	W73818	Hs.110028	ESTs	3.64
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.61
5	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	3.58
	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.56
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	3.56
	412654	AI093480		hypothetical protein FLJ11896	3.56
	414386	X00442	Hs.75990	haptoglobin	3.54
10	451035	AU076785	Hs.430	plastin 1 (I isoform)	3.52
	436473	AI193122	Hs.132275	ESTs	3.51
	406714	AI219304	Hs.266959	hemoglobin, gamma G	3.46
	414586	AA306160	Hs.16488	lymphocyte cytosolic protein 1 (L-plasti	3.45
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	3.45
15	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	3.39
	452813	U54727	Hs.191445	ESTs	3.36
	442831	AI798959	Hs.131686	ESTs	3.35
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	3.34
	445330	R52656	Hs.21691	ESTs	3.31
20	436001	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	3.31
	431681	AK000378	Hs.267566	hypothetical protein FLJ20371	3.29
	432314	AA533447	Hs.312989	ESTs	3.28
	435129	AI381659	Hs.267086	ESTs	3.28
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.24
25	422607	Z45471	Hs.118684	stromal cell-derived factor 2	3.21
	421205	AL137540	Hs.102541	netrin 4	3.20
	428582	BE336699	Hs.185055	BENE protein	3.20
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.19
	424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	3.17
30	421233	AA209534	Hs.284243	tetraspan NET-6 protein	3.17
	429350	AI754634	Hs.131987	ESTs	3.16
	428727	AF078847	Hs.191356	general transcription factor IIH, polype	3.16
	434850	Z43161	Hs.283714	30 kDa protein	3.13
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.12
35	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spl	3.11
	416114	AI695549	Hs.183868	glucuronidase, beta	3.10
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	3.09
	444212	AW503976	Hs.10649	basement membrane-induced gene	3.08
	422442	AA324998	Hs.147066	signal transducer and activator of trans	3.08
40	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	3.08
	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	3.07
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.07
	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypotheti	3.06
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	3.04
45	428106	BE620016	Hs.182470	PTD010 protein	3.04
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	3.04
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.03
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.02
	423067	AA321355	Hs.285401	colony stimulating factor 2 receptor, be	3.01
50	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	2.96
	415000	AW025529	Hs.239812	Homo sapiens serologically defined breas	2.96
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	2.96
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	2.96
	419660	BE280337	Hs.194693	solute carrier family 7 (cationic amino	2.96
55	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.95
	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	2.94
	416883	AW140128	Hs.184902	ESTs	2.92
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	2.92
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	2.92
60	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.92
	429640	U83508	Hs.2463	angiopoietin 1	2.91
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	2.91
	401958			Target Exon	2.90
	416926	H03109	Hs.263395	HT018 protein	2.90
65	433691	AA605012		ESTs	2.88
	441892	AB028981	Hs.8021	KIAA1058 protein	2.87
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.87
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.87
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	2.87
70	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	2.87
	435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	2.86
	422050	AA302741	Hs.25786	ESTs, Moderately similar to JC5238 galac	2.85
	451356	AA748418	Hs.164577	ESTs	2.85
	442085	AA975688	Hs.159955	ESTs	2.84
75	427704	AW971063	Hs.292882	ESTs	2.83
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	2.83
	441965	AA972712	Hs.269737	ESTs	2.82
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	2.82
	450056	BE047394	Hs.8208	ESTs, Weakly similar to S71512 hypotheti	2.80
80	407245	X90568	Hs.172004	titin	2.80
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.80
	446601	AI312783	Hs.155772	Homo sapiens thymic stromal co-transport	2.80
	432195	AJ243669	Hs.8127	KIAA0144 gene product	2.80

449088	AI654048	Hs.196556	ESTs	2.80
416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.80
406648	AA563730	Hs.277477	major histocompatibility complex, class	2.79
412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	2.78
433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	2.78
440255	AI932285	Hs.160569	ESTs	2.78
410057	R66634	Hs.268107	multimerin	2.77
417497	AW402482	Hs.82212	CD53 antigen	2.77
446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.76
431884	AA521246	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.75
409969	AW514668	Hs.194258	ESTs, Moderately similar to ALU5_HUMAN A	2.75
436729	BE621807		transmembrane 4 superfamily member 1	2.75
431451	AA761378	Hs.192013	ESTs	2.74
413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.74
447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	2.74
418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	2.74
424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.74
443194	AI954968		matrix Gla protein	2.71
443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.71
452870	AW502761	Hs.30909	KIAA0430 gene product	2.70
430334	AI824719	Hs.143251	ESTs	2.70
437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	2.70
432279	N95104	Hs.274260	ATP-binding cassette, sub-family C (CFTR	2.70
413950	AA249096	Hs.32793	ESTs	2.70
430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	2.70
431710	AI735482		ESTs	2.70
448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	2.69
451154	AA015879	Hs.33536	ESTs	2.69
424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	2.69
446899	NM_005397	Hs.16426	podocalyxin-like	2.68
418031	AA648744	Hs.269493	ESTs	2.68
453902	BE502341	Hs.3402	ESTs	2.68
405121			mitogen-activated protein kinase 8 inter	2.68
410163	AF151977	Hs.59260	NTT5 protein	2.67
429632	AW195336	Hs.148910	ESTs	2.67
437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	2.67
455004	AW850303		gb:IL3-CT0219-191199-030-F09 CT0219 Homo	2.67
444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	2.67
401113			solute carrier family 22 (organic cation	2.66
419462	AF071076	Hs.112255	nucleoporin 98kD	2.66
407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-lin	2.66
419175	AW270037		KIAA0779 protein	2.66
408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.66
452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.66
430592	AJ224864	Hs.9688	leukocyte membrane antigen (IRC1)	2.65
446830	BE179030		Human DNA sequence from clone RP5-1174N9	2.64
433327	AI674779	Hs.126744	ESTs	2.64
424868	AI568170	Hs.96886	ESTs	2.64
429854	R55508	Hs.99472	ESTs	2.63
427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.63
456711	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	2.63
419777	D60134	Hs.270975	ESTs	2.63
414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	2.62
427596	AA449506	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.62
452445	AB002438	Hs.29596	Homo sapiens mRNA from chromosome 5q21-2	2.62
447482	AB033059	Hs.18705	KIAA1233 protein	2.62
419110	AA234171	Hs.187626	ESTs	2.62
450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	2.62
419828	T81422	Hs.14922	ESTs	2.62
427202	BE272922	Hs.173936	interleukin 10 receptor, beta	2.62
412491	W31589	Hs.73957	RAB5A, member RAS oncogene family	2.61
436496	AA281959	Hs.5210	glia maturation factor, gamma	2.61
435053	AW629386		ESTs	2.61
435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.61
425976	C75094	Hs.334514	NG22 protein	2.60
412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	2.60
430539	AK001489		ADP-ribosylation factor-like 1	2.60
419825	AI754011	Hs.7326	ESTs	2.59
412577	Z22968	Hs.74076	CD163 antigen	2.58
425894	AW954011	Hs.180711	ESTs	2.58
410883	D43767	Hs.66742	CCL17 chemokine (TARC) (SCYA17)	2.58
441028	AI333660	Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	2.58
413949	AA316077	Hs.75639	Human TB1 gene mRNA, 3' end	2.58
434943	AI929819	Hs.92909	chromosome 21 open reading frame 50	2.58
443605	H06865	Hs.134131	ESTs	2.57
425017	AL119305	Hs.26409	ESTs	2.57
440334	BE276112	Hs.7165	zinc finger protein 259	2.56
426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.56
425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.56
407174	T79938	Hs.77062	leukocyte immunoglobulin-like receptor,	2.56
443834	AI741510	Hs.173548	ESTs	2.55
427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	2.55
420539	AA282735	Hs.44004	AD031 protein	2.55

	421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	2.54
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.54
	422994	AW891802	Hs.296276	ESTs	2.54
	411992	AW816214	Hs.143055	ESTs	2.54
5	451180	H61899	Hs.171937	steroid dehydrogenase-like	2.54
	415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.53
	429752	H52348	Hs.36636	ESTs	2.53
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.53
	453329	T97205	Hs.193400	ESTs, Weakly similar to 2109260A B cell	2.53
10	436503	AJ277750	Hs.183924	ubiquitin associated and SH3 domain cont	2.52
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.52
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.52
	435943	R60194	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.52
	452253	AA928891	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H	2.52
15	442506	BE566411	Hs.41726	ESTs	2.52
	419972	AL041465	Hs.182982	golgin-67	2.52
	431074	BE072772	Hs.8997	ESTs, Moderately similar to A46010 X-lin	2.52
	449129	AI631602	Hs.258949	ESTs	2.52
	440524	R71264	Hs.16798	ESTs	2.51
20	419203	AA488719	Hs.190151	ESTs	2.51
	404370			Target Exon	2.51
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.51
	439219	N33883	Hs.41322	ESTs	2.51
	428044	AA093322	Hs.301404	RNA binding motif protein 3	2.50
25	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.50
	437644	AA748575	Hs.136748	lectin-like NK cell receptor	2.50
	442566	R37337	Hs.12111	ESTs	2.50
	409317	U20165	Hs.53250	bone morphogenetic protein receptor, typ	2.50
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.50
30	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	2.50
	415165	AW887604	Hs.78065	complement component 7	2.50
	435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	2.50

TABLE 38B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
412654	1350_1	BG743181 AI830050 BE695688 AA126591 AI903503 R26045 N62894 N63950 AA131619 AI681480 N79626 AA461603 R78979 AW608865 N66622 BF448838 AA779000 AA460314 AI092721 AI870182 AI436284 AI494151 AI127704 AI127702 BE349350 AI093480 AA115264 AA131567 R26840 R78885
433691	2203511_1	AI223854 AI129852 AA605012
436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
443194	19335_1	BI754027 BF696071 AI351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA993445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568964 BF725590 AI004210 AI809799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AA155854 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 D57214 BE045265 AA541785

		BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 F27562 AA614749 D56645 F20774 F30660 F25646 AW023542 AA827300 AA582214 AI701289 AA228293 AI906950 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518 AV704158 BE439643 AA910666 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA451625 AA916141 AL572719 AV707258 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553696 AA916094 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215
431710	1611592_1	AI422419 AA514370 AI741678 AI735482 AI735081 AI371436
455004	1089114_1	AW850587 AW850589 AW850318 AW850303
419175	35068_1	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
446830	41421_1	BC020595 BI488430 BG168023 BE179030 AW294203 BF849776 AA459064 AI917452 AW403072 W27419 BF914568 BF798468 AW370558 T35055 AW370623 AA399232 AA214221 AW802987 BF902228 AW370622 BF819597 AW370567 BF914313 AW954040 BF060706 AA194237 T25074 C01285 BI489433
435053	124009_1	AI332638 AA663215 AW629386
430539	31268_1	AK001489 AU129447 BF959274 BG565452 AI245327 AU116848 BF358559 BF358554 BF358570 BG678119 AL515852 AU154607 AI357567 AW874359 AI122554 AA406478 AI091013 AI866679 AI686163 AA662158 AA911580 D31095 AI302576 BF588761 AU151560 AU143828 AI291610 AW169600 D31161 AA905362 C21179 BE327258 D31474 AW439053 D31309 BF756901 BI838626 BF979839 AU149562 BM142116 AU156455 AA452028 AW473972 AW468490 AA410271 AI475944 BF821859 AA658188 AI360390 AA226320 F37355 F27660 F36093 AA152126 BF930021 BF375775 AW821784 AW975085 W16475 D31031 BG696392 AW860676 AW752864 BI013705 BF965715 BF326604 AW821786

TABLE 38C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406617	8439858	Plus	36430-36552
401958	3258613	Plus	108411-108629
405121	8102330	Minus	35816-36004,36587-36684
401113	9966541	Minus	19419-19959
404370	7631003	Plus	127868-128244

TABLE 40A: 656 genes upregulated in fibrosis relative to normal body tissues

Table 40A lists about 656 genes upregulated in fibrosis relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 95th percentile of fibrosis AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1

442275; AW449467; Hs.54795; Homo sapiens secretoglobin, family 3A, m; Uteroglobin;TM=M;SS=Y; 39.47
428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA segment, Ch; LBP_BPI_CETP_C;TM=M;SS=Y; 32.35
439335; AA742697; Hs.62492; NM_052863:Homo sapiens secretoglobin, fa; none;; 28.49
406964; M21305; ; FGENES predicted novel secreted protein; none,none; 27.90
425211; M18667; Hs.1867; progastricsin (pepsinogen C); asp;TM=M;SS=M; 27.90
441835; AB036432; Hs.184; advanced glycosylation end product-speci; homeobox,Acyltransferase,notch,EGF,ank,Acyltransferase; 27.23
446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8;; 24.97
428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10;; 24.38
431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22_Claudin,none; 23.35
409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibrinogen_C;; 23.29
431089; BE041395; Hs.374629; ESTs, Weakly similar to unknown protein ; none,none; 18.23
425371; D49441; Hs.155981; mesothelin; none;TM=M;SS=M; 18.17
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP;TM=M;SS=M; 17.64
421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospha; Ribosomal_L20,Na_Pi_cotrans;TM=Y;SS=N; 17.33
421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase (acid c; SAPA,Surfactant_B,none; 16.81
419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); Glyco_hydro_18,CBM_14;TM=M;SS=Y; 16.24
419092; J05581; Hs.89603; mucin 1, transmembrane; SEA;TM=Y;SS=M; 16.06
426174; AA547959; Hs.115838; Homo sapiens similar to Echinoidin (LOC1; none,none; 15.84
406672; M26041; Hs.198253; major histocompatibility complex, class ; ig,MHC_II_alpha;TM=M;SS=M; 15.42
421110; AJ250717; Hs.1355; cathepsin E; asp;; 15.08
444342; NM_014398; Hs.10887; similar to lysosome-associated membrane ; Lamp;TM=Y;SS=M; 14.94

406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 14.36
443709; AI082692; Hs.134662; ESTs; SNF,fn3,none; 14.05
428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3;TM=Y;SS=M; 13.88
457200; U33749; Hs.197764; thyroid transcription factor 1; homeobox;TM=M;SS=N; 13.86
432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA S-100 pro; none,none; 13.82
422355; AW403724; Hs.300697; coagulation factor VII (serum prothrombi; none,ig; 13.62
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 13.47
415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN,sugar_tr;TM=Y;SS=M; 13.35
431164; AA493650; Hs.94367; thyroid transcription factor 1; none,homeobox; 13.32
414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 12.83
400269; ; Hs.253495; Eos Control; lectin_c,Collagen,Xlink;; 12.30
424310; AA338648; Hs.50334; testes development-related NYD-SP22; none;TM=M;SS=N; 11.81
451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1; ABC_tran,SRP54;TM=Y;SS=M; 11.79
452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine ; none,none; 11.68
445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM;; 11.56
423778; Y09267; Hs.132621; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 11.41
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 11.31
430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior ; none,none; 11.25
407910; AA650274; Hs.41296; fibronectin leucine rich transmembrane p; fn3,LRR,LRRCT,LRRNT;TM=Y;SS=M; 11.15
451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF,WIF;; 11.07
430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 11.07
411020; NM_006770; Hs.67726; macrophage receptor with collagenous str; SRCR,Collagen;TM=Y;SS=M; 11.05
446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin;; 11.01
438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.97
413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 10.93
432231; AA339977; Hs.274127; CLST 11240 protein; none;TM=M;SS=M; 10.81
416402; NM_000715; Hs.1012; complement component 4-binding protein, ; sushi;TM=M;SS=M; 10.77
418156; W17056; Hs.83623; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.63
436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 10.58
421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen ; none;TM=Y;SS=M; 10.57
418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial: hemopexin,Peptidase_M10,Astacin,PG_binding_1;; 10.33
419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fn3,wap;; 10.30
407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 10.28
441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 10.26
453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPase;TM=M;SS=N; 10.22
435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 10.09
423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alph; vwa,Cache;TM=M;SS=N; 10.03
415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 10.02
408562; AI436323; Hs.31141; roundabout (axon guidance receptor, Dros; ig,fn3;TM=M;SS=N; 10.02
448782; AL050295; Hs.362806; KIAA0758 protein; 7tm_2,ig,GPS,SEA;TM=Y;SS=N; 9.86
419235; AW470411; Hs.288433; neurotrimin; none,none; 9.79
415992; C05837; Hs.145807; hypothetical protein FLJ13593; none;TM=Y;SS=M; 9.74
418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 9.70
439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.69
442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 9.68
446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 9.64
408380; AF123050; Hs.44532; diubiquitin; ubiquitin;TM=M;SS=N; 9.54
438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 9.52
449494; AW237014; Hs.315369; aquaporin 4; MIP,none; 9.51
456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none,none; 9.42
446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4_HUMAN ALU S; none,none; 9.41
421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); none,none; 9.19
407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell ; Ribosomal_S14,ank,pkinase,death,none; 9.16
456034; AW450979; ; gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su; none,none; 9.15
407788; BE514982; Hs.38991; S100 calcium-binding protein A2; efhand,S_100,S_100,efhand; 9.15
416965; N26223; Hs.160436; MDAC1; none;NA;NA; 9.03
443324; R44013; Hs.164225; ESTs; none,none; 9.03
435575; AF213457; Hs.44234; triggering receptor expressed on myeloid; ig;TM=Y;SS=M; 9.00
440273; AI805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fis, clone L; none,none; 8.99
424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374 gene NF2 ; Zn_carbOpept,none; 8.80
409203; AA780473; Hs.687; cytochrome P450, subfamily IVB, polypept; p450;TM=M;SS=Y; 8.76
423387; AJ012074; Hs.348500; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSC;TM=Y;SS=M; 8.74
443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 8.73
425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 8.68
418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 8.56
421563; NM_006433; Hs.105806; granulysin; none;; 8.55
450726; AW204600; Hs.355462; HUMPSPBA Human pulmonary surfactant-asso; SAPA,Surfactant_B,none; 8.51
419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 8.51
424450; AL137526; Hs.374425; dynein intermediate chain 2; WD40;; 8.42
402474; ; ; NM_004079:Homo sapiens cathepsin S (CTSS; Peptidase_C1;; 8.41
458079; AI796870; Hs.54277; Homo sapiens similar to RIKEN cDNA 28100; none;TM=M;SS=N; 8.40
424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 8.36
453310; X70697; Hs.553; solute carrier family 6 (neurotransmitte; SNF,5HT_transporter;TM=Y;SS=N; 8.34
448140; AF146761; Hs.20450; BCM-like membrane protein precursor; ig;TM=Y;SS=N; 8.33
404240; ; ; NM_018950:Homo sapiens major histocompat; ig,MHC_I;TM=Y;SS=M; 8.28
459702; AI204995; ; gb:an03c03.x1 Stratagene schizo brain S1; none,none; 8.17
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.17
442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 8.12
446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22_Claudin,none; 8.07
420137; AA306478; Hs.95327; CD3D antigen, delta polypeptide (TIT3 co; ITAM;TM=Y;SS=M; 8.01
435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig;TM=M;SS=M; 7.99
432441; AW292425; Hs.163484; intron of hepatocyte nuclear factor-3 al; Fork_head,none; 7.99
409208; Y00093; Hs.172631; integrin, alpha X (antigen CD11C (p150),; vwa,FG-GAP,integrin_A,vwa,integrin_A,FG-GAP; 7.94

432606; NM_002104; Hs.3066; granzyme K (serine protease, granzyme 3;; trypsin;TM=Y;SS=M; 7.92
442832; AW206560; Hs.253569; ESTs; none,none; 7.90
412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN cDNA 2210; none;TM=M;SS=N; 7.89
427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, r; ig;TM=Y;SS=M; 7.86
443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin,none; 7.84
418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 7.79
447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazaro; none;TM=Y;SS=N; 7.78
423961; D13666; Hs.136348; periostin (OSF-2os); Fasciclin;TM=M;SS=M; 7.73
424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none;TM=M;SS=N; 7.72
438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig,MHC_II_alpha,none; 7.65
456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, com; none,PK,PK_C,myosin_head,RhoGAP; 7.64
427792; M63928; Hs.180841; tumor necrosis factor receptor superfami; SRP14,TNFR_c6;; 7.63
436954; AA740151; Hs.130425; ESTs; none,none; 7.58
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2;; 7.56
407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC;TM=Y;SS=M; 7.55
417105; X60992; Hs.81226; CD6 antigen; SRCR;TM=Y;SS=M; 7.51
414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig;TM=Y;SS=M; 7.46
444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 7.40
432222; AI204995; ; gb:an03c03.x1 Stratagene schizo brain S1; none,none; 7.38
422667; H25642; Hs.132821; ESTs; FMO-like,FMO-like; 7.37
444527; NM_005408; Hs.11383; small inducible cytokine subfamily A (Cy; IL8;; 7.36
457411; AW085961; Hs.130093; iroquois-class homeobox protein IRX2; none,none; 7.32
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Recep_L_domain,YLP,none; 7.32
419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227 hypotheti; none,none; 7.30
438873; AI302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fis, clone L; none,none; 7.27
424027; AW337575; Hs.201591; ESTs; 7tm_2,HRM,none; 7.26
428927; AA441837; Hs.90250; Homo sapiens hypothetical protein FLJ231; none,none; 7.24
432435; BE218886; Hs.282070; ESTs; none,none; 7.22
428467; AK002121; Hs.184465; hypothetical protein FLJ11259; none;TM=Y;SS=M; 7.21
416030; H15261; Hs.21948; ESTs; none,none; 7.20
433293; AF007835; Hs.32417; hypothetical protein MGC2742; none;TM=M;SS=N; 7.18
418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase,Activin_recp,pkinase,Activin_recp; 7.16
420656; AA279098; Hs.187636; ESTs; none,none; 7.14
427698; AW972594; Hs.335499; ESTs; none,none; 7.11
432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase;TM=M;SS=N; 7.06
413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT,none; 7.04
430413; AW842182; Hs.241392; small inducible cytokine A5 (RANTES); IL8;TM=M;SS=Y; 7.04
452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q,Collagen;; 7.03
421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 7.01
418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M;SS=N; 6.97
452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide,TGF-beta,none; 6.96
458124; AW005548; Hs.124590; ESTs; none,none; 6.94
422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 6.93
411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, ; inositol_P,ig;TM=M;SS=N; 6.92
428820; AA436187; Hs.172631; integrin, alpha M (complement component ; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 6.90
423575; C18863; Hs.163443; intron of periostin (OSF-2os); Fasciclin,none; 6.89
419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cytotoxic T-lymp; trypsin;TM=M;SS=M; 6.89
450954; AI904740; Hs.25691; receptor (calcitonin) activity modifying; none;TM=Y;SS=M; 6.87
425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 6.84
425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fis, clone L; LRR;TM=M;SS=N; 6.81
414991; C17898; ; Homo sapiens up-regulated by BCG-CWS (LO; Zip,none; 6.80
410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM;TM=Y;SS=M; 6.80
422163; AF027208; Hs.112360; prominin (mouse)-like 1; none;TM=Y;SS=M; 6.79
445885; AI734009; Hs.127699; KIAA1603 protein; none,none; 6.77
436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 6.77
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;; 6.76
424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2,HRM;TM=Y;SS=M; 6.75
416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3;TM=M;SS=N; 6.73
426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54); ig,ICAM_N;TM=M;SS=M; 6.71
417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; ig,abhydrolase; 6.70
412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin_c; 6.70
428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 6.68
421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.65
439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 6.62
428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 6.60
453142; AA033648; Hs.7473; Homo sapiens gap junction protein, alpha; connexin;TM=Y;SS=M; 6.60
432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none,none; 6.56
448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 6.54
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;SS=N; 6.51
446932; AA961459; Hs.125644; ESTs; none,LRR,LRRNT; 6.50
427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180),; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 6.48
425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; ig,pkinase;TM=M;SS=M; 6.47
447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 6.46
431745; AW972448; Hs.163425; Novel FGENESH predicted cadherin repeat ; none,none; 6.43
417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; WHEP-TRS,tRNA-synt_1b;; 6.41
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 6.40
429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lung and nas; none;; 6.39
409340; BE174629; Hs.321130; hypothetical protein MGC2771;
aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 6.37
413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO;TM=M;SS=N; 6.36
451820; AW058357; Hs.199248; ESTs; 7tm_1;TM=Y;SS=M; 6.34
408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2;TM=Y;SS=N; 6.32
424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD_Synth,Idh,Idh_C,pkinase;; 6.32

444090; S69115; Hs.10306; natural killer cell group 7 sequence; PMP22_Claudin;TM=Y;SS=M; 6.31
416819; U77735; Hs.80205; pim-2 oncogene; pkinase;; 6.30
421659; NM_014459; Hs.106511; protocadherin 17; cadherin;TM=M;SS=M; 6.27
415198; AW009480; Hs.943; natural killer cell transcript 4; none;TM=M;SS=N; 6.26
424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 6.24
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 6.23
452194; AI694413; Hs.373599; olfactory receptor, family 2, subfamily ; none,none; 6.22
424144; AA454033; Hs.41644; AKAP-associated sperm protein; RIIa;; 6.21
414142; AW366397; Hs.334485; hemicentin (fibulin 6); EGF,ig,tsp_1,hormone4,squash,TIL,Adeno_E3_CR1;TM=M;SS=M; 6.21
442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482 hypotheti; none,none; 6.20
420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin (vascula; cadherin,Cadherin_C_term;TM=Y;SS=M; 6.19
421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 6.17
440452; AI925136; Hs.55150; ESTs, Weakly similar to CAYP_HUMAN CALCY; none;NA;NA; 6.17
421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 6.16
452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t; Y_phosphatase,none; 6.15
410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP,GBP_C;TM=Y;SS=M; 6.13
415765; NM_005424; Hs.78824; tyrosine kinase with immunoglobulin and ; EGF,fn3,ig,pkinase,laminin_EGF;TM=M;SS=Y; 6.12
430478; NM_014349; Hs.241535; apolipoprotein L, 3; MotA_ExbB;TM=Y;SS=M; 6.12
413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 6.09
446608; N75217; Hs.175622; ESTs; Armadillo_seg,HEAT_PBS;TM=M;SS=M; 6.08
430378; Z29572; Hs.2556; tumor necrosis factor receptor superfami; IL2;; 6.08
426116; AA868729; Hs.144694; ESTs; none,none; 6.06
445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 6.05
426721; AA383588; Hs.288545; ESTs, Weakly similar to T29012 hypotheti; zf-C2H2;TM=M;SS=N; 6.05
429228; AI553633; Hs.356828; ESTs; none,none; 6.05
421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase;; 6.04
437669; AI358105; Hs.123164; ESTs, Weakly similar to malch to ESTs AA; none,pkinase,pkinase_C; 6.03
419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 6.02
428667; AI375550; Hs.346868; nucleolar protein p40; homolog of yeast ; none,none; 6.01
432731; R31178; Hs.287820; fibronectin 1; fn1,fn2,fn3,none; 5.95
446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 5.95
450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2;; 5.94
418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide (p32); ig;TM=Y;SS=M; 5.94
424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 5.94
408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmin;TM=M;SS=N; 5.94
438670; AI275803; Hs.123428; ESTs; none;NA;NA; 5.91
424238; AA337401; Hs.137635; ESTs; none;TM=M;SS=M; 5.90
444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 5.89
423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 prot; ion_trans,IQ,none; 5.88
409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 5.81
407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, ; ig;TM=Y;SS=M; 5.81
411125; AA151647; Hs.66877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 5.80
420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TiT3 com; ITAM;TM=M;SS=M; 5.79
431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr;TM=Y;SS=N; 5.79
413441; AI929374; Hs.75367; Src-like-adapter; SH2,SH3;TM=M;SS=N; 5.79
443257; AI334040; Hs.11614; HSPC065 protein; trypsin;TM=M;SS=N; 5.76
415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig;TM=Y;SS=N; 5.70
435299; AI745456; Hs.343026; ESTs, Weakly similar to T20593 hypotheti; none;NA;NA; 5.69
415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 5.67
436772; AW975688; Hs.348918; metallothionein 1E (functional); 7tm_2,HRM,none; 5.67
431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none,none; 5.66
419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetas; WHEP-TRS,tRNA-synt_1b,none; 5.66
421859; AA356620; Hs.108947; KIAA0050 gene product; ank,PH,ArfGap;; 5.64
407756; AA116021; Hs.38260; ubiquitin specific protease 18; UCH-1,UCH-2;; 5.63
425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 5.63
423533; NM_014339; Hs.129751; interleukin 17 receptor; none;TM=Y;SS=M; 5.63
419577; L36531; Hs.91296; integrin, alpha 8; integrin_A,FG-GAP;TM=Y;SS=N; 5.61
452561; AI692181; Hs.49169; KIAA1634 protein; TPR,PDZ,WW,Guanylate_kin;TM=M;SS=N; 5.61
428677; AI657119; Hs.351582; troponin I, cardiac; none;TM=M;SS=N; 5.60
425509; AF079363; Hs.158213; sperm associated antigen 6; Armadillo_seg,HEAT_PBS;TM=M;SS=N; 5.58
453852; AW961818; Hs.211592; MUM2 protein; pkinase,DAG_PE-bind,C2,pkinase_C,none; 5.57
421924; BE514514; Hs.109606; coronin, actin-binding protein, 1A; WD40,Idh_C;TM=M;SS=N; 5.57
448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 5.55
431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 5.53
410257; BE244044; Hs.61469; hypothetical protein; none,none; 5.53
441965; AA972712; Hs.269737; ESTs; pkinase,Activin_recp,TSPN,Collagen; 5.52
413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; integrin_B,Glyco_hydro_56;; 5.52
424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT_bind,STAT_prot,none; 5.50
447357; AI375922; Hs.132821; ESTs; FMO-like,FMO-like; 5.46
422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin,Defensin_propep;TM=M;SS=M; 5.46
447033; AI357412; Hs.157601; Predicted gene: Eos cloned; secreted w/V; none,none; 5.45
417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR;TM=M;SS=M; 5.45
436057; AJ004832; Hs.5038; neuropathy target esterase; cNMP_binding,ion_trans,Patatin;TM=Y;SS=M; 5.41
417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 5.41
439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 5.40
452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 5.40
443623; AA345519; Hs.9641; complement component 1, q subcomponent, ; C1q,Collagen;; 5.40
446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 5.38
437275; AW976035; Hs.292396; ESTs, Weakly similar to A47582 B-cell gr; none,Frizzled,Fz; 5.37
419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino ; aa_permeases;TM=Y;SS=M; 5.37
449853; AF006823; Hs.24040; potassium channel, subfamily K, member 3; ion_trans;TM=Y;SS=M; 5.36
442434; AA995787; Hs.129583; ESTs; IRK,none; 5.36
428065; AI634046; Hs.157313; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 5.36

445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,arf,TK;; 5.33
425638; NM_012337; Hs.158450; nasopharyngeal epithelium specific prote; none;TM=M;SS=N; 5.32
419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;SS=N; 5.32
452416; AA026115; Hs.114777; ESTs; none,Porphobil_deam; 5.29
425205; NM_005854; Hs.155106; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 5.29
440475; AI807671; Hs.24040; potassium channel, subfamily K, member 3; ion_trans,none; 5.28
417355; D13168; Hs.82002; endothelin receptor type B; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 5.28
436120; AI248193; Hs.119860; ESTs; heme_1,none; 5.27
418307; U70867; Hs.83974; solute carrier family 21 (prostaglandin ; OATP_N,OATP_C;TM=Y;SS=M; 5.27
409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 5.26
421554; AW137676; Hs.97775; ESTs; none,none; 5.23
408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none,none; 5.22
410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 5.21
421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2 (; 7tm_1;TM=Y;SS=M; 5.19
400261; ; Hs.1802; Eos Control; ig,MHC_II_beta;TM=Y;SS=M; 5.19
436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 5.18
408761; AA057264; Hs.238936; ESTs, Weakly similar to (defline not ava; 7tm_1,none; 5.17
425023; AW956889; Hs.154210; EDG-1 (endothelial differentiation, sph; 7tm_1;TM=Y;SS=M; 5.16
452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 5.16
451220; AF124251; Hs.26054; novel SH2-containing protein 3; SH2;TM=M;SS=N; 5.15
417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 5.14
424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation ant; PAAD_DAPIN,HIN;; 5.14
451099; R52795; Hs.25954; interleukin 13 receptor, alpha 2; fn3;TM=Y;SS=M; 5.13
427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a l; 7tm_1;TM=Y;SS=M; 5.12
423196; AK001866; Hs.125139; hypothetical protein FLJ11004; none;TM=M;SS=N; 5.12
433671; AW138797; Hs.132906; 19A24 protein; ig;TM=M;SS=M; 5.11
426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2;TM=M;SS=N; 5.06
431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subuni; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 5.05
418185; AW958272; Hs.347326; intercellular adhesion molecule 2 (ICAM; none;TM=Y;SS=M; 5.05
437352; AL353957; Hs.284181; hypothetical protein DKFZp434P0531; DUF221;TM=Y;SS=M; 5.03
457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDc;TM=M;SS=N; 5.02
452924; AW560939; Hs.97199; complement component C1q receptor; EGF,lectin_c,Tissue_fac,Xlink,TIL;TM=Y;SS=M; 5.02
426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR m; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 4.99
432805; X94630; Hs.3107; CD97 antigen; 7tm_2,EGF,GPS,FecCD;TM=Y;SS=M; 4.95
434883; AW361538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;; 4.95
414291; AI289619; Hs.13040; G protein-coupled receptor 86; 7tm_1;TM=Y;SS=M; 4.94
428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU S; none,rrm; 4.92
451154; AA015879; Hs.33536; ESTs; TIMP,none; 4.92
435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-Hacid_DH_C;TM=M;SS=N; 4.90
413011; AW068115; Hs.821; biglycan; LRR,LRRNT;; 4.90
422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); rrm,ig; 4.89
417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr_redox;TM=Y;SS=M; 4.88
412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc;TM=M;SS=N; 4.88
439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1,LRR;TM=Y;SS=N; 4.87
405102; ; ; C15001220*:gi|4469558|gb|AAD21311.1| (AF; DAG_PE-bind,PH,RhoGEF,DC1;; 4.86
422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1,kazal,A2M,A2M_N;TM=Y;SS=M; 4.84
432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.83
414936; C14774; ; gb:C14774 Clontech human aorta polyA mRN; ank,pkinase,death,none; 4.82
430152; AB001325; Hs.234642; aquaporin 3; MIP;TM=Y;SS=M; 4.82
444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 4.81
410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-recept; SH2,Y_phosphatase,DSPc;TM=M;SS=N; 4.81
453107; NM_016113; Hs.279746; vanilloid receptor-like protein 1; ank,ion_trans;TM=Y;SS=N; 4.80
433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;; 4.80
422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 4.78
419542; AA366037; Hs.90911; solute carrier family 16 (monocarboxylic; none,none; 4.76
438899; AF085833; Hs.135624; ESTs; none,PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 4.75
427418; AA402587; Hs.356667; LAT1-3TM protein; none,none; 4.75
431924; AK000850; Hs.272203; Homo sapiens cDNA FLJ20843 fis, clone AD; SH3,none; 4.73
424218; AF031824; Hs.143212; cystatin F (leukocystatin); cystatin;; 4.72
414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17,none; 4.72
416178; AI808527; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.71
430037; BE409649; Hs.227789; mitogen-activated protein kinase-activat; pkinase;TM=M;SS=N; 4.71
451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none,none; 4.71
453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP,integrin_A,NIF; 4.71
408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 4.70
438543; AA810141; Hs.192182; ESTs; SH2,pkinase,none; 4.70
424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;SS=N; 4.70
438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 4.70
422164; NM_014312; Hs.112377; cortic al thymocyte receptor (X. laevis ; ig,Gemini_mov;TM=Y;SS=M; 4.69
414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 4.69
425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-; aldo_ket_red,none; 4.67
432314; AA533447; Hs.285173; ESTs; Xlink,none; 4.66
453518; AW503205; Hs.27268; gb:UI-HF-BN0-akt-g-03-0-UI.r1 NIH_MGC_50; SH3,PH,RhoGEF;TM=M;SS=N; 4.66
418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH;TM=M;SS=N; 4.66
446063; AI720140; Hs.151079; ESTs; ISK_Channel,none; 4.65
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh;; 4.65
431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 4.65
443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, ; none,PDZ,LIM,pkinase; 4.65
414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 4.64
427535; R29543; Hs.2164; pro-platelet basic protein (includes pla; IL8;TM=M;SS=M; 4.64
437119; AI379921; Hs.177043; XP_171387 similar to rhotekin; none,none; 4.63
411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK;; 4.63
429784; M69796; Hs.30; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=N; 4.62

415934; NM_000928; Hs.992; phospholipase A2, group IB (pancreas); phoslip;; 4.61
408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none,none; 4.61
426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase;TM=M;SS=N; 4.59
444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligas; WW,HECT,RNA_pol_A,none; 4.59
408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FlID,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M;SS=N; 4.59
431087; H12723; Hs.290791; ESTs; ion_trans,none; 4.58
425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 4.58
422427; AA310514; Hs.96692; ESTs; PH,Ets,CH,spectrin,Ca_channel_B,none; 4.57
441527; W19504; Hs.7884; solute carrier family 21 (organic anion ; OATP_N,OATP_C;TM=Y;SS=N; 4.56
416464; NM_000132; Hs.79345; coagulation factor VIII, procoagulant co; Cu-oxidase,F5_F8_type_C;; 4.56
421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4;TM=Y;SS=M; 4.56
422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3;TM=M;SS=N; 4.55
444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC,death,TNFR_c6; 4.55
428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled; Nramp;TM=Y;SS=N; 4.55
410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 4.54
426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 4.54
450086; AW016343; Hs.233301; ESTs; ank,death,ZU5,NMU,none; 4.54
438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear transl; HLH,PAS,IL8;TM=M;SS=N; 4.54
414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase;TM=M;SS=N; 4.53
429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M;SS=N; 4.53
427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6,ET,PLA2_inh;; 4.53
411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 4.53
434158; T86534; Hs.14372; ESTs; adenylatekinase,none; 4.52
431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep_L_domain,none; 4.52
447341; AF106941; Hs.18142; arrestin, beta 2; arrestin,arrestin_C,PX,PH,PLDc; 4.52
447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of ; SH3,PH;TM=M;SS=N; 4.51
417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3,pkinase;TM=M;SS=N; 4.51
422893; X98411; Hs.380077; myosin IF; SH3,myosin_head,IQ;TM=M;SS=N; 4.51
407202; N58172; Hs.109370; ESTs; F5_F8_type_C,pkinase,Ets,none; 4.51
447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sa; zf-C2H2,zf-C3HC4,UIM;TM=M;SS=N; 4.51
450747; AI064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 4.50
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 4.50
453856; AA804789; Hs.379109; PDZ-LIM protein mystique; LIM,PDZ;TM=M;SS=N; 4.49
432744; AA988835; Hs.38664; ESTs; none,none; 4.49
419032; W81330; Hs.99877; ESTs, Highly similar to JAK3B [H.sapiens; pkinase,SH2,Insulin,pkinase,SH2; 4.48
444009; AI380792; Hs.135104; ESTs; TNFR_c6,TIL,none; 4.48
426416; AW612744; Hs.169824; killer cell lectin-like receptor subfami; lectin_c;TM=Y;SS=M; 4.48
412802; U41518; Hs.74602; aquaporin 1 (channel-forming integral pr; MIP;TM=Y;SS=M; 4.48
447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 4.47
408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed; efhand,ion_trans,K_tetra,none; 4.47
435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none;TM=M;SS=N; 4.46
413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;; 4.45
423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 4.45
434308; N51517; Hs.47282; ESTs; pkinase,pkinase_C,none; 4.45
434448; W26667; Hs.184581; Homo sapiens cDNA FLJ14821 fis, clone OV; pkinase,pkinase_C;; 4.45
417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;; 4.44
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 4.44
430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 4.44
436001; AW903849; Hs.173840; HUEL (C4orf1)-interacting protein; ig;TM=M;SS=M; 4.44
452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1,OATP_C;TM=Y;SS=N; 4.43
418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2,none; 4.43
410068; AI633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3;TM=M;SS=N; 4.43
449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain,none; 4.42
451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate,; IQ,7tm_1;TM=M;SS=N; 4.42
410598; AI817130; Hs.9195; Homo sapiens cDNA FLJ13698 fis, clone PL; RasGEF,PRK; 4.42
439411; AA044876; Hs.58043; ESTs, Weakly similar to CYA2_HUMAN ADENY; guanylate_cyc;TM=Y;SS=M; 4.42
433179; AW362945; Hs.162459; ESTs; Armadillo_seg,none; 4.42
414849; AW372721; Hs.291623; ESTs, Weakly similar to unnamed protein ; pkinase,none; 4.42
409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase_C,CARD;TM=M;SS=N; 4.41
445903; AI347487; Hs.132781; class I cytokine receptor; fn3;TM=Y;SS=N; 4.41
438507; AA809052; Hs.356627; ESTs; none,none; 4.41
409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfami; TNF;TM=Y;SS=M; 4.40
453037; AA045175; Hs.17914; ESTs; none;TM=Y;SS=M; 4.40
412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi;TM=Y;SS=M; 4.40
451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin_N;; 4.40
415149; X12451; Hs.78056; cathepsin L; Peptidase_C1;; 4.39
408105; AW152207; Hs.270977; ESTs, Weakly similar to I38022 hypothetl; Y_phosphatase,carb_anhydrase,DSPc,none; 4.39
423099; NM_002837; Hs.123641; protein tyrosine phosphatase, receptor t; fn3,Y_phosphatase,DSPc,COX6C;TM=M;SS=M; 4.39
438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 4.39
433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20;; 4.39
429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;; 4.39
426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2,BH4,none; 4.38
434511; R28982; Hs.18106; ESTs; pkinase,Glyco_hydro_39; 4.38
448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;SS=N; 4.37
447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3,ig,Y_phosphatase,MAM;TM=Y;SS=M; 4.36
432583; AW023624; Hs.162282; potassium channel TASK-4; potassium chan; ion_trans,X;TM=Y;SS=M; 4.36
413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 4.36
426828; NM_000020; Hs.172670; activin A receptor type II-like 1; pkinase,Activin_recp;TM=M;SS=M; 4.36
449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 4.36
437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO3_cotransp;TM=Y;SS=N; 4.36
429670; L01087; Hs.211593; protein kinase C, theta; DAG_PE-bind,pkinase,pkinase_C,DNA_pol_viral_N,PHD,DC1;TM=M;SS=N; 4.35
421195; BE464560; Hs.133017; ESTs; none,none; 4.35

415758; BE270465; Hs.78793; protein kinase C, zeta; pkinase,DAG_PE-bind,pkinase_C,OPR;; 4.35
457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metalfothio_5;TM=M;SS=N; 4.34
419150; T29618; Hs.89640; TEK tyrosine kinase, endothelial (venous; EGF,fn3,pkinase,ig,laminin_EGF,DSL;TM=Y;SS=M; 4.34
440675; AW005054; Hs.279788; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase,none; 4.34
429657; D13626; Hs.2465; KIAA0001 gene product; putative G-protei; 7tm_1;TM=Y;SS=M; 4.34
414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 4.34
425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinas; SH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.34
452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.33
407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.33
452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H; SH3,none; 4.33
434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.32
445330; R52656; Hs.21691; ESTs; 7tm_1,none; 4.32
437527; AI241019; Hs.145644; ESTs; PIP5K,none; 4.32
437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 ; TIMP,pkinase,DAG_PE-bind,RBD; 4.31
416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; ig,ITAM,Zn_clus;TM=Y;SS=M; 4.31
416269; AA177138; Hs.161671; ESTs; pkinase,DAG_PE-bind,RBD,none; 4.30
425458; H89317; Hs.182889; ESTs; ion_trans,none; 4.30
424206; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 4.29
451876; T63141; ; gb:yb99a12.s1 Stratagene lung (937210) H; SH3,none; 4.29
417801; AA417383; Hs.82582; integrin, beta-like 1 (with EGF-like rep; EGF;; 4.29
435240; AI025435; Hs.117532; ESTs; GHMP_kinases,none; 4.27
444051; N48373; Hs.10247; activated leucocyte cell adhesion molecu; none,none; 4.26
423523; AW299828; Hs.193580; ESTs; none,none; 4.26
426274; D38122; Hs.2007; tumor necrosis factor (ligand) superfami; TNF;TM=Y;SS=N; 4.26
425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M;SS=N; 4.26
448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 4.26
418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 4.26
427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 4.26
416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,vwc,TSPN;; 4.25
436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.25
436494; AA720997; Hs.128295; ESTs; none,CAP_GLY,HCO3_cotransp,Glyco_hydro_63,PH; 4.24
439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.24
418255; AW135405; Hs.37251; ESTs; pkinase,none; 4.24
400328; X87344; ; transporter 2, ATP-binding cassette, sub; none;TM=Y;SS=N; 4.24
405121; ; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;; 4.24
425795; AJ000479; Hs.159543; EDG-6 (endothelial differentiation, G-p; 7tm_1;TM=Y;SS=M; 4.23
406786; AW161678; Hs.111334; ferritin, light polypeptide; ferritin;TM=M;SS=N; 4.23
449843; R65337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 4.23
445657; AW612141; Hs.279575; Homo sapiens G-protein coupled receptor ; 7tm_1;TM=Y;SS=M; 4.23
413795; AL040178; Hs.142003; ESTs; none,pkinase,LRR,LRRCT; 4.22
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 4.22
447687; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 4.22
417318; AW953937; Hs.240845; ESTs; SH3,PH,RhoGEF;; 4.21
424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 4.21
408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, com; none,none; 4.20
432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 4.20
424618; L29472; Hs.1802; major histocompatibility complex, class ; ig,MHC_II_beta;TM=Y;SS=M; 4.19
445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 4.19
432882; NM_013257; Hs.279696; serum/glucocorticoid regulated kinase-li; pkinase,PX,pkinase_C;; 4.19
425481; AW978162; Hs.372811; ESTs; none,Oxysterol_BP; 4.19
429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M;SS=N; 4.18
401083; ; ; NM_016582*:Homo sapiens peptide transpor; PTR2;TM=Y;SS=M; 4.18
420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 4.18
424377; AF081675; Hs.146322; killer cell lectin-like receptor subfami; lectin_c;TM=Y;SS=M; 4.17
424148; BE242274; Hs.1741; integrin, beta 7; integrin_B,EGF,metalthio,PSI;TM=Y;SS=M; 4.17
421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig,none; 4.17
452100; AI668668; Hs.379032; inositol polyphosphate-5-phosphatase, 75; Exo_endo_phos,RhoGAP,none; 4.17
413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylin; SH2,SH3,C2,PH,PI-PLC-Y,PI-PLC-X,PDGF;; 4.17
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,ig; 4.17
444034; AL161957; Hs.10177; pleckstrin homology domain interacting p; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,Ribosomal_S15,bromodomain,WD40;TM=M;SS=N; 4.16
450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.16
407245; X90568; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M;SS=N; 4.16
418962; AA714835; Hs.271863; ESTs; RhoGAP,SH2,pkinase,POLO_box,none; 4.15
410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 4.15
425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.15
446967; AI699629; Hs.156781; ESTs; none,none; 4.14
432176; AW090386; Hs.112278; arrestin, beta 1; arrestin,arrestin_C,none; 4.14
452571; W31518; Hs.34665; ESTs; none;TM=M;SS=N; 4.14
425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.14
410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;; 4.14
417871; AA521368; Hs.24252; ESTs; tBB,Armadillo_seg,none; 4.13
429819; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (fr; none,none; 4.12
424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;; 4.12
429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase,RGS;TM=M;SS=N; 4.12
413019; BE281604; Hs.75140; low density lipoprotein-related protein-; none;TM=M;SS=Y; 4.12
434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;SS=N; 4.11
434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 4.11
449656; AA002008; Hs.188633; ESTs; PIP5K,none; 4.11
406403; ; ; NM_002162*:Homo sapiens intercellular ad; ig;TM=Y;SS=M; 4.10
427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 4.10
437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,RIO1,none; 4.10
432885; AA595607; Hs.368129; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,pkinase_C,none; 4.10

411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;SS=N; 4.10
418342; BE002723; Hs.334330; leptin receptor; ICE_p20,DED,ICE_p10,ICE_p20,DED; 4.10
424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 4.10
435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;SS=N; 4.10
422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 4.10
437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none;TM=Y;SS=M; 4.10
432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH,RhoGAP,SH3;TM=M;SS=N; 4.09
435140; AA668123; Hs.134170; ESTs; none,none; 4.09
422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.08
428483; AI908539; Hs.184592; KIAA0344 gene product; none,none; 4.08
446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3,none; 4.07
431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV_H; 4.07
409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0627 (f; ABC_tran,ABC_membrane;TM=M;SS=M; 4.07
441518; AW161697; Hs.294150; ESTs; Y_phosphatase,DSPc,none; 4.07
442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 4.06
436982; AB018305; Hs.5378; spondin 1, (f-spondin) extracellular mat; tsp_1,Reeler;; 4.05
420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP,7tm_1; 4.05
439549; AW937885; Hs.137314; ESTs; SH2,none; 4.04
419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.04
418836; AI655499; Hs.161712; ESTs; pkinase,Activin_recp,PDZ,ZU5,death; 4.04
408806; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fis, clone C; SH3,PDZ,Guanylate_kin,none; 4.04
432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanylate_kin,none; 4.03
426086; T94907; Hs.188572; ESTs; PH,Ets,CH,spectrin,Ca_channel_B,none; 4.03
418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 4.03
412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;SS=N; 4.03
416350; AF188625; Hs.189507; phospholipase A2, group IID; phoslip;TM=M;SS=Y; 4.02
434457; AF141332; Hs.200333; apolipoprotein B48 receptor; none;TM=M;SS=N; 4.02
414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;SS=N; 4.02
425694; U51333; Hs.159237; hexokinase 3 (white cell); hexokinase,hexokinase2;TM=M;SS=N; 4.02
449943; AF104266; Hs.24212; latrophilin; 7tm_2,GPS,Gal_Lectin,OLF,Latrophilin,HRM;TM=Y;SS=M; 4.01
408938; AA059013; Hs.22607; ESTs; fn3,Y_phosphatase,carb_anhydrase,none; 4.01
426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affin; none;TM=M;SS=M; 4.00
422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB;TM=Y;SS=M; 4.00
410726; AI623659; Hs.15936; ESTs; pkinase,pro_isomerase,none; 4.00
428318; BE300110; Hs.183842; ubiquitin B; lipocalin,aldedh,ubiquitin,IRK;; 4.00
440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 3.99
429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 3.99
414700; H63202; Hs.38163; ESTs; 7tm_1;TM=Y;SS=M; 3.99
432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase,Sema,PSI,TIG,A4_EXTRA;TM=M;SS=M; 3.99
456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;SS=N; 3.98
427541; AI798983; Hs.375835; solute carrier family 35 (CMP-sialic aci; none,none; 3.98
440248; AA876138; Hs.369458; ESTs; SH2,none; 3.98
437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR_c6,laminin_EGF;TM=Y;SS=N; 3.98
425262; D87119; Hs.155418; GS3955 protein; pkinase;; 3.98
420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetr; transmembrane4;TM=Y;SS=M; 3.98
437151; AA745618; Hs.380121; BANP homolog, SMAR1 homolog; none,none; 3.98
443574; U83993; Hs.321709; purinergic receptor P2X, ligand-gated io; P2X_receptor;TM=Y;SS=M; 3.97
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M;SS=N; 3.97
411574; BE242842; Hs.6760; protein tyrosine kinase 9-like (A6-relat; LRR,LRRCT,TIR,cofilin_ADF;TM=M;SS=N; 3.97
432639; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo; none,IRK; 3.97
457675; AF119917; Hs.306574; Homo sapiens PRO3098 mRNA, complete cds; none;; 3.97
445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2,PH;TM=M;SS=N; 3.96
437157; BE048860; Hs.17287; ESTs; IRK,none; 3.96
453641; AA444140; Hs.90960; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 3.96
446714; W73818; Hs.110028; ESTs; 7tm_1,7tm_1; 3.96
427648; AI376722; Hs.180062; proteasome (prosome, macropain) subunit,; proteasome;; 3.96
453686; AL110326; Hs.304679; ESTs, Moderately similar to Z195_HUMAN Z; none,lectin_c,lig_chan; 3.96
457718; F18572; Hs.22976; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase,pkinase; 3.95
428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4,LIM;TM=M;SS=N; 3.95
435411; AW444619; Hs.138211; ESTs; none,pkinase; 3.94
440209; H05049; Hs.247837; neurexin 3; laminin_G,EGF,none; 3.94
416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 3.94
435272; AA906415; Hs.110041; ESTs; none,pkinase; 3.93
402550; ; ; Target Exon; none,none; 3.93
425233; Z17861; Hs.155216; E1B-55kDa-associated protein 5; SPRY,SAP,pkinase,fn3,ig; 3.93
410073; AW408163; Hs.58488; catenin (cadherin-associated protein), a; Stathmin,Vinculin;; 3.92
453548; AL079983; Hs.116774; integrin, alpha 1; none,vwa,FG-GAP,integrin_A; 3.92
417226; AW505054; Hs.4283; ESTs; pkinase,RGS,PH,myosin_head,Myosin_tail; 3.92
446755; AW451473; Hs.16134; serine/threonine kinase 10; pkinase,TYA;TM=M;SS=N; 3.92
452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp,STAS;; 3.92
418516; NM_006218; Hs.85701; phosphoinositide-3-kinase, catalytic, al; PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B,none; 3.91
423069; W15613; Hs.1613; adenosine A2a receptor; 7tm_1;TM=Y;SS=M; 3.91
414443; AU077268; Hs.76144; platelet-derived growth factor receptor,; ig,pkinase;TM=Y;SS=N; 3.91
434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone H; pkinase,none; 3.91
429615; AF258627; Hs.211562; ATP-binding cassette, sub-family A (ABC1; ABC_tran;TM=Y;SS=M; 3.91
414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;; 3.91
442831; AI798959; Hs.131686; ESTs; ABC_tran,PRK,ABC_tran; 3.91
441657; BE314696; Hs.7936; BAT1-associated protein 2; SH3;TM=M;SS=N; 3.91
438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypotheti; lipoxygenase,PLAT,none; 3.90
447560; AF065214; Hs.18858; phospholipase A2, group IVC (cytosolic, ; PLA2_B;TM=M;SS=N; 3.90
437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 3.89
429379; NM_014840; Hs.200596; KIAA0537 gene product; pkinase,RIO1;TM=M;SS=N; 3.89
410179; W27723; Hs.59498; cell division cycle 2-like 5 (cholineste; pkinase;; 3.89

428713; AA432067; Hs.268551; ESTs, Moderately similar to CYA4 RAT ADE; pkinase;; 3.89
456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 3.89
425190; AW028302; Hs.155079; protein phosphatase 2, regulatory subuni; B56;TM=M;SS=N; 3.89
426752; X69490; Hs.172004; titin; fn3,ig,pkinase,SGXXSG;TM=M;SS=N; 3.89
417767; BE242241; Hs.82542; acyloxyacyl hydrolase (neutrophil); Lipase_GDSL;TM=M;SS=M; 3.88
414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dep; Man-6-P_recep;TM=M;SS=M; 3.88
416140; AI918035; Hs.301196; roundabout (axon guidance receptor, Dros; none,none; 3.88
434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe co; fn3;TM=Y;SS=M; 3.88
410011; AB020641; Hs.57856; PFTAIRE protein kinase 1; pkinase;TM=M;SS=N; 3.87
406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gen; none,none; 3.87
425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;; 3.87
441859; AW194364; Hs.9877; interleukin-4 induced gene-1 protein (Fl; Amino_oxidase,FAD_binding_3,TBC;TM=M;SS=N; 3.87
439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like;TM=M;SS=N; 3.87
415392; Z44067; Hs.10957; ESTs; PIP5K,none; 3.86
416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 3.86
414649; AI672727; Hs.76753; endoglin (CD105 antigen) (ENG); none;TM=Y;SS=M; 3.85
425729; L22647; Hs.159360; prostaglandin E receptor 1 (subtype EP1); 7tm_1;TM=Y;SS=M; 3.85
414496; W73853; Hs.355424; ESTs; pkinase,F5_F8_type_C,adh_short,none; 3.84
412204; AI125507; Hs.24937; ESTs; ig,rrm,none; 3.84
434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin;; 3.84
444981; AW855398; Hs.12210; hypothetical protein FLJ13732 similar to; SH2;TM=M;SS=N; 3.84
412309; M23892; Hs.73809; arachidonate 15-lipoxygenase; lipoxygenase,PLAT;; 3.84
405545; ; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.84
407143; C14076; Hs.332329; EST; none;TM=Y;SS=M; 3.84
420593; AA280356; Hs.187634; ESTs; B56,none; 3.84
413420; AW410235; Hs.75348; proteasome (prosome, macropain) activato; PA28_alpha,PA28_beta,biopterin_H;; 3.83
448253; H25899; Hs.201591; ESTs; 7tm_2,HRM,none; 3.83
444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHIT; ABC_tran,PRK,GBP;TM=Y;SS=N; 3.83
430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 3.83
423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, be; fn3;TM=Y;SS=M; 3.83
458188; AW297226; Hs.137840; ESTs, Moderately similar to SIX4_HUMAN H; pkinase,WD40; 3.82
426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (f; pkinase,none; 3.82
428791; AA435661; Hs.264750; ESTs; zf-C3HC4,none; 3.82
438068; AI927209; Hs.306210; Homo sapiens cDNA: FLJ23133 fis, clone L; NusG;; 3.82
453370; AI470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=N; 3.82
419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1,BAH,zf-CXXC,DNA_methylase; 3.82
410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none,none; 3.82
420679; X57152; Hs.165843; fibrillarin; CK_II_beta,Fibrillarin,WD40;TM=M;SS=N; 3.82
417916; NM_006416; Hs.82921; solute carrier family 35 (CMP-sialic aci; DUF6;TM=Y;SS=M; 3.81
425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, de; none,none; 3.81
417365; D50683; Hs.82028; transforming growth factor, beta recepto; pkinase,WD40;TM=Y;SS=N; 3.64
414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigeni; DAN;TM=M;SS=M; 3.52
422398; AI476149; Hs.334489; hypothetical protein FLJ21992; SH2,SH3;; 3.51
418432; M14156; Hs.85112; insulin-like growth factor 1 (somatomedi; Insulin;; 3.50
459705; BE082764; Hs.270252; ESTs, Weakly similar to androgen recepto; none,C2,WW,HECT; 3.48
425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3,ig,Y_phosphatase,MAM;TM=Y;SS=M; 3.38
415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 3.37
433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR;; 3.24
426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolo; EGF,cadherin,laminin_G;TM=Y;SS=M; 3.11
419721; NM_001650; Hs.315369; aquaporin 4; MIP,none; 2.99
433147; AF091434; Hs.43080; platelet derived growth factor C; PDGF,CUB;; 2.91
417976; BE565892; Hs.83077; interleukin 18 (interferon-gamma-inducin; none;TM=M;SS=N; 2.89
439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.59
426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.23
411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none,none; 2.07
428800; M57627; Hs.193717; interleukin 10; IL10;; 1.10

TABLE 40B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
414991	1785136_1	D78831 C17898 D78863
409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
414936	1782849_1	C14774 C17911 D79033
451876	2328579_1	T63141 AI821021 BF370092 BF370127 BF370060 T62998
432639	1237887_1	AW973785 H60163 AA557608

TABLE 40C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
404240	5002624	Minus	116132-116407,116653-116922
405102	8076881	Minus	120922-121296
405121	8102330	Minus	35816-36004,36587-36684
401083	3242744	Plus	33192-33360
406403	9256305	Minus	151426-151680
402550	7652009	Minus	80413-80673
405545	1054740	Plus	118677-118807,119091-119296,121626-12182

TABLE 41A: 556 GENES UP-REGULATED IN PANCREATIC TUMORS OR PANCREATITIS RELATIVE TO NORMAL TISSUES

Table 41A lists about 556 genes up-regulated in pancreatic tumors or pancreatitis relative to normal tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of pancreatic cancer/median of normal pancreas

Pkey	ExAccn	UnigeneID	Unigene Title	R1
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	7.25
431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.64
444995	AJ272265	Hs.12230	secreted phosphoprotein 2, 24kD	3.56
453863	X02544	Hs.572	orosomucoid 1	114.18
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	922.40
421344	AW631030	Hs.103665	villin-like	2.19
416018	AW138239	Hs.76977	proprotein convertase subtilisin/kexin t	61.10
438091	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	607.40
418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	228.20
418969	W33191	Hs.28907	hypothetical protein FLJ20258	4.97
443162	T49951	Hs.9029	DKFZP434G032 protein	38.01
423096	AA732684	Hs.278428	progestin induced protein	189.60
413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	11.06
448243	AW369771	Hs.52620	integrin, beta 8	116.90
421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-236D15	21.52
407788	BE514962	Hs.38991	S100 calcium-binding protein A2	8.74
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	3.11
432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	307.70
457059	BE561665	Hs.177677	exosome component Rrp40	33.60
451945	BE504055	Hs.211420	ESTs	7.31
453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	133.70
443247	BE614387	Hs.333893	c-Myc target JPO1	349.10
410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	330.00
416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	3.78
413635	AI272727	Hs.249163	fatty acid hydroxylase	3.53
433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	73.90
414774	X02419	Hs.77274	plasminogen activator, urokinase	3.39
410639	BE269047	Hs.65234	hypothetical protein FLJ20596	1.72
410541	AA065003	Hs.64179	syntenin-2 protein	10.29
427722	AK000123	Hs.180479	hypothetical protein FLJ20116	6.79
429612	AF062649	Hs.252587	pituitary tumor-transforming 1	4.62
407604	AW191962	Hs.249239	collagen, type VIII, alpha 2	366.30
431193	AW749505	Hs.296770	KIAA1719 protein	6.99
442080	AW444761	Hs.44565	ESTs	118.00
427670	BE612888	Hs.180224	myosin regulatory light chain	2.73
445921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	647.30
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	738.90
441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	66.43
407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.03
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	7.73
416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	227.30
418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	115.60
452355	N54926	Hs.29202	G protein-coupled receptor 34	192.20
419481	AI879195	Hs.90606	15 kDa selenoprotein	119.90
407230	AA157857	Hs.182265	keratin 19	12.11
418525	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	6.63
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	592.10
411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	120.40
445517	AF208855	Hs.12830	hypothetical protein	117.40
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.25
428385	AF112213	Hs.184062	putative Rab5-interacting protein	3.12
448663	BE614599	Hs.106823	hypothetical protein MGC14797	135.20
406867	AA157857	Hs.182265	keratin 19	11.32
417426	NM_002291	Hs.82124	laminin, beta 1	406.20

406366	AF026692	Hs.105700	secreted frizzled-related protein 4	0.62
401201	#(NOCAT)		Target Exon	0.75
420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	0.63
405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.75
442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	0.67
405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.83
403207	#(NOCAT)		C2000960:gi|131432|sp|P23132|LITH_BOVIN	0.80
427858	NM_001971	Hs.21	elastase 1, pancreatic	0.98
426004	AW600300	Hs.124123	ESTs, Moderately similar to SYNL RAT SYN	0.88
401541	NA		Target Exon	0.91
429793	AI417638	Hs.114648	estrogen regulated gene 1	0.85
423058	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.81
433110	D56494	Hs.3191	rat regenerating islet-derived-like, hum	0.72
425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	0.95
416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	0.87
412470	M93283	Hs.73923	pancreatic lipase-related protein 1	0.89
431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	0.97
419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.95
412688	AW583062	Hs.74502	chymotrypsinogen B1	0.95
427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.07
420937	AW965719	Hs.1340	colipase, pancreatic	0.99
418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	1.02
410839	NM_006849	Hs.66581	protein disulfide isomerase	1.00
437986	AA774575	Hs.121776	testis expressed sequence 11	1.02
415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	1.06
427965	D00306	Hs.181289	elastase 3, pancreatic (protease E)	1.22
406399	#(NOCAT)		NM_003122*:Homo sapiens serine protease	1.08
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.11
414061	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	1.22
421243	AW873803	Hs.102876	pancreatic lipase	1.13
419263	AW583874	Hs.89832	insulin	1.12
424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.13
408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductanc	1.32
436217	T53925	Hs.107	fibrinogen-like 1	1.72
435975	AL118990	Hs.41997	alpha-1-B glycoprotein	1.60
431330	X69532	Hs.2777	inter-alpha (globulin) inhibitor, H1 pol	2.02
414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	1.82
415003	M11437	Hs.77741	kininogen	3.83
422281	M36803	Hs.1504	hemopexin	2.14
414910	X12662	Hs.289057	arginase, liver	97.90
417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	236.70
400836	#(NOCAT)		Target Exon	2.47
452983	L32140	Hs.531	afamin	117.10
419768	T72104	Hs.93194	apolipoprotein A-I	4.87
413841	M34276	Hs.75576	plasminogen	374.00
400560	#(NOCAT)		NM_030878*:Homo sapiens cytochrome P450,	144.50
419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	266.50
425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	77.80
426205	D63521	Hs.167877	leukocyte cell-derived chemotaxin 2	169.80
414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	3.60
443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	400.40
429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	4.72
428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	5.26
425260	L47726	Hs.1870	phenylalanine hydroxylase	73.78
443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	182.20
413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	335.00
413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	173.40
421126	M74587	Hs.102122	insulin-like growth factor binding prote	565.30
407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	86.20
413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	477.20
452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	201.50
416402	NM_000715	Hs.1012	complement component 4-binding protein,	426.10
425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	1.10
421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	0.62
406672	M26041	Hs.198253	major histocompatibility complex, class	4.02
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	5.34
421712	AK000140	Hs.107139	hypothetical protein	5.62
417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	8.85
442896	R37725	Hs.261108	ESTs	157.70
410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	137.70
428486	AW583497	Hs.184604	pancreatic polypeptide	2.59
457489	AI693815	Hs.127179	cryptic gene	3.23
404866	NA		ENSP00000251112*:Sodium/potassium-transp	2.84
432874	W94322	Hs.279651	melanoma inhibitory activity	2.48
445891	AW391342	Hs.199460	ESTs	70.38
404682	NA		C9001188*:gi|12738842|ref|NP_073725.1| p	1.38
429547	AW009166	Hs.99376	ESTs	6.85
441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	5.21
422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.74
446868	AV660737	Hs.135100	ESTs	102.10
404287	NA		C6001909:gi|704441|dbj|BAA18909.1| (D298	242.70
443267	AW450630	Hs.133851	ESTs	98.90
451635	AA018899	Hs.127179	cryptic gene	2.16

	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	131.70
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	128.70
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	92.90
	410309	BE043077	Hs.278153	ESTs	108.80
5	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	170.10
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	75.70
	449592	AI655494	Hs.195718	ESTs	4.58
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	188.50
	406685	M18728		gb:Human nonspecific crossreacting antig	1123.60
10	411573	AB029000	Hs.70823	KIAA1077 protein	995.60
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	11.32
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	8.38
	428698	AA852773	Hs.334838	KIAA1866 protein	662.00
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	4.00
15	432596	AJ224741	Hs.278461	matrilin 3	283.50
	428824	W23624	Hs.173059	ESTs	4.55
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.01
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.21
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	4.80
20	448844	AI581519	Hs.177164	ESTs	362.80
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	133.90
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	128.20
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	13.83
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	316.00
25	452571	W31518	Hs.34665	ESTs	245.50
	443646	AI085198	Hs.164226	ESTs	189.40
	436032	AA150797	Hs.109276	latexin protein	291.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	252.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	278.20
30	430407	H23551	Hs.30974	ESTs	6.20
	419235	AW470411	Hs.288433	neurotrimin	423.50
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.01
	444301	AK000136	Hs.10760	asporin (LRR class 1)	499.90
	427333	AF067797	Hs.176658	aquaporin 8	1.05
35	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	4.33
	407777	AA161071	Hs.71465	squalene epoxidase	3.64
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	1.47
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	3.98
	453935	AI633770	Hs.42572	ESTs	2.08
40	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	3.84
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	14.21
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	315.70
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.53
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	3.13
45	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	9.33
	440484	BE328156	Hs.150356	ESTs	1.03
	447395	AI418412	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	1.09
	440099	AL080058	Hs.6909	DKFZP564G202 protein	14.74
	434665	AA642125		gb:nr60c01.s1 NCI_CGAP_Lym3 Homo sapiens	0.98
50	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	2.23
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	329.40
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.71
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.69
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.70
55	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	3.19
	429010	Y18198	Hs.194725	one cut domain, family member 2	1.96
	414420	AA043424	Hs.76095	immediate early response 3	2.54
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	3.30
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	312.80
60	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	177.80
	406173	#(NOCAT)		ENSP00000250148*:Growth hormone variant	1.46
	403776	#(NOCAT)		ENSP00000226542*:Small inducible cytokin	121.80
	403574	NA		Target Exon	16.12
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.94
65	458449	H04482	Hs.29019	ESTs	71.60
	409958	NM_001523	Hs.57697	hyaluronan synthase 1	1.77
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	3.13
	451181	AI796330	Hs.207461	ESTs	68.00
	440508	BE267911	Hs.196970	ESTs	38.00
70	429636	AA455692	Hs.163232	ESTs	30.70
	419570	W68738		gb:zd37g06.s1 Soares_fetal_heart_NbHH19W	1.02
	431779	AW971178	Hs.268571	apolipoprotein C-I	3.36
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.20
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	3.94
75	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	1171.10
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	809.50
	440482	AA886658	Hs.50873	ESTs	9.95
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	30.70
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	82.90
80	452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	26.01
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	5.38
	409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	0.54
	420876	AA918425	Hs.177744	ESTs	0.89

	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	0.94
	401732	#(NOCAT)		NM_001176*:Homo sapiens Rho GDP dissocia	1.13
	404142	NA		Target Exon	1.33
	424165	AW582904	Hs.142255	islet amyloid polypeptide	2.95
5	413880	AI660842	Hs.110915	interleukin 22 receptor	1.34
	407007	U22961		gb:Human mRNA clone with similarity to L	1.57
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.48
	432855	AF017988	Hs.279565	secreted frizzled-related protein 5	1.28
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.31
10	445730	AI624342	Hs.170042	ESTs	2.14
	406666	V00495	Hs.184411	albumin	2.95
	435849	BE305242	Hs.16098	claudin 2	1.96
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	2.49
	430272	X04898	Hs.237658	apolipoprotein A-II	3.29
15	412374	X01388	Hs.73849	apolipoprotein C-III	2.42
	419276	BE165909	Hs.306881	MSTP043 protein	83.40
	415448	T68645	Hs.952	solute carrier family 10 (sodium/bile ac	3.52
	423541	AA296922	Hs.129778	gastrointestinal peptide	3.16
	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	6.24
20	425551	AA359252	Hs.126485	hypothetical protein FLJ12604; KIAA1692	14.67
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	4.30
	428786	Y16577	Hs.2314	mannose-binding lectin (protein C) 2, so	92.10
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	203.30
	451253	H48299	Hs.26126	claudin 10	1.37
25	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.38
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	7.04
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.84
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.65
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	9.28
30	422237	M13149	Hs.1498	histidine-rich glycoprotein	34.26
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	1.92
	414386	X00442	Hs.75990	haptoglobin	8.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	1.74
	452689	F33868	Hs.284176	transferrin	6.51
35	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	35.08
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	170.30
	428874	W32133	Hs.194366	transthyretin (prealbumin, amyloidosis t	2.34
	405849	#(NOCAT)		Target Exon	103.10
	405281	#(NOCAT)		NM_002864:Homo sapiens pregnancy-zone pr	31.20
40	419078	M93119	Hs.89584	insulinoma-associated 1	6.28
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.89
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.80
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.82
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	13.15
45	450400	AI694722	Hs.279744	ESTs	5.22
	413916	N49813	Hs.75615	apolipoprotein C-II	8.60
	444632	AI184027	Hs.146986	ESTs, Weakly similar to FATH_HUMAN CADHE	71.30
	415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.70
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.65
50	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	3.01
	436961	AW375974	Hs.156704	ESTs	164.60
	446319	AW207590	Hs.160711	ESTs	1.88
	427899	AA829286	Hs.332053	serum amyloid A1	6.98
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.12
55	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	132.20
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.23
	406319	NA		CX000780:gi|6679197|ref|NP_032800.1| pol	51.50
	404286	NA		C6001909:gi|704441|dbj|BAA18909.1| (D298	1.75
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	52.90
60	406293	NA		Target Exon	68.30
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	102.43
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	206.30
	425200	BE255203	Hs.155101	ATP synthase, H transporting, mitochondr	5.76
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	200.10
65	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	97.70
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.96
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	30.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.66
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	193.80
70	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.05
	420001	J05064	Hs.1282	complement component 6	159.00
	449038	AL133084	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	39.10
	423184	NM_004428	Hs.1624	ephrin-A1	2.39
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	327.90
75	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	90.50
	445593	AW203963	Hs.150896	ESTs	49.20
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	3.12
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.93
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	39.90
80	417940	R28205	Hs.24230	ESTs	57.20
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	2.51
	439920	H05430	Hs.288433	neurotrimin	1.91
	432542	AW083920	Hs.16098	claudin 2	3.47

	410418	D31382	Hs.63325	transmembrane protease, serine 4	3.82
	415989	AI267700	Hs.317584	ESTs	182.50
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.84
	400024			AFFX control - HUMRGE/M10098_5	4.82
5	418067	AI127958	Hs.83393	cystatin E/M	4.19
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.92
	405909	NA		Target Exon	71.80
	448811	AI590371	Hs.174759	ESTs	6.74
	430044	AA464510	Hs.152812	ESTs	14.91
10	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	757.80
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	1.65
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapi	104.70
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	143.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	311.80
15	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	63.00
	422330	D30783	Hs.115263	epiregulin	141.70
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	2.59
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	181.90
	430691	C14187	Hs.103538	ESTs	95.80
20	401682	NA		Target Exon	6.17
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	318.60
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.51
	442560	AA365042	Hs.228598	ESTs, Weakly similar to 2004399A chromos	3.90
	414812	X72755	Hs.77367	monokine induced by gamma interferon	434.60
25	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	6.58
	421430	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	35.10
	419693	AA133749	Hs.301350	FXYD domain-containing ion transport reg	2.45
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	8.56
	448437	AW470125		gb:xw60c04.x1 NCI_CGAP_Pan1 Homo sapiens	79.80
30	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	147.30
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	30.07
	424586	NM_003401	Hs.150930	X-ray repair complementing defective rep	55.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	405.20
	438746	AI885815	Hs.184727	ESTs	3.57
35	456032	AW957446	Hs.301711	ESTs	136.80
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	36.10
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	9.93
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	146.40
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	20.60
40	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.58
	437157	BE048860	Hs.120655	ESTs	91.80
	404285	NA		C6001909:gi|704441|dbj|BAA18909.1| (D298	123.80
	424036	AA770688	Hs.28777	H2A histone family, member L	5.26
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	130.40
45	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	48.80
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	3.15
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	253.20
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	80.00
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	3.05
50	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.66
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	23.02
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	78.10
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	1.74
	421298	AW172431	Hs.13012	ESTs	133.10
55	422424	AI186431	Hs.296638	prostate differentiation factor	2.65
	421582	AI910275	Hs.1406	trefoil factor 1 (pS2)	5.17
	401480	NA		Target Exon	73.70
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	137.70
	409757	NM_001898	Hs.123114	cystatin SN	9.36
60	449722	BE280074	Hs.23960	cyclin B1	162.70
	452240	AI591147	Hs.61232	ESTs	151.90
	415165	AW887604	Hs.78065	complement component 7	2.85
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	290.30
	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.89
65	409041	AB033025	Hs.50081	KIAA1199 protein	334.10
	453331	AI240665	Hs.8895	ESTs	12.85
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	12.42
	453160	AI263307	Hs.239884	H2B histone family, member L	156.40
	444015	AI472865	Hs.135534	ESTs	14.60
70	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	87.20
	448045	AJ297436	Hs.20166	prostate stem cell antigen	526.20
	422426	W79117	Hs.58559	ESTs	58.30
	450737	AW007152	Hs.203330	ESTs	281.00
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	31.25
75	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	78.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	212.10
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	3.40
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	3.48
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	281.50
80	431753	X76029	Hs.2841	neuromedin U	60.50
	428651	AF196478	Hs.188401	annexin A10	508.30
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	85.80
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	55.30

	435039	AW043921	Hs.130526	ESTs	64.00
	447033	AI357412	Hs.157601	ESTs	123.20
	433578	BE336886	Hs.3416	adipose differentiation-related protein	9.22
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	525.70
5	411274	NM_002776	Hs.69423	kallikrein 10 (KLK10) (PRSSL1) (nes1)	44.36
	452705	H49805	Hs.246005	ESTs	120.10
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	92.30
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	29.37
	422562	AI962060	Hs.118397	AE-binding protein 1	3.84
10	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	27.80
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.09
	440868	R79707	Hs.263339	ESTs, Moderately similar to I38022 hypot	76.30
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.37
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	3.44
15	426320	W47595	Hs.169300	transforming growth factor, beta 2	138.10
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	3.45
	459309	AA040620	Hs.5672	hypothetical protein AF140225	127.80
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	361.20
	422553	AI697720	Hs.171455	ESTs, Weakly similar to T31613 hypotheti	136.60
20	432375	BE536069	Hs.2962	S100 calcium-binding protein P	6.87
	400534	#(NOCAT)		C22000015:gi|12741327|ref|XP_008833.2| z	89.00
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.78
	423739	AA398155	Hs.97600	ESTs	135.60
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	148.50
25	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	87.70
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	76.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	110.60
	419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (	234.60
	428471	X57348	Hs.184510	stratifin	3.72
30	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	437.90
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	219.20
	419842	AA765489	Hs.104350	ESTs	3.80
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	606.80
	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.62
35	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	258.70
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	304.80
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	8.78
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	10.95
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	199.70
40	438199	AW016531	Hs.122147	ESTs	67.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfami	107.20
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.59
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	3.45
	421937	AI878857	Hs.109706	hematological and neurological expressed	3.17
45	427961	AW293165	Hs.143134	ESTs	109.30
	422043	AL133649	Hs.110953	retinoic acid induced 1	2.98
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	276.50
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	5.28
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	27.85
50	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	342.30
	424086	AI351010	Hs.102267	lysyl oxidase	213.50
	432731	R31178	Hs.287820	fibronectin 1	185.10
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	106.10
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.27
55	417308	H60720	Hs.81892	KIAA0101 gene product	405.30
	438146	Z36842	Hs.57548	ESTs	8.38
	424800	AL035588	Hs.153203	MyoD family inhibitor	172.10
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	45.70
	408380	AF123050	Hs.44532	diubiquitin	11.18
60	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	149.10
	422963	M79141	Hs.13234	ESTs	33.60
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.73
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	8.96
	424897	D63216	Hs.153684	frizzled-related protein	312.40
65	421110	AJ250717	Hs.1355	cathepsin E	790.80
	411789	AF245505	Hs.72157	DKFZP564I1922 protein	3.17
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	8.52
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	558.00
	406837	R70292	Hs.156110	immunoglobulin kappa constant	4.36
70	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.83
	421470	R27496	Hs.1378	annexin A3	242.90
	407242	M18728		gb:Human nonspecific crossreacting antig	36.91
	432101	AI918950	Hs.123642	EphA3	221.60
	406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	5.34
75	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	292.00
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	184.90
	435202	AI971313	Hs.170204	KIAA0551 protein	64.80
	407216	N91773	Hs.102267	lysyl oxidase	73.70
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	3.20
80	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	288.70
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	502.60
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	6.13
	441020	W79283	Hs.35962	ESTs	178.90

	453857	AL080235	Hs.35861	DKFZP586E1621 protein	504.30
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	242.10
	413435	X51405	Hs.75360	carboxypeptidase E	7.30
	436476	AA326108	Hs.33829	bHLH protein DEC2	247.20
5	406747	AI925153	Hs.217493	annexin A2	110.00
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	112.10
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	583.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	6.56
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	460.90
10	444665	BE613126	Hs.47783	B aggressive lymphoma gene	204.40
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	7.75
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	14.61
	424560	AA158727	Hs.150555	protein predicted by clone 23733	99.80
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	242.20
15	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	17.88
	410668	BE379794	Hs.65403	hypothetical protein	4.18
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	116.40
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	60.30
	442577	AA292998	Hs.163900	ESTs	4.18
20	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	334.20
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	8.16
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	375.30
	445133	AW157646	Hs.153506	ESTs	292.40
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	4.38
25	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfami	89.00
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	322.10
	410687	U24389	Hs.65436	lysyl oxidase-like 1	9.10
	417409	BE272506	Hs.82109	syndecan 1	4.05
	426471	M22440	Hs.170009	transforming growth factor, alpha	138.60
30	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	250.50
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.89
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.76
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.79
	408491	AI088063	Hs.7882	ESTs	8.25
35	437802	AI475995	Hs.122910	ESTs	4.54
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	175.10
	421155	H87879	Hs.102267	lysyl oxidase	170.10
	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-447F3	2.91
	439867	AA847510	Hs.161292	ESTs	261.60
40	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	723.00
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	251.70
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	155.50
	457180	R26022	Hs.194662	calponin 3, acidic	68.00
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	17.19
45	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	5.32
	425139	AW630488	Hs.325820	protease, serine, 23	371.90
	432978	AF126743	Hs.279884	DNAJ domain-containing	7.27
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	19.30
	421991	NM_014918	Hs.110488	KIAA0990 protein	190.50
50	421814	L12350	Hs.108623	thrombospondin 2	15.02
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	28.57
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	519.20
	413048	M93221	Hs.75182	mannose receptor, C type 1	240.60
	404210	#(NOCAT)		NM_005936:Homo sapiens myeloid/lymphoid	404.60
55	452862	AW378065	Hs.8687	ESTs	364.20
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	226.20
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	4.31
	427390	AI432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	10.41
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	22.46
60	451295	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene	23.74
	448569	BE382657	Hs.21486	signal transducer and activator of trans	5.68
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	190.80
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	230.50
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	361.90
65	422545	X02761	Hs.287820	fibronectin 1	8.81
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	7.30
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	267.20
	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	5.07
	431512	BE270734	Hs.2795	lactate dehydrogenase A	270.10
70	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	504.60
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	10.62
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.80
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	14.01
	428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f	9.15
75	434423	NM_006769	Hs.3844	LIM domain only 4	297.30
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	486.20
	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	9.73
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	762.90
	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	7.81
80	400133	NA		Eos Control	357.00
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1150.30
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.50
	446019	AI362520	Hs.279789	histone deacetylase 3	11.26

426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	459.50
422687	AW068823	Hs.119206	insulin-like growth factor binding prote	2.68
432401	NM_013330	Hs.274479	NME7	4.99
437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	7.65

Table 41B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
419570	1860604_1	W68738 W68831
423733	231476_1	AA330281 0AA330232 AW962521
434665	390530_1	AA642125 AA654516
448437	763310_1	AW470125 AI734872 AI749559 AW856504 AI583942 AW779036 AW843429 AW844876 AI520713 AW847236

Table 41C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400534	6981826	Minus	278637-279292
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400836	8954179	Plus	677-1188
401201	9743387	Minus	138534-138629,139234-139294,140121-140335,142033-142479
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401541	8072607	Minus	50018-50158
401682	4755167	Plus	13022-13473
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,20067-20130,20215-20414
403207	7630829	Plus	89914-90033,90729-90855,91131-91198
403574	8101156	Plus	5542-6176
403776	7770611	Minus	1414-1513,1624-1756
404142	9856692	Minus	80316-80459
404210	5006246	Plus	169926-170121
404285	2326514	Plus	32282-32416
404286	2326514	Plus	51086-51301
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404866	9366919	Minus	11743-11929
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405849	7651817	Minus	17705-18287
405909	7705180	Minus	86985-87233
406173	7230224	Plus	12925-13213
406293	5686274	Minus	17646-17953
406319	9211730	Minus	82320-82561
406399	9256288	Minus	63448-63554

TABLE 42A: 574 genes upregulated in pancreatic cancer relative to normal body tissues

Table 42A lists about 574 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
R2 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1; R2

426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin,toxin_4;SS=M; 107.29; 1.07
415934; NM_000928; Hs.992; phospholipase A2, group IB (pancreas); phoslip;SS=M; 83.67; 1.06
421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61
406399; ; ; NM_003122*:Homo sapiens serine protease ; kazal;SS=M; 55.49; 1.08
444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 53.65; 43.61

406685; M18728; ; gb:Human nonspecific crossreacting antig; ig;TM=M;SS=M; 52.73; 22.83
428698; AA852773; Hs.334838; KIAA1866 protein; none;NA;NA; 32.44; 13.11
437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO3_cotransp;TM=Y;; 29.80; 1.46
428874; W32133; Hs.194366; transthyretin (prealbumin, amyloidosis t; Transthyretin;SS=M; 29.42; 1.94
444754; T83911; Hs.374341; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 28.78; 3.13
418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUSS protein d; none;TM=M;SS=M; 28.61; 0.98
438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 25.38; 3.63
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;SS=M; 24.64; 7.21
417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 23.77; 6.74
414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 22.96; 4.57
418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 22.31; 5.42
425573; AB006423; Hs.158308; serine (or cysteine) proteinase inhibito; serpin,GCV_H;TM=M;SS=M; 21.91; 1.03
433110; D56494; Hs.3191; rat regenerating islet-derived-like, hum; lectin_c;TM=M;SS=M; 21.90; 0.60
426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M;; 21.41; 19.89
453863; X02544; Hs.572; orosomucoid 1; lipocalin,aldedh,ubiquitin,IRK;SS=M; 20.80; 8.12
421126; M74587; Hs.102122; insulin-like growth factor binding prote; thyroglobulin_1,IGFBP;SS=Y; 20.60; 8.48
451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin_N;SS=M; 19.25; 3.53
413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT,none; 18.38; 2.53
420332; NM_001756; Hs.1305; serine (or cysteine) proteinase inhibito; serpin;TM=M;SS=M; 18.19; 2.29
438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 17.67; 4.80
417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;SS=M; 17.08; 6.37
427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a l; 7tm_1;TM=Y;SS=M; 16.89; 7.15
441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 16.59; 7.74
445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 16.28; 9.22
431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 15.96; 2.38
444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B,Endonuclease,Phosphodiest;TM=Y;SS=M; 15.65; 1.33
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;; 15.53; 4.34
419355; AA428520; Hs.90061; progesterone binding protein; heme_1;TM=Y;SS=M; 15.45; 10.50
426006; R49031; Hs.22627; ESTs; pkinase,TBC; 15.17; 0.58
433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;SS=M; 14.84; 3.04
422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c;SS=M; 14.71; 2.89
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 14.28; 11.47
408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran,ABC_membrane,PRK,Bac_export_3;TM=Y;; 13.98; 1.18
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.81; 7.69
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;; 13.59; 2.24
425988; BE045897; Hs.53985; ESTs, Weakly similar to I38022 hypotheti; none,none; 13.54; 0.95
409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase_C,CARD;TM=M;; 13.48; 3.59
429556; AW139399; Hs.98988; ESTs; none;TM=M;; 13.20; 1.16
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 12.83; 7.72
427286; AW732802; Hs.2132; epidermal growth factor receptor pathway; SH3,TonB_boxC;TM=M;; 12.72; 9.01
431912; AI660552; Hs.356183; ESTs, Weakly similar to A56154 Abl subst; none,Acyl-CoA_dh,Acyl-CoA_dh_M,Acyl-CoA_dh_N; 12.72; 6.72
412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1;TM=Y;SS=M; 12.71; 12.56
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisoIV,HATPase_c;SS=M; 12.52; 4.92
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 12.38; 7.59
428157; AI738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 12.34; 11.53
424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 12.32; 3.02
414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig;TM=Y;SS=M; 12.29; 2.21
415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;; 12.16; 4.14
427283; AL119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodi; Sulfatase,Somatomedin_B,Phosphodiest,Endonuclease;TM=M;SS=Y; 11.97; 5.93
434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK;TM=Y;; 11.76; 1.58
426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 11.75; 3.56
412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi;TM=Y;SS=M; 11.67; 3.77
450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin,ldl_recept_a,none; 11.65; 4.52
439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 11.56; 5.46
431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh,ldh_C,SH3,pkinase,UBA;TM=M;; 11.55; 5.11
429638; AI916662; Hs.211577; kinectin 1 (kinesin receptor); bZIP,Tropomyosin,spectrin,LBP_BPI_CETP,B56,M;TM=Y;SS=M; 11.47; 4.65
445133; AW157646; Hs.198689; ESTs; efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FliD,bZIP,Tropomyosin,Myc-LZ,M,ldh_C,CH,AIP3;TM=M;; 11.41; 12.62
411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activa; SH2,SH3,C2,PH,RasGAP;TM=M;SS=M; 11.24; 9.95
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 11.19; 4.16
422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;; 11.17; 5.98
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;; 11.14; 9.09
440594; AW445167; Hs.126036; ESTs; none,none; 11.05; 16.45
425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;SS=M; 11.05; 10.38
427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M;; 11.05; 4.70
448811; AI590371; Hs.199460; ESTs; none;TM=Y;; 10.85; 9.69
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;; 10.72; 8.65
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;; 10.51; 12.97
424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD_Synth,ldh,ldh_C,pkinase;SS=M; 10.37; 6.35
436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;; 10.36; 2.74
427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, r; ig;TM=Y;SS=M; 10.34; 3.14
417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3,pkinase;TM=M;; 10.34; 4.47
418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 10.21; 4.58
451820; AW058357; Hs.199248; ESTs; 7tm_1;TM=Y;SS=M; 10.18; 2.67
413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 10.17; 8.35
429752; H52343; Hs.36636; ESTs; pkinase,pkinase; 10.13; 12.35
452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN,sugar_tr;TM=Y;SS=M; 10.08; 8.74
421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 10.05; 6.06
452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 9.98; 3.16
416389; AA180072; Hs.149846; integrin, beta 5; integrin_B,none; 9.85; 9.59
421044; AF061871; Hs.101302; Human DNA sequence from clone RP1-238D15; fn3,vwa,Collagen,TSPN;TM=M;SS=M; 9.78; 5.96
446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 9.75; 2.64
405102; ; ; C15001220*:gi|4469558|gb|AAD21311.1| (AF; DAG_PE-bind,PH,RhoGEF,DC1;SS=M; 9.74; 1.88
418693; AI750878; Hs.87409; thrombospondin 1; EGF,tsp_1,vwc,TSPN,tsp_3;SS=M; 9.72; 6.94

426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR m; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 9.68; 10.58
448105; AW591433; Hs.298241; Transmembrane protease, serine 3; ldl_recept_a,trypsin;TM=Y;SS=M; 9.67; 4.06
456266; L29073; Hs.198726; cold shock domain protein A; 7tm_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36
410240; AL157424; Hs.61289; synaptojanin 2; Exo_endo_phos,Syja_N,rrm,Gram-ve_porins;TM=M;; 9.62; 3.77
457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;; 9.60; 8.05
456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A; none;TM=Y;; 9.57; 3.77
416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3;TM=M;; 9.56; 10.50
437158; AW090198; Hs.348709; KIAA1150 protein; none;NA;NA; 9.55; 8.87
426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;; 9.47; 5.67
403344; ; ; NM_000341:Homo sapiens solute carrier fa; alpha-amylase;TM=Y;; 9.47; 1.42
449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra,Ion_trans,none; 9.46; 3.12
433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M;; 9.42; 4.01
444838; AV651680; Hs.208558; ESTs; Integrin_A,FG-GAP,none; 9.42; 1.87
439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none,none; 9.41; 5.55
428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46
411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 9.38; 6.32
432810; AA863400; Hs.374489; ESTs; none,Skp1,AAA; 9.38; 4.36
427581; NM_014788; Hs.179703; KIAA0129 gene product; SPRY,zf-B_box;TM=M;; 9.34; 8.26
413109; AW389845; Hs.110855; ESTs, similar to leukemia virus receptor; PHO4,none; 9.34; 4.67
428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;; 9.31; 4.24
408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 9.24; 7.12
448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23; 6.03
437672; AW748265; Hs.5741; flavohemoprotein b5?; heme_1,NAD_binding,lipoxygenase,FAD_binding_6;TM=M;; 9.22; 10.72
416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 9.20; 4.46
409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb_propeptide,Tub;SS=M; 9.19; 16.46
413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none,START; 9.15; 2.18
418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiest;TM=Y;SS=M; 9.14; 3.03
452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t; Y_phosphatase,none; 9.14; 11.75
417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF;SS=M; 9.11; 4.29
427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;; 9.06; 9.68
431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M;; 9.05; 5.61
413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;; 9.04; 5.79
437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSPc;TM=M;; 9.02; 5.75
418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestin; cadherin;TM=Y;SS=M; 8.94; 5.01
446406; AI553681; Hs.348490; Arg/Abl-interacting protein ArgBP2; Sorb,none; 8.91; 1.77
428820; AA436187; Hs.172631; integrin, alpha M (complement component ; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 8.85; 4.74
434398; AA121098; Hs.3838; serum-inducible kinase (SNK); pkinase,POLO_box;TM=M;; 8.78; 4.54
453902; BE502341; Hs.3402; ESTs; none,none; 8.72; 3.71
433334; AI927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 8.70; 3.71
450247; AF123303; Hs.24713; hypothetical protein; efhand,mito_carr;TM=Y;SS=M; 8.68; 3.40
432101; AI918950; Hs.123642; EphA3; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 8.62; 5.62
410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 8.61; 13.53
422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 8.55; 4.82
425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;; 8.50; 3.18
419111; AA234172; Hs.137418; ESTs; none,IRK; 8.47; 7.51
430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 8.45; 3.46
447574; AF162666; Hs.18895; tousled-like kinase 1; pkinase;TM=M;; 8.45; 5.30
447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 8.44; 6.30
419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;; 8.43; 4.87
405555; ; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;; 8.39; 0.68
417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR;TM=M;SS=M; 8.35; 4.74
405556; ; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;; 8.31; 0.87
407687; AK002011; Hs.37558; hypothetical protein FLJ11149; lys,ig,FAD_Synth,ldh,ldh_C,pkinase;SS=M; 8.28; 3.12
408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 8.27; 5.65
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.26; 5.49
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2;SS=M; 8.24; 8.91
405204; ; ; NM_002086*:Homo sapiens growth factor re; SH2,SH3;TM=M;; 8.23; 6.43
426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073;SS=M; 8.20; 6.11
428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xe; pkinase;TM=M;; 8.18; 8.37
450375; AA009647; Hs.352537; a disintegrin and metalloproteinase doma; Reprolysin,Pep_M12B_propep,disintegrin,Reprolysin,Pep_M12B_propep,disintegrin; 8.17; 12.24
443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 8.15; 4.61
413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalyti; PKI;SS=M; 8.15; 11.12
428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 8.13; 1.15
425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; per; none;TM=M;; 8.12; 4.54
425836; AW955696; Hs.90960; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 8.11; 7.47
406366; ; ; secreted frizzled-related protein 4; trypsin;SS=M; 8.05; 0.69
429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, ; C2,PLA2_B;TM=M;; 8.04; 5.20
458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 8.02; 1.93
425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (sol; PEPCK;TM=M;; 7.97; 19.33
445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none,none; 7.90; 11.44
449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00
426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg,HEAT_PBS;; 7.83; 11.16
400408; S75765; ; Homo sapiens delta CCK-B gene, partial c; 7tm_1,none; 7.81; 0.78
448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 simil; sugar_tr;TM=Y;SS=M; 7.78; 7.02
457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substra; SH3;TM=M;; 7.75; 2.63
409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;; 7.72; 2.68
447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;; 7.68; 2.40
421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg;SS=M; 7.49; 6.57
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2,none; 7.47; 2.53
417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi;TM=M;SS=M; 7.38; 5.60
436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78

428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3;TM=Y;SS=M; 7.26; 11.00
426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 7.25; 7.22
413880; AI660842; Hs.110915; interleukin 22 receptor; Tissue_fac;TM=Y;SS=M; 7.24; 0.98
418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M;; 7.22; 6.45
413441; AI929374; Hs.75367; Src-like-adapter; SH2,SH3;TM=M;; 7.20; 5.72
426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 7.13; 3.97
428474; AB023182; Hs.184523; KIAA0965 protein; pkinase;TM=M;; 7.13; 5.43
421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer, estroge; trefoil,Gastrin;SS=M; 7.08; 21.61
449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 7.07; 6.18
452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PL; pkinase,Activin_recp,none; 6.94; 4.82
451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene ; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 6.92; 15.34
430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU S; Y_phosphatase,Adaptin_N,Y_phosphatase; 6.88; 1.94
441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG; 7tm_1,ldl_recept_a,LRR;SS=M; 6.86; 0.97
410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 6.83; 7.24
425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3,ig,Y_phosphatase,MAM;TM=Y;SS=M; 6.83; 11.43
400539; ; ; Target Exon; none;TM=M;; 6.70; 1.19
431113; AK000673; Hs.274337; hypothetical protein FLJ20666; pkinase;TM=M;; 6.65; 2.21
445280; AW055063; Hs.343220; v-crk avian sarcoma virus CT10 oncogene ; SH2,SH3,none; 6.61; 10.66
425834; NM_001639; Hs.1957; amyloid P component, serum; pentaxin;TM=M;SS=M; 6.57; 2.20
435706; W31254; Hs.7045; GL004 protein; PDEase,GAF,none; 6.55; 11.44
415906; AI751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone H; Ephrin,none; 6.45; 5.25
408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none,none; 6.42; 9.14
432336; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase;TM=M;; 6.42; 4.12
417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y;; 6.42; 2.26
446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1;TM=Y;SS=M; 6.41; 4.54
444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 6.38; 3.55
412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPc;SS=M; 6.35; 4.95
422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha;TM=M;; 6.35; 3.56
452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1,OATP_C;TM=Y;; 6.32; 11.02
422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB;TM=Y;SS=M; 6.32; 5.15
407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none,Ribosomal_S13,Galactosyl_T,Zip,adh_short,zf-C3HC4; 6.30; 8.35
428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3;TM=M;SS=Y; 6.29; 3.51
408847; AW290997; Hs.30346; ESTs; pkinase,ig,none; 6.28; 3.63
428179; AI127772; Hs.279696; serum/glucocorticoid regulated kinase-li; pkinase,PX,pkinase_C;SS=M; 6.28; 3.50
443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none,none; 6.26; 7.48
425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 6.25; 3.98
448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;; 6.21; 4.10
428180; AI129767; Hs.182874; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;; 6.18; 4.62
409245; AA361037; Hs.356436; tRNA isopentenylpyrophosphate transferas; Armadillo_seg;TM=M;; 6.17; 11.15
417952; AI192838; Hs.372643; dual-specificity tyrosine-(Y)-phosphoryl; pkinase,none; 6.17; 3.05
445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2,PH;TM=M;; 6.16; 11.90
425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none;TM=M;; 6.10; 2.96
426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf,Ca_channel_B,SH3; 6.03; 3.17
408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc;TM=M;; 5.99; 2.55
441364; AA447849; Hs.286660; Homo sapiens cDNA: FLJ22182 fis, clone H; 7tm_3,none; 5.97; 13.12
414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 5.92; 6.47
418506; AA084248; Hs.85339; Unknown protein for MGC:29643; none,none; 5.91; 1.94
436345; AA873008; Hs.121572; ESTs; CARD,BIR,zf-C3HC4,CARD,BIR,zf-C3HC4; 5.90; 1.40
414087; W19712; ; gb:zb36d03.r1 Soares_parathyroid_tumor_N; pkinase,none; 5.85; 0.90
430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.77; 1.24
431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none,none; 5.71; 4.00
427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6,ET,PLA2_inh;SS=M; 5.71; 3.83
414171; AA360328; Hs.865; RAP1A, member of RAS oncogene family; pkinase,DAG_PE-bind,RBD,ras,DC1,GFP;TM=M;; 5.69; 3.07
418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 5.68; 12.92
425317; AW205118; Hs.210546; interleukin 21 receptor; none;TM=Y;SS=M; 5.60; 5.45
417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase;TM=M;; 5.59; 4.19
400151; ; ; Eos Control; AT_hook,DNA_mis_repair,HATPase_c,UQ_con;TM=M;; 5.53; 8.13
450139; AK001838; Hs.355608; serum/glucocorticoid regulated kinase; none,none; 5.52; 8.61
418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 5.52; 10.04
433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kin; pkinase,none; 5.51; 6.75
424701; NM_005923; Hs.151988; mitogen-activated protein kinase kinase ; pkinase;TM=M;; 5.47; 4.58
415875; AA894876; Hs.5687; protein phosphatase 1B (formerly 2C), ma; PP2C;TM=M;; 5.43; 5.30
408761; AA057264; Hs.238936; ESTs, Weakly similar to (defline not ava; 7tm_1,none; 5.42; 2.59
415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;; 5.37; 8.69
444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20 ; pkinase,RIO1,APH,KOW;TM=M;; 5.36; 3.32
410434; AF051152; Hs.53668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 5.36; 3.94
429023; NM_000312; Hs.2351; protein C (inactivator of coagulation fa; EGF,trypsin,gla;SS=M; 5.31; 4.30
421559; NM_014720; Hs.105751; Ste20-related serine/threonine kinase; pkinase,UVR;TM=M;; 5.31; 3.26
429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;; 5.27; 3.12
440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP;TM=M;; 5.26; 4.82
411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 5.25; 11.26
428234; U93553; Hs.183123; nuclear receptor subfamily 5, group A, m; hormone_rec,zf-C4;SS=M; 5.20; 1.11
408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos;TM=M;; 5.19; 6.25
408657; AA782601; Hs.173328; ESTs; B56,none; 5.18; 5.47
438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate_kin,PDZ,SH3; 5.17; 4.02
438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypotheti; lipoxygenase,PLAT,none; 5.16; 2.91
442200; AW590572; Hs.235768; ESTs; none,none; 5.11; 4.22
418736; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none,none; 5.06; 2.71
419088; AI538323; Hs.367688; integrin, beta 8; Integrin_B,none; 5.07; 3.53
414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip;TM=M;SS=Y; 5.05; 3.42
408414; AI114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell ; fn3,ig;TM=Y;SS=M; 5.05; 3.41
430407; H23551; Hs.30974; ESTs; pkinase,PBD,none; 5.03; 1.63
427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.00; 5.14

452194; AI694413; Hs.373599; Ubiquitin-like protein FAT10??? - diubiq; none,none; 4.98; 2.65
410073; AW408163; Hs.58488; catenin (cadherin-associated protein), a; Stathmin,Vinculin;SS=M; 4.97; 10.60
409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 4.96; 2.87
432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y_phosphatase;SS=M; 4.88; 21.69
433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 4.79; 5.47
421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm_1;TM=M;; 4.75; 5.41
414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M;; 4.74; 9.76
417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 4.73; 4.58
430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;; 4.66; 5.61
452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none,none; 4.63; 6.62
427333; AF067797; Hs.176658; aquaporin 8; MIP;TM=Y;SS=M; 4.63; 0.80
431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subuni; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 4.58; 11.38
428065; AI634046; Hs.157313; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 4.55; 4.51
428562; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 4.54; 8.76
416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;SS=M; 4.54; 19.57
450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.49; 10.47
414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 4.41; 7.27
447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.41; 10.25
433208; AW002834; Hs.24095; ESTs; arf,Ca_channel_B,SH3; 4.39; 12.14
403208; ; ; Target Exon; lectin_c,none; 4.37; 0.76
440486; BE243513; Hs.7212; hypothetical protein PP1044; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 4.36; 10.34
414278; AA330116; Hs.355877; Human glucose transporter pseudogene; none,none; 4.35; 7.95
424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS;SS=M; 4.34; 6.23
422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin_A,none; 4.32; 5.85
418721; NM_002731; Hs.87773; protein kinase, cAMP-dependent, catalyti; pkinase,pkinase_C;SS=M; 4.31; 3.09
412330; NM_005100; Hs.788; A kinase (PRKA) anchor protein (gravin) ; none;TM=M;; 4.25; 12.74
421939; BE169531; Hs.109727; TAK1-binding protein 2; KIAA0733 protein; zf-RanBP,CUE;TM=M;; 4.25; 12.54
414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;SS=M; 4.24; 6.91
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 4.22; 5.27
415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig;TM=Y;; 4.16; 7.22
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 4.16; 9.27
445496; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArfGap;TM=M;; 4.15; 23.43
436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 4.14; 3.76
414462; BE622743; Hs.301064; arfaptin 1; none,none; 4.08; 13.43
435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-Hacid_DH_C;TM=M;; 4.06; 9.12
431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr;TM=Y;; 4.04; 10.05
429379; NM_014840; Hs.200598; KIAA0537 gene product; pkinase,RIO1;TM=M;; 4.00; 6.35
429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M;; 3.98; 5.66
405203; ; ; NM_002086*:Homo sapiens growth factor re; SH2,SH3;TM=M;; 3.95; 17.71
409335; NM_001502; Hs.53985; glycoprotein 2 (zymogen granule membrane; zona_pellucida;TM=M;SS=M; 3.94; 0.58
446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 3.89; 7.59
413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanylate_kin;TM=M;; 3.84; 8.89
438000; AI825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M;; 3.83; 4.22
418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 3.81; 6.45
450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M;; 3.78; 8.49
417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 3.77; 4.22
456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M;; 3.68; 4.92
438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 3.59; 12.12
414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 3.58; 10.93
429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 3.57; 5.10
415088; AI077288; Hs.374374; serum/glucocorticoid regulated kinase; none,none; 3.56; 4.60
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 3.55; 4.52
448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;; 3.54; 8.19
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 3.52; 9.70
400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor,; integrin_A,FG-GAP;TM=Y;; 3.45; 6.44
445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M;; 3.41; 6.03
418255; AW135405; Hs.37251; ESTs; pkinase,none; 3.41; 13.97
408822; AW500715; Hs.57079; Homo sapiens cDNA FLJ13267 fis, clone OV; PIP5K,none; 3.40; 8.97
426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase;TM=M;; 3.39; 11.24
431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 3.39; 5.10
414291; AI289619; Hs.13040; G protein-coupled receptor 86; 7tm_1;TM=Y;SS=M; 3.38; 10.25
457329; AI634860; Hs.247043; type 1 tumor necrosis factor receptor sh; Peptidase_M1;SS=M; 3.38; 13.78
411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 3.36; 4.17
443710; AI928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha,none; 3.32; 20.33
454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;; 3.31; 6.94
408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 3.29; 3.07
426728; NM_007118; Hs.367689; triple functional domain (PTPRF interact; SH3,ig,pkinase,PH,spectrin,RhoGEF;TM=M;; 3.27; 14.90
427202; BE272922; Hs.173936; interleukin 10 receptor, beta; Tissue_fac;TM=Y;SS=M; 3.24; 4.49
413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;; 3.24; 12.27
425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 3.23; 13.40
417534; NM_004998; Hs.82251; myosin IE; SH3,myosin_head,IQ;TM=M;; 3.21; 15.21
458097; AW341135; Hs.58104; ESTs; none,SH3,PID; 3.21; 7.34
437928; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epimerase/N-ac; hexokinase,FGGY,ROK,Epimerase_2;SS=M; 3.20; 8.38
425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 3.19; 5.09
416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none,none; 3.18; 4.17
453489; AA300067; Hs.102000; hypothetical protein DKFZp434N185; F5_F8_type_C,pkinase,Ets,F5_F8_type_C,pkinase,Ets; 3.17; 7.88
414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_PI4_kinase;TM=M;; 3.16; 4.71
412767; AA233808; Hs.286241; protein kinase, cAMP-dependent, regulato; SH3,7tm_2,cadherin,GPS,laminin_G,EGF,laminin_EGF,Sulfate_transp,STAS,cNMP_binding,RIIa; 3.16; 7.19
415662; AW972481; Hs.170610; ESTs, Highly similar to G01887 MEK kinas; pkinase,none; 3.16; 7.21
407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 3.15; 22.66

437175; AW968078; Hs.87773; protein kinase, cAMP-dependent, catalyti; pkinase,pkinase_C,none; 3.14; 11.72
409270; BE090051; Hs.23120; PIST; fn3,pkinase,PDZ,DUF139;TM=Y;SS=M; 3.09; 7.81
419591; AF090900; Hs.91393; Homo sapiens cDNA: FLJ21887 fis, clone H; PDZ,L27;TM=M;; 3.06; 5.46
447225; R62676; Hs.17820; Rho-associated, coiled-coil containing p; PH,pkinase,HR1,none; 3.04; 13.05
412692; AF044288; Hs.74515; aryl hydrocarbon receptor nuclear transl; HLH,PAS,PAC;TM=M;; 2.95; 12.28
409274; NM_003930; Hs.52644; SKAP55 homologue; SH3,PH;SS=M; 2.90; 14.62
417707; AL035786; Hs.82425; actin related protein 2/3 complex, subun; none;TM=M;; 2.90; 11.00
427045; H86504; Hs.173328; protein phosphatase 2, regulatory subuni; B56;TM=M;; 2.89; 6.12
431177; NM_003304; Hs.250687; transient receptor potential channel 1; ion_trans,ank;TM=Y;; 2.89; 6.53
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;; 2.87; 9.18
418546; AA224827; ; gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens ; vwa,integrin_A,FG-GAP,none; 2.86; 9.94
446668; W58353; Hs.285123; Homo sapiens mRNA full length insert cDN; NDK,PH,Oxysterol_BP;SS=M; 2.85; 14.25
454080; AI199711; Hs.576; fucosidase, alpha-L- 1, tissue; Alpha_L_fucos;TM=M;SS=M; 2.81; 28.84
432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 2.80; 10.53
433000; U26710; Hs.3144; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,UBA,Cbl_N,Cbl_N2,Cbl_N3;; 2.77; 10.93
444488; AW192879; Hs.355660; ancient conserved domain protein 4; none,none; 2.77; 12.58
417904; AI750762; Hs.82911; protein tyrosine phosphatase type IVA, m; Y_phosphatase,DSPc;TM=M;; 2.76; 12.78
425204; NM_002436; Hs.1861; membrane protein, palmitoylated 1 (55kD); SH3,PDZ,Guanylate_kin;SS=M; 2.74; 5.71
419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS,zf-C2H2,SET; 2.73; 12.50
410793; AW581906; Hs.66392; intersectin 1 (SH3 domain protein); SH3,efhand,C2,PH,RhoGEF,M;SS=M; 2.73; 9.84
446081; AA972412; Hs.13755; f-box and WD-40 domain protein 2; WD40,F-box,Ribosomal_L14;TM=M;; 2.71; 12.29
414443; AU077266; Hs.76144; platelet-derived growth factor receptor,; ig,pkinase;TM=Y;; 2.71; 10.53
452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 2.69; 12.53
423533; NM_014339; Hs.129751; interleukin 17 receptor; none;TM=Y;SS=M; 2.67; 8.59
422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 2.67; 12.22
453915; AA588721; Hs.12284; ribosomal protein L44; none,T-box; 2.65; 6.38
416810; AF035606; Hs.80019; programmed cell death 6; efhand;TM=M;; 2.61; 13.89
439658; AA332057; Hs.6639; hypothetical protein MGC15440; none;TM=M;SS=M; 2.58; 10.19
449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3,none; 2.56; 19.04
412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C ; MARCKS;SS=M; 2.55; 14.99
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Recep_L_domain,YLP,none; 2.52; 14.71
409098; AA132672; Hs.7984; pleckstrin homology, Sec7 and coiled/coi; PH,Sec7;TM=M;; 2.51; 14.51
413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex;TM=Y;SS=M; 2.49; 9.28
422070; AF149785; Hs.111126; pituitary tumor-transforming 1 interacti; TCTP;TM=M;SS=Y; 2.45; 12.49
452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase;TM=M;; 2.44; 6.68
427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none;TM=M;; 2.43; 7.97
446287; BE247683; Hs.14611; dual specificity phosphatase 11 (RNA/RNP; DSPc;SS=M; 2.41; 9.51
410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none,none; 2.41; 14.01
424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24,FKBP;TM=Y;; 2.40; 5.98
447580; AI953360; Hs.88201; ESTs; none,none; 2.36; 11.63
426276; AW881411; Hs.169078; hypothetical protein FLJ23018; hormone_rec,zf-C4;TM=M;; 2.34; 13.34
424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF;; 2.33; 12.17
429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase,RGS;TM=M;; 2.32; 15.80
439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M;; 2.32; 12.48
453648; W21493; Hs.28329; hypothetical protein FLJ14005; none,none; 2.31; 13.19
443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin,none; 2.31; 8.51
453327; AW500180; Hs.356109; tryptophanyl-tRNA synthetase; rrm,vwa,FG-GAP; 2.30; 13.02
439256; AA322302; Hs.183302; PCTAIRE protein kinase 2; none,none; 2.26; 10.36
424467; AI929392; Hs.350026; DnaJ (Hsp40) homolog, subfamily B, membe; DnaJ,pkinase,UBA,pkinase_C;SS=M; 2.26; 11.82
426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 2.26; 12.54
456607; AI660190; Hs.106070; cyclin-dependent kinase inhibitor 1C (p5; CDI;TM=M;; 2.25; 13.11
423960; AA164516; Hs.136309; SH3-containing protein SH3GLB1; SH3,none; 2.20; 20.05
424058; AL121516; Hs.138617; thyroid hormone receptor interactor 12; HECT,WWE;TM=M;; 2.20; 13.38
446644; NM_003272; Hs.15791; transmembrane 7 superfamily member 1 (up; none;TM=Y;SS=M; 2.18; 15.68
411218; H46440; Hs.180628; dynamin 1-like; dynamin_2,dynamin,GED,none; 2.18; 13.83
414721; X90392; Hs.77091; ribosomal protein L10; Exo_endo_phos,Ribosomal_L10e,Acyltransferase,SCP;TM=M;SS=M; 2.14; 11.24
421759; AA027968; Hs.107979; small membrane protein 1; none;TM=Y;SS=M; 2.14; 14.03
416240; NM_001981; Hs.79095; epidermal growth factor receptor pathway; efhand,DUF164;TM=M;; 2.13; 12.86
435521; W23814; Hs.6361; mitogen-activated protein kinase kinase ; none,none; 2.12; 11.08
409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;; 2.12; 14.05
453064; R40334; Hs.89463; potassium large conductance calcium-acti; none,none; 2.12; 8.96
409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2,SH3,RhoGAP,none; 2.08; 11.60
414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 2.06; 14.23
414496; W73853; Hs.355424; ESTs; pkinase,F5_F8_type_C,adh_short,none; 2.05; 13.45
450455; AL117424; Hs.25035; chloride intracellular channel 4; none,TNF; 2.05; 19.04
449906; NM_005638; Hs.24167; synaptobrevin-like 1; synaptobrevin,NTF2;TM=Y;; 2.04; 13.34
422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;SS=M; 2.03; 12.60
434935; BE561824; Hs.273369; uncharacterized hematopoietic stem/proge; none;TM=M;; 2.02; 10.52
433427; At816449; Hs.171889; cholinephosphotransferase 1; SH2,CDP-OH_P_transf;TM=M;; 2.02; 16.87
410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 2.02; 9.37
440481; AA182907; Hs.7200; Homo sapiens, clone MGC:16714, mRNA, com; pkinase,RCC1;TM=M;; 2.02; 12.31
434645; AF255303; Hs.112227; membrane-associated nucleic acid binding; zf-CCCH,gpdh,Adeno_E1B_55K,zf-C3HC4;TM=M;; 2.00; 9.15
410113; AW996564; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone H; pkinase,none; 1.99; 10.64
414636; AL120259; Hs.76691; stannin; none;TM=M;SS=Y; 1.95; 7.72
408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase,none; 1.95; 14.95
422690; AU077275; Hs.119222; suppression of tumorigenicity 13 (colon ; TPR;TM=M;; 1.94; 10.91
427881; BE538296; Hs.323834; cytochrome c oxidase subunit Va; none,GKAP; 1.93; 20.57
433387; L76528; Hs.3260; presenilin 1 (Alzheimer disease 3); Presenilin,7tm_3,oxidored_q5_N;TM=Y;; 1.92; 12.58
453938; AF082569; Hs.36794; D-type cyclin-interacting protein 1; B56;TM=M;; 1.90; 12.74
433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) ; none;TM=M;; 1.89; 23.27
447791; BE241859; Hs.19575; CGI-11 protein; V-ATPase_H,Armadillo_seg;TM=M;; 1.88; 12.82
426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone H; adenylatekinase,none; 1.88; 14.95

432650; D00860; Hs.56; phosphoribosyl pyrophosphate synthetase ; none,none; 1.88; 12.70
424250; AF073310; Hs.143648; insulin receptor substrate 2; PH,IRS;TM=M;; 1.86; 19.50
424482; BE268621; Hs.149155; voltage-dependent anion channel 1; Euk_porin;SS=M; 1.85; 11.29
425335; BE394327; Hs.296267; fotilstatin-like 1; efhand,kazal,arf,ras,7tm_1;TM=M;; 1.85; 13.62
426122; NM_006925; Hs.166975; splicing factor, arginine/serine-rich 5; rrm;SS=M; 1.83; 10.88
451579; AW607731; Hs.26670; Human PAC clone RP3-515N1 from 22q11.2-q; kringle;TM=Y;SS=M; 1.83; 20.35
428901; AI929568; Hs.146668; KIAA1253 protein; 7tm_2,UPF0073,TMS_TDE;TM=Y;SS=M; 1.83; 19.00
453963; AA040311; Hs.28959; ESTs; pkinase,Activin_recp,none; 1.82; 15.25
417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB;; 1.81; 14.20
414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigeni; DAN;TM=M;SS=M; 1.81; 22.29
425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M;; 1.80; 18.30
417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown prot; none;NA;NA; 1.80; 6.28
424805; AF230904; Hs.153260; c-Cbl-interacting protein; SH3;TM=M;; 1.80; 11.99
420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M;; 1.79; 25.25
416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 1.78; 15.25
437708; AB033020; Hs.5801; KIAA1194 protein; LRR,Exo_endo_phos;TM=M;; 1.77; 11.11
439877; H39685; Hs.258730; tryptase beta 1; pkinase;SS=M; 1.77; 21.91
440256; U23841; Hs.18851; hypothetical protein FLJ10875; none,UBA,UBX; 1.76; 12.95
425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 1.76; 21.01
414703; BE243877; Hs.374366; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 1.75; 20.03
443693; AI344782; Hs.349261; DnaJ (Hsp40) homolog, subfamily C, membe; rrm,DnaJ,TPR;TM=M;; 1.75; 13.29
437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC_tran,GTP_EFTU,ABC_membrane,none; 1.75; 8.75
413796; AW408094; Hs.75545; interleukin 4 receptor; fn3,granulin;TM=M;SS=M; 1.74; 14.73
438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyrosine kinas; pkinase,SH2,adenylatekinase,none; 1.73; 24.10
429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,ig,none; 1.73; 31.59
421456; AW579842; Hs.104557; hypothetical protein FLJ10697; zf-C2H2,DUF18,efhand,C2,PI-PLC-Y,PI-PLC-X;TM=M;; 1.73; 16.87
444252; R21135; Hs.54985; ESTs; none,none; 1.71; 10.40
442819; BE622721; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; none,pkinase,PBD; 1.69; 14.02
447918; AI129320; Hs.115175; ESTs, Highly similar to JC5818 gamma-act; pkinase,SAM,none; 1.69; 17.14
429279; AB018271; Hs.198689; KIAA0728 protein; Myosin_tail,efhand,spectrin,GAS2,Myosin_tail; 1.68; 14.21
450440; AB024334; Hs.25001; tyrosine 3-monooxygenase/tryptophan 5-mo; 14-3-3;TM=M;; 1.67; 24.67
413423; AU076684; Hs.75350; vinculin; Vinculin,none; 1.65; 29.28
420972; AW814616; Hs.31431; hypothetical protein FLJ12171; Fructosamin_kin;SS=M; 1.65; 10.75
416884; M60484; Hs.80350; protein phosphatase 2 (formerly 2A), cat; Metallophos;SS=M; 1.63; 24.55
436719; Y11192; Hs.5299; aldehyde dehydrogenase 5 family, member ; lipocalin,aldedh,ubiquitin,IRK;SS=M; 1.61; 11.20
419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 1.61; 14.93
414176; BE140638; Hs.75794; EDG-2 (endothelial differentiation, lys; 7tm_1,CRCB;TM=Y;; 1.61; 8.03
431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT;SS=M; 1.60; 24.37
412347; AW970026; Hs.73818; ubiquinol-cytochrome c reductase hinge p; UCR_hinge,G-alpha,arf;TM=M;; 1.59; 18.09
423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;; 1.59; 10.99
426552; BE297660; Hs.170328; moesin; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 1.58; 25.97
428216; M18468; Hs.183037; protein kinase, cAMP-dependent, regulato; cNMP_binding,RIIa;SS=M; 1.56; 10.58
421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;SS=M; 1.56; 13.51
448581; NM_002709; Hs.21537; protein phosphatase 1, catalytic subunit; none,none; 1.55; 12.33
417098; AB017365; Hs.173859; frizzled (Drosophila) homolog 7; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 1.55; 13.77
437076; AA961260; Hs.5443; BCL2-associated athanogene 5; BAG,Hanta_nucleocap;TM=M;; 1.54; 10.93
426653; AA530892; Hs.171695; dual specificity phosphatase 1; Rhodanese,DSPc,Y_phosphatase;TM=M;; 1.54; 11.88
421143; AB024536; Hs.102171; immunoglobulin superfamily containing le; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 1.53; 23.05
414457; AW514320; Hs.76159; ATPase, H transporting, lysosomal (vacuo; pkinase,ATP-synt_C,none; 1.53; 32.59
414382; AW380339; Hs.8068; hematopoietic PBX-interacting protein; M;TM=M;; 1.52; 8.66
450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm;TM=M;; 1.52; 11.74
402705; ; ; activator of S phase kinase; AhpC-TSA;TM=M;SS=M; 1.51; 26.85
426268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;SS=M; 1.50; 24.04
414604; AU076649; Hs.76556; growth arrest and DNA-damage-inducible 3; none;TM=M;; 1.50; 14.35
445584; AF217518; Hs.8360; PTD012 protein; none;SS=M; 1.49; 12.00
407232; X04526; ; gb:Human liver mRNA for beta-subunit sig; WD40;TM=M;; 1.49; 19.32
424206; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 1.48; 13.21
458761; AF090922; Hs.152738; mitochondrial ribosomal protein L11; ER_lumen_recept,Ribosomal_L11,Ribosomal_L11_N;TM=Y;SS=M; 1.48; 12.50
426340; Z97989; Hs.169370; FYN oncogene related to SRC, FGR, YES; BNR,SH2,SH3,pkinase;TM=Y;SS=M; 1.48; 17.75
414166; AW388941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPc,tsp_1,Ribosomal_S21,rvp;TM=M;; 1.46; 20.47
452516; AA058630; Hs.29759; RNA POLYMERASE I AND TRANSCRIPT RELEASE ; none;SS=M; 1.46; 12.72
414240; AL046742; Hs.75842; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;SS=M; 1.45; 14.38
420532; AA248016; Hs.194110; hypothetical protein PRO2730; pkinase,WD40;SS=M; 1.43; 13.92
402575; ; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.43; 13.71
414765; X07854; Hs.77269; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;; 1.41; 24.62
448423; BE390905; Hs.21198; translocase of outer mitochondrial membr; TPR;TM=M;SS=M; 1.41; 10.70
422587; AI879352; Hs.118625; hexokinase 1; hexokinase,hexokinase2;TM=M;; 1.41; 19.31
415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 1.40; 11.21
446108; AL036596; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmin;TM=M;; 1.40; 13.98
427721; AI582843; Hs.180455; RAD23 (S. cerevisiae) homolog A; ubiquitin,UBA,integrin_B;SS=M; 1.39; 15.01
417891; W79410; Hs.82687; protein phosphatase 1, regulatory (inhib; none;TM=M;; 1.39; 15.97
427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M;; 1.39; 14.49
446334; U52427; Hs.14839; polymerase (RNA) II (DNA directed) polyp; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 1.38; 12.58
447042; AB035863; Hs.182217; succinate-CoA ligase, ADP-forming, beta ; ligase-CoA,ATP-grasp,Zip,CPSase_L_D2,GARS_B;TM=Y;SS=M; 1.37; 11.37
427705; AI870421; Hs.180394; signal recognition particle 14kD (homolo; SRP14,TNFR_c6;SS=M; 1.37; 22.05
425969; AW576265; Hs.301763; KIAA0554 protein; SH3,FCH,HR1;TM=M;; 1.37; 13.68
433572; AL046859; Hs.3407; protein kinase (cAMP-dependent, catalyti; PK;SS=M; 1.35; 12.43
410597; W16518; Hs.279518; amyloid beta (A4) precursor-like protein; Kunitz_BPTI,A4_EXTRA,Coprogen_oxidas;TM=Y;SS=M; 1.35; 22.54
418424; Y13622; Hs.85087; latent transforming growth factor beta b; EGF,TB,spidertoxin,granulin,ANF_receptor;SS=M; 1.34; 12.09
442603; AL035719; Hs.303091; pleckstrin homology, Sec7 and coiled/coi; PH,Sec7;TM=M;; 1.34; 11.40
418043; AW377752; Hs.83341; AXL receptor tyrosine kinase; fn3,ig,pkinase;TM=Y;SS=M; 1.31; 10.79

439278; AF077046; Hs.6518; ganglioside expression factor 2; MAP1_LC3,aminotran_3;TM=M;; 1.31; 15.89
425875; AU077333; Hs.160483; erythrocyte membrane protein band 7.2 (s; PBP,Band_7;TM=M;; 1.31; 17.93
407744; AB020629; Hs.38095; ATP-binding cassette, sub-family A (ABC1; ABC_tran,PRK;TM=Y;SS=M; 1.29; 10.95
420679; X57152; Hs.99853; fibrillarin; CK_II_beta,Fibrillarin,WD40;TM=M;; 1.29; 18.69
427397; AI929685; Hs.177656; calmodulin 1 (phosphorylase kinase, delt; efhand,RmaAD;SS=M; 1.29; 15.68
424661; M29551; Hs.151531; protein phosphatase 3 (formerly 2B), cat; Metallophos;TM=M;; 1.28; 13.39
428950; BE311879; Hs.194673; phosphoprotein enriched in astrocytes 15; DED;TM=M;; 1.27; 11.15
440820; AL031846; Hs.356416; plakophilin 4; none,none; 1.26; 10.65
448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG;SS=M; 1.25; 12.07
447386; NM_006289; Hs.375001; KIAA1027 protein; Band_41,I_LWEQ,Apolipoprotein,IRS;SS=M; 1.22; 10.65
433053; BE301909; Hs.279952; glutathione S-transferase subunit 13 hom; HCCA_isomerase;TM=M;; 1.20; 15.78
440708; AF038962; Hs.7381; voltage-dependent anion channel 3; Euk_porin,Enterotoxin_A,PHO4,none; 1.20; 14.06
417069; AA442192; Hs.374980; cytochrome c oxidase subunit VIII; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 1.18; 16.91
402559; ; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.16; 15.49
426636; BE242634; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT;TM=M;; 1.14; 10.99
428773; BE256236; Hs.193163; bridging integrator 1; BAR,SH3;SS=M; 1.14; 11.38
406906; Z25424; ; gb:H.sapiens protein-serine/threonine ki; none,none; 1.13; 12.97
443932; AW888222; Hs.9973; tensin; SH2,WW,PID,none; 1.07; 15.41
421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61
414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 22.96; 4.57
442573; H93366; Hs.7567; branched chain aminotransferase 1, cytos; aminotran_4,none; 21.41; 1.15
451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin_N;SS=M; 19.25; 3.53
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;; 15.53; 4.34
421340; F07783; Hs.1369; decay accelerating factor for complement; sushi;SS=M; 14.84; 19.59
422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c;SS=M; 14.71; 2.89
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 14.28; 11.47
412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1;TM=Y;SS=M; 12.71; 12.56
451820; AW058357; Hs.199248; ESTs; 7tm_1;TM=Y;SS=M; 10.18; 2.67
418693; AI750878; Hs.87409; thrombospondin 1; EGF,tsp_1,vwc,TSPN,tsp_3;SS=M; 9.72; 6.94
448105; AW591433; Hs.298241; Transmembrane protease, serine 3; ldl_recept_a,trypsin;TM=Y;SS=M; 9.67; 4.06
456266; L29073; Hs.198726; cold shock domain protein A; 7tm_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36
413095; AA494359; Hs.30715; potassium voltage-gated channel, lsk-rel; none,START; 9.15; 2.18
417933; X02308; Hs.82962; thymidylate synthetase; thymidylat_synt,MR_MLE,MR_MLE_N;SS=M; 8.97; 5.01
433334; AI927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55
433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20;SS=M; 8.31; 4.23
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.26; 5.49
426513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00
453459; BE047032; Hs.257789; ESTs; none,none; 7.40; 0.60
436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78
426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 7.25; 7.22
426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 7.13; 3.97
419966; X04430; Hs.93913; interleukin 6 (interferon, beta 2); IL6;SS=Y; 6.93; 3.43
457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma 2 viral on; ras,Idh;SS=M; 6.90; 2.85
420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 6.88; 3.10
417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y;; 6.42; 2.26
427969; NM_001963; Hs.2230; epidermal growth factor (beta-urogastron; EGF,ldl_recept_b,EB;TM=M;SS=M; 6.37; 1.07
430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.77; 1.24
427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6,ET,PLA2_inh;SS=M; 5.71; 3.83
418283; S79895; Hs.83942; cathepsin K (pycnodysostosis); Peptidase_C1;SS=M; 5.59; 38.68
458471; AV648609; Hs.194240; ESTs; none,none; 5.23; 1.05
433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
433293; AF007835; Hs.32417; hypothetical protein MGC4309; none;TM=M;; 4.56; 4.96
410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); EGF,TB,wnt,EB,TIL;SS=M; 4.32; 26.87
417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD;TM=Y;SS=M; 4.26; 9.04
414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 3.94; 1.16
439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 3.76; 2.21
419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 3.47; 2.24
419749; X73608; Hs.93029; sparc/osteonectin, cwcv and kazal-like d; kazal,thyroglobulin_1;SS=M; 3.37; 7.10
436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 3.15; 3.27
428093; AW594506; Hs.104830; ESTs; none,none; 2.81; 3.40
459683; AI674906; Hs.199460; gb:wc73f02.x1 NCI_CGAP_Pan1 Homo sapiens; none;TM=Y;; 2.77; 1.36
414443; AU077268; Hs.76144; platelet-derived growth factor receptor,; Ig,pkinase;TM=Y;; 2.71; 10.53
430451; AA836472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase;SS=M; 2.26; 14.59
428953; AA306610; Hs.346183; tumor necrosis factor receptor superfami; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD;; 2.21; 6.33
435496; AW840171; Hs.265398; PAR-6 beta; none,none; 2.17; 2.00
418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Reprolysin,Pep_M12B_propep,EGF;TM=Y;SS=M; 1.91; 13.06
414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigeni; DAN;TM=M;SS=M; 1.81; 22.29
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 1.52; 8.40
452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-FeII_Oxy;TM=M;; 1.49; 3.29
432199; AI693815; Hs.127179; cryptic gene; none;TM=M;SS=M; 1.23; 1.60
453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,ldl_recept_a,none; 1.00; 3.92
445418; AW139377; Hs.127179; cryptic gene; none,none; 1.00; 2.45
451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc_N_term;TM=M;; 1.00; 1.87
447993; AW139525; Hs.170362; ESTs; none,none; 1.00; 1.30

TABLE 42B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
414087	1632850_1	W19712 BE247277
400151	9575_21	BC006850 U07418 NM_000249 U07343 AL574783 BI090482 BG684481 AA385302 BG196167 BI091720 BG195132 AI680106 AI457552 AA402478 BG249688 AA347119 BG755996 BG822578
418546	242836_1	T59706 AA224827 T59643 BE156903

TABLE 42C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406399	9256288	Minus	63448-63554
405102	8076881	Minus	120922-121296
403344	8569726	Plus	70823-70990
405555	1552511	Plus	153405-153564,154623-154876,155272-15540
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
405204	7230116	Plus	126569-126754
406366	9256126	Minus	10639-10800,10890-11023,11113-11293
400539	7574902	Plus	8559-8721
403208	7630829	Minus	147706-147903,148667-148804
405203	7230116	Plus	125295-125463
402705	8782736	Plus	89961-90114,90773-90895,91131-91261
402575	9884830	Minus	109742-109883
402559	9864273	Plus	33539-33715

TABLE 43A: 43 genes upregulated in pancreatic cancer relative to normal body tissues

Table 43A lists about 43 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins particularly useful for diagnostic or prognostic applications. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
R2 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1; R2

446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin;SS=M; 44.95; 2.17
421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;SS=M; 35.40; 29.13
411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M;; 30.10; 13.59
446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8;SS=Y; 29.33; 16.08
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;SS=M; 24.64; 7.21
452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide,TGF-beta,none; 23.81; 10.74
407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagon; TGF-beta,DAN;SS=Y; 22.33; 10.20
404682; ; ; C9001188*:gi|12738842|ref|NP_073725.1| p; none;TM=M;; 17.72; 1.40
413554; AA319146; Hs.75426; secretogranin II (chromogranin C); Granin;TM=M;SS=Y; 17.36; 2.01
428392; H10233; Hs.2265; secretory granule, neuroendocrine protei; none;TM=M;SS=M; 16.82; 1.70
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;; 15.53; 4.34
419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;SS=M; 15.40; 3.70
428242; H55709; Hs.2250; leukemia inhibitory factor (cholinergic ; LIF_OSM;SS=M; 14.85; 6.58
421340; F07783; Hs.1369; decay accelerating factor for complement; sushi;SS=M; 14.84; 19.59
409757; NM_001898; Hs.123114; cystatin SN; cystatin;SS=M; 14.61; 12.75
425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 14.35; 17.22
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.81; 7.69
409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin_B,laminin_EGF;SS=M; 13.05; 7.72
432596; AJ224741; Hs.278461; matrilin 3; EGF,vwa;SS=M; 12.80; 9.91
422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin,Defensin_propep;TM=M;SS=M; 12.79; 4.69
421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 11.36; 2.22
429547; AW009166; Hs.99376; FGENESH predicted novel secreted protein; none,none; 10.25; 5.62
422424; AI186431; Hs.296638; prostate differentiation factor; TGF-beta;SS=M; 9.96; 1.88
428505; AL035451; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46
409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb_propeptide,Tub;SS=M; 9.19; 16.46
418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55
452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB;SS=M; 7.46; 4.96

421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer, estroge; trefoil,Gastrin;SS=M; 7.08; 21.61
423634; AW959906; Hs.1690; heparin-binding growth factor binding pr; none;TM=M;SS=M; 6.78; 12.19
426486; AW583497; Hs.184604; pancreatic polypeptide; hormone3;TM=M;SS=Y; 6.29; 3.51
443646; AI085198; Hs.164226; ESTs; EGF,tsp_1,vwc,TSPN,tsp_3,none; 6.17; 4.25
457489; AI693815; Hs.127179; cryptic gene; none;TM=M;SS=M; 5.19; 2.79
450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; none;SS=M; 5.01; 7.43
422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3,EGF;SS=M; 4.87; 9.40
426322; J05068; Hs.2012; transcobalamin I (vitamin B12 binding pr; Cobalamin_bind;SS=M; 4.71; 11.74
414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;SS=M; 4.24; 6.91
428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA;TM=Y;; 3.52; 8.43
422048; NM_012445; Hs.288126; spondin 2, extracellular matrix protein; tsp_1;TM=M;SS=M; 3.45; 7.69
424667; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2,hemopexin,Peptidase_M10;SS=M; 3.43; 10.37
417931; W95642; Hs.82961; trefoil factor 3 (intestinal); trefoil;SS=M; 2.98; 9.65
445417; AK001058; Hs.12680; Homo sapiens cDNA FLJ10196 fis, clone HE; tsp_1,Reprolysin,Pep_M12B_propep,none; 2.97; 5.74
432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 2.80; 10.53
431462; AW583572; Hs.256311; granin-like neuroendocrine peptide precu; none,none; 2.70; 1.99

TABLE 43C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404682	9797231	Minus	40977-41150

TABLE 44A: 754 GENES UP-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 44A lists about 754 genes up-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	ExAccn	UnigeneID	Unigene Title
100042	M10098		AFFX control - HUMRGE/M10098_3
101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h
103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa
104743	AA021157	Hs.33619	Homo sapiens cDNA FLJ20096 fis, clone CO
104996	AA112307	Hs.105894	hypothetical protein FLJ21919
105437	AA252191	Hs.25199	hypothetical protein
108258	AA063269		gb:zm02a09.s1 Stratagene corneal stroma
109086	AA166695	Hs.270737	tumor necrosis factor (ligand) superfami
109279	AA196625	Hs.86080	ESTs
109779	F10527	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur
111794	R32647	Hs.23545	ESTs
112531	R69798	Hs.29036	ESTs
112784	R96306	Hs.191290	ESTs
113293	T67026	Hs.187403	ESTs
115416	AA283893	Hs.337079	ESTs
116548	D20433		gb:HUMGS01407 Human promyelocyte Homo sa
116565	D45533	Hs.129691	hypothetical protein FLJ21603
118104	N55332	Hs.39785	ESTs
119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa
119336	T55340	Hs.208238	ESTs
120101	W95414	Hs.55497	EST
120715	AA292700		gb:zs59a06.s1 NCI_CGAP_GCB1 Homo sapiens
120872	AA357993	Hs.96996	ESTs
121010	AA398355	Hs.97330	ESTs
121509	AA412092	Hs.97888	ESTs
121722	AA419482	Hs.98674	similar to proline-rich protein 48
122265	AA436838	Hs.98906	EST
123206	AA489681	Hs.102248	Homo sapiens cDNA: FLJ22105 fis, clone H
123490	AA599723		gb:ag11c07.s1 Gessler Wilms tumor Homo s
124198	H53099	Hs.198271	NADH dehydrogenase (ubiquinone) 1 alpha
124294	H90573	Hs.102298	EST
125067	T86429	Hs.111725	ESTs
125153	W38294		
125330	AA401804	Hs.114574	ESTs
125335	T86620	Hs.16230	hypothetical protein FLJ20619
125361	T90348	Hs.183404	ESTs
125439	AA826305		gb:PM0-LT0017-031299-001-c07 LT0017 Homo
125535	R17430	Hs.22215	secretogranin III
125583	R22272	Hs.86022	ESTs
125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
125742	H81181	Hs.261023	hypothetical protein FLJ20958

125795	T98190	Hs.7756	proteasome (prosome, macropain) 26S subu
125858	H11549	Hs.31066	ESTs
125865	H12876	Hs.283078	hOAT4
126039	AA160575	Hs.181102	p30 DBC protein
126143	N29315	Hs.266331	hypothetical protein MGC4595
126177	H93164	Hs.129750	hypothetical protein FLJ10546
126219	N36368	Hs.293483	ESTs, Weakly similar to similar to C. el
126221	AI248169	Hs.172965	ESTs
126262	C75147	Hs.143764	ESTs, Weakly similar to unknown [H.sapi
126277	N39132	Hs.15441	Crm (Cramped Drosophila)-like
126292	AA491328		gb:aa65d09.r1 NCI_CGAP_GCB1 Homo sapiens
126293	Z18870	Hs.248121	G protein-coupled receptor 22
126353	AI243114	Hs.94031	ESTs
126556	AA491325	Hs.112227	membrane-associated nucleic acid binding
126559	R15866	Hs.170263	tumor protein p53-binding protein, 1
126609	W87435	Hs.186802	ESTs
126616	AA348581	Hs.134605	ESTs
126628	AI357886	Hs.170994	hypothetical protein MGC10946
126636	AA001527		gb:zf56g09.r1 Soares retina N2b4HR Homo
126861	AA742428	Hs.144432	ESTs
126990	AA215510	Hs.191650	ESTs
127017	AA740146	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l
127049	AA235966	Hs.291811	ESTs
127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil
127331	F20186		gb:HSPD05873 HM3 Homo sapiens cDNA clone
127357	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
127368	AA434362	Hs.193326	fibroblast growth factor receptor-like 1
127374	AA448728	Hs.312110	ESTs, Weakly similar to I38022 hypothet
127429	AA961490	Hs.293751	ESTs, Moderately similar to TPTE_HUMAN P
127490	W52891	Hs.7278	cryptochrome 2 (photolyase-like)
127502	AA614422	Hs.183502	ESTs
127647	AI087279	Hs.148410	ESTs
127650	AA873776	Hs.261957	ESTs
127676	D31237	Hs.279938	HSPC067 protein
127746	AI239495	Hs.120189	ESTs
127812	AA749094	Hs.291434	ESTs
127824	AI208365	Hs.127811	ESTs
127933	AA811102	Hs.303581	ESTs, Moderately similar to ALU1_HUMAN A
128006	AA058693	Hs.129908	KIAA0591 protein
128011	AI347067	Hs.124636	ESTs
128038	AA868782	Hs.137024	ESTs
128058	AI126617	Hs.132449	ESTs
128199	AI073548	Hs.164597	ESTs
128308	AI079496	Hs.134169	ESTs
128389	AI142639	Hs.146662	ESTs
128410	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
129199	H90914	Hs.200332	hypothetical protein FLJ20651
130998	C00810	Hs.293981	guanine nucleotide binding protein (G pr
134409	AA281600	Hs.164915	small nuclear RNA activating complex, p
134578	AA194724	Hs.224137	hypothetical protein
134644	S83308	Hs.87224	SRY (sex determining region Y)-box 5
100262	D38500	Hs.278468	postmeiotic segregation increased 2-like
100676	HG3044-HT3742	Hs.287820	fibronectin 1
100704	HG3242-HT3419	Hs.166110	calcium channel, voltage-dependent, alph
100787	HG3872-HT4142	Hs.302063	immunoglobulin heavy constant mu
100873	HG4333-HT4603	Hs.17364	zinc finger protein 79 (pT7)
100943	HG880-HT880		gb:PM0-SN0019-280300-001-D11 SN0019 Homo
100996	J03909	Hs.14623	interferon, gamma-inducible protein 30
101046	K01160		
101371	M13232	Hs.36989	coagulation factor VII (serum prothrombi
101461	M22430	Hs.76422	phospholipase A2, group IIA (platelets,
101697	M64358		gb:Human rhom-3 gene, exon.
101909	S69265		
102199	U21128	Hs.79914	lumican
102275	U30998	Hs.17752	phosphatidylserine-specific phospholipas
102295	U32581	Hs.168052	KIAA0421 protein
102319	U34587	Hs.66578	corticotropin releasing hormone receptor
102383	U40622	Hs.150930	X-ray repair complementing defective rep
102470	U49835	Hs.154138	chitinase 3-like 2
102544	U57721	Hs.169139	kynureninase (L-kynurenine hydrolase)
102649	U68133		gb:U68133 Human cell line PCI-O6A Homo s
102798	U88898		gb:Human endogenous retrovirus H proteas
102804	U89942	Hs.83354	lysyl oxidase-like 2
102851	V00532	Hs.93907	interferon, alpha 14
102852	V00571	Hs.75294	corticotropin releasing hormone
102860	X00368		gb:Human prolactin gene 5' region.
103262	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)
103484	Y08374	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
103559	Z19585	Hs.75774	thrombospondin 4
103658	Z74615	Hs.172928	collagen, type I, alpha 1
103719	AA054109	Hs.4273	hypothetical protein FLJ13159
103876	AA226865	Hs.8203	endomembrane protein emp70 precursor iso
103897	AA248870	Hs.55058	EH-domain containing 4

103906	AA249437	Hs.317403	hypothetical protein MGC2744
103985	AA313880	Hs.99872	fetal Alzheimer antigen
104056	AA397529	Hs.58297	CLLL8 protein
104209	AB000221	Hs.16530	small inducible cytokine subfamily A (Cy
104386	H41895	Hs.144164	ESTs, Moderately similar to ALU8_HUMAN A
104398	H53555	Hs.36790	ESTs, Weakly similar to putative p150 [H
104422	H86858	Hs.132909	ESTs
104561	R60100	Hs.323817	DKFZP547E1010 protein
104593	R81267	Hs.98640	hypothetical protein FLJ21069
104643	AA004701	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone K
104673	AA007633	Hs.20010	ESTs
104681	AA009832	Hs.34500	ESTs
104711	AA017254	Hs.32794	ESTs
104812	AA034111	Hs.124187	ESTs
104877	AA047437	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
104886	AA053348	Hs.339699	growth differentiation factor 11
104924	AA058532	Hs.28774	ESTs, Weakly similar to I38022 hypotheti
105071	AA136532	Hs.29475	ESTs
105105	AA151872	Hs.87016	hypothetical protein FLJ22938
105203	AA195660	Hs.7882	ESTs
105317	AA233926	Hs.52620	integrin, beta 8
105617	AA280687	Hs.4069	glucocorticoid modulatory element bindin
105707	AA291012	Hs.37617	ESTs, Weakly similar to A53933 myosin I
105754	AA302657	Hs.192028	ESTs
105770	AA347964	Hs.269873	Homo sapiens clone IMAGE:297403, mRNA se
105882	AA400292	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
105883	AA400490	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com
105890	AA400766	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,
106080	AA418046	Hs.35124	ESTs
106090	AA418909	Hs.169333	hypothetical protein DKFZp761E2110
106096	AA419609	Hs.170121	protein tyrosine phosphatase, receptor t
106124	AA423987	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
106308	AA436186	Hs.30662	ESTs
106438	AA449199	Hs.21342	ESTs
106660	AA460936	Hs.27056	KIAA1284 protein
106731	AA465657	Hs.29205	alpha integrin binding protein 63
106880	AA488889	Hs.32425	ESTs
107055	AA600152	Hs.29419	ESTs
107151	AA621169	Hs.8687	ESTs
107183	C20974	Hs.12114	vanin 1
107231	D59299	Hs.34727	ESTs, Moderately similar to I38759 zinc
107490	W74158	Hs.103189	lipopolysaccharide specific response-68
107572	AA001903	Hs.59962	ESTs
107620	AA005039	Hs.60171	ESTs
107801	AA019433	Hs.285803	Homo sapiens cDNA FLJ10674 fis, clone NT
107817	AA020781	Hs.60847	ESTs
107823	AA021057	Hs.60836	ESTs
107857	AA024687	Hs.61208	ESTs
107882	AA025630	Hs.231967	ALL1 fused gene from 5q31
108005	AA037769	Hs.194293	ESTs, Weakly similar to I54374 gene NF2
108092	AA045961	Hs.184029	hypothetical protein DKFZp761A052
108115	AA047291	Hs.165216	ESTs
108214	AA058661	Hs.60764	ESTs
108382	AA074885	Hs.67726	macrophage receptor with collagenous str
108409	AA075578		gb:zm88h03.r1 Stratagene ovarian cancer
108436	AA078801		gb:zm94a09.s1 Stratagene colon HT29 (937
108625	AA101983	Hs.283022	triggering receptor expressed on myeloid
108631	AA102553	Hs.334337	ESTs
108763	AA127539	Hs.281397	hypothetical protein AD034
108852	AA133131		gb:zm25d03.s1 Stratagene pancreas (93720
108931	AA147186		gb:zo38d01.s1 Stratagene endothelial cel
108976	AA151480	Hs.91202	ESTs
109026	AA157811		gb:zo35d07.s1 Stratagene colon (937204)
109170	AA180352	Hs.191472	ESTs, Weakly similar to ALU1_HUMAN ALU
109303	AA206126	Hs.269291	ESTs
109326	AA210719		gb:zr88e04.s1 NCI_CGAP_GCB1 Homo sapiens
109345	AA213774	Hs.203396	ESTs
109404	AA224594	Hs.86941	ESTs
109473	AA233151	Hs.81796	ESTs
109725	F10003	Hs.79658	casein kinase 1, epsilon
109794	F10684	Hs.23687	ESTs
109835	H00615	Hs.170044	ESTs
109896	H04794	Hs.30489	ESTs
109918	H05641	Hs.216701	Homo sapiens mRNA; cDNA DKFZp564I0816 (f
109950	H08200	Hs.268770	ESTs, Weakly similar to 2004399A chromos
110078	H15054	Hs.318773	KIAA1836 protein
110182	H20402	Hs.31746	hypothetical protein DKFZp547F072
110213	H23216	Hs.86905	ATPase, H+ transporting, lysosomal (vacu
110310	H38209	Hs.32728	EST
110354	H41280	Hs.22586	ESTs
110413	H48124	Hs.279454	ESTs
110422	H48467	Hs.36094	EST
110433	H49425	Hs.301062	UDP-N-acetyl-alpha-D-galactosamine:polyp

110434	H49446	Hs.26299	ESTs
110553	H58934	Hs.124990	ESTs
110750	N20522	Hs.30981	ESTs
110827	N30077	Hs.14855	ESTs
110829	N30198	Hs.28625	ESTs
110917	N46363	Hs.5170	ESTs
111100	N62522	Hs.20450	BCM-like membrane protein precursor
111112	N63281	Hs.35452	ESTs
111179	N67239	Hs.10760	asporin (LRR class 1)
111185	N67551	Hs.12844	EGF-like-domain, multiple 6
111223	N68921	Hs.334838	KIAA1866 protein
111275	N70970	Hs.35006	ESTs
111443	R01901		gb:Homo sapiens endogenous retrovirus W
111573	R10305	Hs.185683	ESTs
111590	R11157	Hs.75425	ubiquitin associated protein
111671	R19368	Hs.229084	Homo sapiens cDNA FLJ11666 fis, clone H
111732	R25153	Hs.163813	ESTs
111809	R33616	Hs.24688	EST
111829	R36070		gb:Homo sapiens full length insert cDNA
111944	R40606	Hs.21263	suppressor of potassium transport defect
112015	R42836	Hs.23198	ESTs
112023	R43020	Hs.236223	EST
112055	R43621	Hs.26139	ESTs
112334	R56239	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S
112340	R56602	Hs.8904	Ig superfamily protein
112353	R58986	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (f
112467	R65706		gb:yi16g12.s1 Soares placenta Nb2HP Homo
112478	R66067	Hs.28664	ESTs
112533	R69886		gb:yi47f03.s1 Soares placenta Nb2HP Homo
112588	R77302		gb:yi75h08.s1 Soares placenta Nb2HP Homo
112595	R77783	Hs.22404	protease, serine, 12 (neurotrypsin, moto
112676	R86976	Hs.34060	ESTs
112744	R93206	Hs.293762	ESTs, Weakly similar to I38022 hypotheti
112777	R95869	Hs.35467	EST
112817	R98491	Hs.14584	ESTs
112902	T09262	Hs.129190	Human DNA sequence from clone RP5-1046G1
113009	T23699	Hs.7246	ESTs
113151	T51620	Hs.9326	EST
113297	T67161	Hs.13059	ESTs
113398	T82280	Hs.87016	hypothetical protein FLJ22938
113484	T87795	Hs.187543	ESTs
113769	U55966	Hs.22985	alpha2,8-sialyltransferase
113794	W37382	Hs.11090	membrane-spanning 4-domains, subfamily A
113971	W86760	Hs.269172	ESTs
114066	Z38152	Hs.26920	ESTs
114178	Z39063	Hs.17930	chromosome 6 open reading frame 11
114206	Z39294	Hs.27339	EST
114371	Z41835	Hs.27810	ESTs
114428	AA017130	Hs.84790	KIAA0225 protein
114466	AA026970	Hs.135150	lung type-I cell membrane-associated gly
114625	AA084362		gb:zn05b10.r1 Stratagene hNT neuron (937
114862	AA235174	Hs.106432	Homo sapiens cDNA FLJ13410 fis, clone PL
114908	AA236545	Hs.54973	cadherin-like protein VR20
114973	AA250845	Hs.87762	ESTs
115009	AA251561	Hs.48689	ESTs
115055	AA253005	Hs.61753	ESTs
115098	AA256161	Hs.161729	ESTs
115321	AA280805	Hs.191540	ESTs
115385	AA282540	Hs.109694	KIAA1451 protein
115466	AA287008	Hs.285655	ESTs
115479	AA287596	Hs.278188	ESTs, Moderately similar to I54374 gene
115663	AA405838	Hs.40507	ESTs
115689	AA410645	Hs.199014	ESTs, Moderately similar to ALU7_HUMAN A
115748	AA418835	Hs.90286	ESTs
115810	AA426026	Hs.187615	ESTs
115827	AA427890	Hs.83583	actin related protein 2/3 complex, subun
115881	AA435577	Hs.184942	G protein-coupled receptor 64
116148	AA460708	Hs.62905	hypothetical protein FLJ14834
116257	AA481493	Hs.88537	ESTs
116365	AA521080	Hs.46765	ESTs
116941	H77395	Hs.39749	ESTs
116982	H81933	Hs.312582	ESTs
116995	H83928		gb:ys64b03.s1 Soares retina N2b4HR Homo
116997	H84214	Hs.40594	ESTs
117016	H87171	Hs.52170	ESTs
117097	H93608	Hs.41919	EST
117101	H94043	Hs.24341	transcriptional co-activator with PDZ-bi
117238	N20815	Hs.173337	ESTs
117303	N22776	Hs.264079	ESTs
117399	N26480	Hs.43805	lipoma HMGIC fusion partner-like 3
117503	N31963	Hs.44286	ESTs
117544	N33222	Hs.44451	ESTs
117594	N34929	Hs.171984	ESTs

117627	N36113	Hs.44789	ESTs, Weakly similar to B34087 hypothet
117653	N38970	Hs.194214	ESTs
117695	N40953	Hs.45093	EST
117697	N40976		gb:yy80b06.s1 Soares_multiple_sclerosis_
117766	N47807	Hs.46767	EST
117807	N48701	Hs.46523	EST
117816	N48872		gb:yy77a05.s1 Soares_multiple_sclerosis_
117882	N50101	Hs.301406	hypothetical protein PP3501
117987	N51935	Hs.47374	Homo sapiens cDNA FLJ13561 fis, clone PL
118074	N54188	Hs.130323	Homo sapiens, clone IMAGE:3960432, mRNA
118114	N56875	Hs.143212	cystatin F (leukocystatin)
118151	N58276	Hs.229119	EST
118270	N62868	Hs.48653	ESTs
118291	N63076	Hs.138746	EST
118358	N64017	Hs.144633	hypothetical protein DKFZp434F2322
118383	N64529	Hs.49001	EST
118412	N64856	Hs.97437	centrosomal protein 1
118433	N66248	Hs.141609	EST
118600	N69222	Hs.238936	ESTs, Weakly similar to (defline not av
118641	N70298	Hs.49829	ESTs
118643	N70324	Hs.49840	ESTs
118695	N71781	Hs.50081	KIAA1199 protein
118915	N91481	Hs.54713	ESTs
119041	R02591	Hs.284294	Breakpoint cluster region protein, uteri
119069	R27619	Hs.231046	EST
119105	R42357	Hs.91453	ESTs
119154	R61293		gb:yh07a05.s1 Soares infant brain 1NIB H
119241	T12559		gb:CHR90079 Chromosome 9 exon II Homo sa
119269	T16367	Hs.65327	EST
119310	T40427		gb:ya01a06.s2 Stratagene lung (937210) H
119345	T63474	Hs.90696	EST
119353	T66867	Hs.187402	ESTs
119390	T89122	Hs.249712	ESTs, Weakly similar to ALU1_HUMAN ALU
119423	T99544	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU
119428	W02129	Hs.55242	EST
119529	W38053		
119795	W73370	Hs.339722	ESTs, Highly similar to S03917 fibronec
119817	W74257	Hs.159690	ESTs
119831	W78050	Hs.58419	DKFZP586L2024 protein
119930	W86471	Hs.151624	hypocretin (orexin) receptor 2
120039	W92548	Hs.94985	ESTs
120256	AA169801	Hs.98710	hypothetical protein
120284	AA182626		gb:zp54e11.s1 Stratagene NT2 neuronal pr
120350	AA211300	Hs.108614	KIAA0627 protein; Drosophila multiple as
120379	AA227849		gb:DKFZp434B1822_r1 434 (synonym: htes3)
120383	AA228030	Hs.123122	FSH primary response (LRPR1, rat) homolo
120420	AA236031	Hs.112885	spinal cord-derived growth factor-B
120437	AA243427	Hs.104311	novel protein with MAM domain
120461	AA251301	Hs.293369	ESTs
120594	AA282054	Hs.5094	ring finger protein 10
120611	AA284178	Hs.110637	homeo box A10
120626	AA285064	Hs.104485	EST
120696	AA291503	Hs.97249	ESTs
120747	AA302976	Hs.96672	ESTs
120749	AA303235		gb:EST14544 Testis tumor Homo sapiens cD
120752	AA311972	Hs.22895	hypothetical protein FLJ23548
120851	AA349662	Hs.174248	ESTs
120866	AA350718	Hs.291272	ESTs
120949	AA397830	Hs.98347	ESTs, Weakly similar to JC5308 testis-sp
120996	AA398281	Hs.308114	ESTs
121038	AA398536	Hs.97365	ESTs
121065	AA398658	Hs.97300	ESTs
121067	AA398662	Hs.97302	ESTs
121071	AA398678	Hs.139355	ESTs
121082	AA398722		gb:zl75h07.s1 Soares_testis_NHT Homo sap
121172	AA400013	Hs.97750	EST, Weakly similar to MPL3 RAT MICROTUB
121191	AA400205	Hs.104447	ESTs
121354	AA405384	Hs.193737	ESTs
121393	AA405981	Hs.262643	ESTs
121399	AA406059	Hs.332700	EST
121479	AA411911	Hs.98110	ESTs
121498	AA412033	Hs.178045	ESTs
121704	AA418743	Hs.98306	KIAA1862 protein
121736	AA421131	Hs.148515	Human clone 23564 mRNA sequence
122198	AA435892	Hs.97541	ESTs
122220	AA436011	Hs.98187	ESTs
122250	AA436692	Hs.98892	EST
122279	AA437209	Hs.234016	ESTs
122286	AA437259	Hs.104944	ESTs
122330	AA442870	Hs.98628	Homo sapiens, clone IMAGE:4214491, mRNA,
122338	AA443311	Hs.98998	ESTs
122355	AA443789	Hs.19978	CGI-30 protein
122590	AA453264	Hs.99310	ESTs

122746	AA458791		gb:aa88c02.s1 Stratagene fetal retina 93
122805	AA460702	Hs.82772	collagen, type XI, alpha 1
122841	AA461536	Hs.288908	WAS protein family, member 2
122899	AA469960	Hs.178420	ESTs, Highly similar to WASP interacting
122933	AA476728	Hs.107537	chromosome 7 open reading frame 2
123005	AA479726	Hs.52620	integrin, beta 8
123142	AA487504	Hs.105718	EST
123153	AA488349	Hs.334808	hypothetical protein MGC4189
123168	AA488881	Hs.105218	EST
123188	AA489092	Hs.177726	ESTs
123276	AA491270	Hs.187946	ESTs
123305	AA496133		gb:zv51e12.s1 Soares_testis_NHT Homo sap
123328	AA496968		gb:aa42g03.s1 Soares_NhHMPu_S1 Homo sapi
123450	AA598913	Hs.111207	ESTs
123464	AA599014	Hs.153321	Homo sapiens cDNA FLJ10577 fis, clone NT
123650	AA609332	Hs.180696	ESTs
123700	AA609606	Hs.191956	ESTs
123858	AA620821	Hs.112911	EST
123863	AA620873	Hs.112916	ESTs
124046	F10243		gb:HSC3CC122 normalized infant brain cDN
124059	F13673	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
124196	H52617	Hs.144167	ESTs
124197	H52921		gb:yq76c09.s1 Soares fetal liver spleen
124229	H62793	Hs.268945	ESTs
124230	H63111	Hs.6655	Homo sapiens EST from clone 208499, full
124241	H65947	Hs.165355	ESTs, Moderately similar to ZN91_HUMAN Z
124251	H68286	Hs.107924	ESTs
124400	N30597	Hs.179152	toll-like receptor 7
124416	N34042	Hs.271674	ESTs
124570	N67117	Hs.102808	ESTs
124575	N68168		gb:za11c01.s1 Soares fetal liver spleen
124588	N69197	Hs.191361	ESTs, Weakly similar to I38022 hypotheti
124598	N70294	Hs.269137	ESTs, Weakly similar to A56194 thromboxa
124655	N93176	Hs.102914	ESTs
124706	R07499	Hs.193612	ESTs, Weakly similar to ALU8_HUMAN ALU
124848	R60135	Hs.203498	EST
124882	R74041	Hs.101539	ESTs
124898	R82846	Hs.273789	ESTs
125086	T91161	Hs.173880	interleukin 1 receptor accessory protein
125145	W38001		
125216	W73409	Hs.103185	ESTs
125342	AI055916	Hs.133552	ESTs
125351	T96520	Hs.324746	alpha-2-HS-glycoprotein
125419	AI076822	Hs.134544	ESTs
125424	T99667	Hs.18564	ESTs
125526	R14487	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f
125539	R17870	Hs.248120	G protein-coupled receptor 21
125633	AA908225	Hs.15463	Homo sapiens, clone IMAGE:2959994, mRNA
125689	R48940	Hs.108043	Friend leukemia virus integration 1
125707	C14616	Hs.284122	Wnt inhibitory factor-1
125790	AA868325	Hs.99962	proteoglycan 2, bone marrow (natural kil
125876	AA324967	Hs.7298	biphenyl hydrolase-like (serine hydrolas
125969	R94247	Hs.88414	BTB and CNC homology 1, basic leucine zi
125970	AI400964	Hs.177516	high density lipoprotein binding protein
125975	AA495891	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv
125985	H54857	Hs.35981	ESTs
126018	H54866	Hs.167583	ESTs
126032	H59735	Hs.269065	ESTs, Highly similar to KIAA0349 [H.sapi
126059	H66582	Hs.308486	ESTs
126107	H79155	Hs.93361	ESTs
126154	AI004105	Hs.190488	Homo sapiens, Similar to nuclear localiz
126199	AI000492	Hs.125829	ESTs
126207	W77936	Hs.83583	actin related protein 2/3 complex, subun
126227	N27236	Hs.269034	ESTs
126269	AA830432	Hs.44701	ESTs
126373	F11606	Hs.6079	B cell RAG associated protein
126378	AA347842		gb:yy62a11.s1 Soares_multiple_sclerosis_
126383	AA885594	Hs.6298	KIAA1151 protein
126403	N73388	Hs.125976	ESTs, Weakly similar to S71949 metallopr
126525	AA884833	Hs.166432	ESTs
126527	AA548559	Hs.103853	hypothetical protein FLJ20043
126566	W67245	Hs.103142	ESTs
126583	W92895	Hs.279746	vanilloid receptor-like protein 1
126610	AA460338	Hs.191391	ESTs
126622	AA699443	Hs.193213	ESTs
126633	AA206993	Hs.315367	Homo sapiens, Similar to hypothetical pr
126727	AA037230	Hs.135084	cystatin C (amyloid angiopathy and cereb
126762	AA064671		gb:zm13b04.s1 Stratagene pancreas (93720
126775	S86382	Hs.957	putative opioid receptor, neuromedin K (
126783	AA126047		gb:zn09d10.s1 Stratagene hNT neuron (937
126882	AA761143	Hs.250581	SWI/SNF related, matrix associated, acti
126945	R51877	Hs.25845	ESTs
126968	AI311457	Hs.99472	ESTs

127070	AA641812	Hs.190037	ESTs
127087	AA380418	Hs.88012	SHP2 interacting transmembrane adaptor
127187	AA297138	Hs.207422	ESTs, Weakly similar to S71949 metallopr
127215	AI246377	Hs.127675	ceroid-lipofuscinosis, neuronal 8 (epile
127229	AA316181	Hs.61635	six transmembrane epithelial antigen of
127278	AA342715		gb:EST48309 Fetal spleen Homo sapiens cD
127299	AA360710	Hs.158480	ESTs
127325	AA393073	Hs.126099	ESTs
127347	AA428350	Hs.58389	hypothetical protein MGC4090
127401	AA921944	Hs.127639	ESTs
127420	AA699582	Hs.82171	Homo sapiens clone 191B7 placenta expres
127438	AI224421	Hs.77100	general transcription factor IIE, polype
127441	AA835684	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH
127449	AI421866	Hs.75722	ribophorin II
127493	AA808081	Hs.291701	ESTs
127505	AA594244	Hs.292245	ESTs, Weakly similar to ALU1_HUMAN ALU S
127620	AI025699	Hs.116200	ESTs
127623	AA773234	Hs.271877	angiopoietin-like 2
127633	AI339609	Hs.268538	potassium voltage-gated channel, isk-rel
127701	AA935466		gb:zf84c06.s1 Soares_pineal_gland_N3HPG
127713	AA638322	Hs.150683	ESTs
127722	AA700444	Hs.189186	ESTs, Weakly similar to ALUD_HUMAN !!!!
127733	AA704680	Hs.189005	ESTs
127816	AA743646	Hs.120604	ESTs, Weakly similar to YA02_HUMAN HYPOT
127966	AI493406	Hs.292514	ESTs
127973	AI336794	Hs.129117	ESTs
127989	AA909267	Hs.132413	ESTs
127997	AI281549	Hs.311054	Homo sapiens mRNA full length insert cDN
128016	N92597	Hs.82689	tumor rejection antigen (gp96) 1
128037	AA868394	Hs.181129	ESTs, Weakly similar to S18968 cyritesti
128053	T65605	Hs.65377	ESTs, Moderately similar to KIAA1399 pro
128066	AA884838	Hs.189171	ESTs
128071	AA889398	Hs.189241	ESTs
128091	AA904559	Hs.129329	ESTs
128113	AI341423	Hs.288433	neurotrimin
128145	AI498467	Hs.166669	solute carrier family 4, sodium bicarbon
128167	AA932961	Hs.85752	uncharacterized hematopoietic stem/proge
128195	AI143866	Hs.127778	ESTs
128265	T95851	Hs.17691	ESTs
128283	AI076570	Hs.134053	ESTs
128309	AI457235	Hs.166479	ESTs
128313	AI051250	Hs.157775	ESTs
128346	AI088907	Hs.160189	ESTs
128359	AI096526	Hs.270244	ESTs, Weakly similar to I38022 hypotheti
128369	F12681	Hs.30445	Homo sapiens cDNA FLJ14687 fis, clone NT
128371	H12876	Hs.283078	hOAT4
128421	T77876	Hs.268589	ESTs
128453	X02761	Hs.287820	fibronectin 1
128496	T83496	Hs.32944	inositol polyphosphate-4-phosphatase, ty
128514	H84261	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA,
128551	H09058	Hs.278398	KIAA1117 protein
128683	AA316862	Hs.9605	cleavage and polyadenylation specific fa
128731	AF005271	Hs.104555	neuropeptide FF-amide peptide precursor
128843	AA234141	Hs.275675	katanin p80 (WD40-containing) subunit B
128988	AA411040	Hs.294140	ESTs
129016	W84524	Hs.184194	transmembrane 4 superfamily member 5
129021	AA426406	Hs.173081	KIAA0530 protein
129095	L12350	Hs.108623	thrombospondin 2
129171	AA234048	Hs.7753	calumenin
129188	M30257	Hs.109225	vascular cell adhesion molecule 1
129410	U25987	Hs.272620	pregnancy specific beta-1-glycoprotein 9
129467	AA410311	Hs.44208	hypothetical protein FLJ23153
129518	AA369807	Hs.112238	ESTs
129534	R73640	Hs.11260	hypothetical protein FLJ11264
129632	L27213	Hs.1176	solute carrier family 4, anion exchanger
129691	X06700	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl
129881	AA458952	Hs.181406	hypothetical protein FLJ22301
129990	N30316		gb:yw75b05.s1 Soares_placenta_8to9weeks_
130049	V01515	Hs.1460	glucagon
130171	AA454177	Hs.245257	ESTs, Weakly similar to A46010 X-linked
130411	AA505009	Hs.169910	KIAA0173 gene product
130479	R44163	Hs.12457	hypothetical protein FLJ10814
130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
130521	U92971	Hs.194351	coagulation factor II (thrombin) recepto
130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITA
130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)
130656	Z20481	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro
130889	D57622	Hs.20985	sin3-associated polypeptide, 30kD
131064	AA598441	Hs.22583	DKFZP434K2235 protein
131070	F13694	Hs.22607	ESTs
131189	L16782	Hs.240	M-phase phosphoprotein 1
131318	X51699	Hs.2558	bone gamma-carboxyglutamate (gla) protei
131506	W47579	Hs.5801	KIAA1194 protein

131551	AA127867	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H
131563	C20547	Hs.302810	Novel human gene mapping to chomosome 20
131830	U33054	Hs.32959	G protein-coupled receptor kinase 2 (Dro
131879	AA017161	Hs.33792	ESTs
132017	W67251	Hs.267659	vav 3 oncogene
132025	U58516	Hs.3745	milk fat globule-EGF factor 8 protein
132096	AA131410	Hs.3964	Homo sapiens clone 24877 mRNA sequence
132159	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi
132164	U84573	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
132180	AA405569	Hs.418	fibroblast activation protein, alpha
132223	R77451	Hs.4245	chromosome 11 hypothetical protein ORF3
132238	AA453446	Hs.42673	ESTs
132406	F09979	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f
132945	N40559	Hs.6129	ATP-binding cassette, sub-family B (MDR/
133185	AA481404	Hs.6686	hypothetical protein DKFZp564O1564
133193	C14015	Hs.303075	EST
133370	AA156897	Hs.72157	DKFZP564I1922 protein
133406	U22172	Hs.179697	Human DNA damage repair and recombinatio
133409	U65918	Hs.73078	deleted in azoospermia-like
133591	T82292	Hs.75111	protease, serine, 11 (IGF binding)
133899	X00588	Hs.77432	epidermal growth factor receptor (avian
134137	F10045	Hs.79347	KIAA0211 gene product
134339	AA478971	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
134421	AA122386	Hs.82985	collagen, type V, alpha 2
134462	U11037	Hs.181300	sel-1 (suppressor of lin-12, C.elegans)-
134515	C20737	Hs.84469	ESTs
134527	T40835	Hs.322978	EST
134711	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro
134824	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor
134854	J03464	Hs.179573	collagen, type I, alpha 2
134921	W60186	Hs.125511	Homo sapiens mRNA; cDNA DKFZp434P1530 (f
135003	H42527	Hs.26102	trichorhinophalangeal syndrome I
135210	W90522	Hs.93589	hypothetical protein DKFZp564B1162
135348	AA442054	Hs.268177	phospholipase C, gamma 1 (formerly subty
100547	HG2149-HT2219		gb:Homo sapiens mucin (mucin) mRNA, part
100572	HG2271-HT2367	Hs.73995	filaggrin
100687	HG3115-HT3291		gb:Human Golli-mbp gene, exon 2.
100695	HG315-HT315	Hs.272620	pregnancy specific beta-1-glycoprotein 9
101447	M21305		gb:Human alpha satellite and satellite 3
102329	U35407	Hs.158084	peroxisome receptor 1
102892	X05232	Hs.83326	matrix metalloproteinase 3 (stromelysin
103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial
103206	X72755	Hs.77367	monokine induced by gamma interferon
103260	X78416	Hs.3155	casein, alpha
103751	AA082824		gb:zo08b08.s1 Stratagene neuroepithelium
104113	AA427510	Hs.181202	hypothetical protein FLJ10038
104316	D61871	Hs.330821	EST
104453	M19169	Hs.123114	cystatin SN
104668	AA007312		gb:EST376458 MAGE resequences, MAGH Homo
104916	AA056588	Hs.155489	NS1-associated protein 1
106151	AA424958	Hs.294132	ESTs
106899	AA490107	Hs.21753	JM5 protein
107379	U93868	Hs.333861	polymerase (RNA) III (DNA directed) (32k
107412	W26105	Hs.287797	integrin, beta 1 (fibronectin receptor,
107652	AA010195	Hs.52642	ESTs, Weakly similar to ALUF_HUMAN !!!!
107754	AA017462	Hs.269244	ESTs
107897	AA026240		gb:no77a05.s1 NCI_CGAP_AA1 Homo sapiens
108238	AA059473	Hs.66783	EST
108497	AA083070		gb:zm85a05.r1 Stratagene ovarian cancer
108710	AA121960		gb:zm24g09.r1 Stratagene pancreas (93720
109012	AA156576	Hs.5947	mel transforming oncogene (derived from
109043	AA159605	Hs.72580	ESTs
109560	F01778	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H
110572	H60523	Hs.37844	EST
110687	H93005	Hs.177311	ESTs
111418	R01084	Hs.19081	ESTs
111507	R07728	Hs.268668	ESTs
111644	R16539	Hs.223649	EST, Moderately similar to Cd-7 Metallo
111919	R39926	Hs.21031	ESTs, Weakly similar to I78885 serine/th
112102	R44840	Hs.326475	ESTs
112229	R50938	Hs.24949	ESTs
112309	R55021		gb:yj76d05.s1 Soares breast 2NbHBst Homo
112368	R59371	Hs.26653	ESTs
112397	R60822	Hs.26805	ESTs, Weakly similar to putative p150 [
112532	R69824	Hs.28313	ESTs
112858	T02963	Hs.4454	ESTs
113170	T54342	Hs.270373	ESTs, Weakly similar to S65657 alpha-1C
113321	T70580	Hs.13759	RAB3A interacting protein (rabin3)-like
113404	T82323	Hs.70337	immunoglobulin superfamily, member 4
113420	T83964	Hs.15400	ESTs, Weakly similar to S65824 reverse
113613	T93337	Hs.17167	ESTs, Highly similar to LRR FLI-I intera
113663	T95909		gb:ye47g07.s1 Soares fetal liver spleen
113790	W33178	Hs.26912	ESTs

113889	W72720		gb:zd61c03.s1 Soares_fetal_heart_NbHH19W
114016	W90671	Hs.11087	ESTs
114251	Z39898	Hs.21948	ESTs
115187	AA261805	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,
115722	AA417297	Hs.59609	ESTs
115775	AA424030	Hs.46627	ESTs
116380	AA598455	Hs.66817	ESTs
116551	D20458	Hs.229071	EST
117009	H85422	Hs.108556	ESTs
117329	N23680	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone H
117523	N32626	Hs.145532	ESTs, Weakly similar to FV1 MOUSE FRIEND
118387	N64579		gb:yz51d11.s1 Morton Fetal Cochlea Homo
118456	N66580		gb:yy69f01.s1 Soares_multiple_sclerosis_
118741	N74042	Hs.50421	KIAA0203 gene product
118771	N74690	Hs.50547	ESTs
119075	R36451	Hs.287820	fibronectin 1
119217	R95778	Hs.237309	EST
119306	T26914	Hs.132785	EAP30 subunit of ELL complex
119347	T64349		gb:yc10d08.s1 Stratagene lung (937210) H
120006	W90108	Hs.10848	KIAA0187 gene product
120441	AA243588	Hs.190035	ESTs
120651	AA287286	Hs.99657	ESTs
120811	AA346854	Hs.52788	fragile X mental retardation, autosomal
121186	AA400156	Hs.339808	hypothetical protein FLJ10120
121599	AA416770	Hs.98255	EST
122146	AA435584	Hs.250173	hypothetical protein FLJ13158
122261	AA436830	Hs.98902	ESTs
122352	AA443725	Hs.159677	ESTs
122433	AA447417	Hs.285491	ESTs
122489	AA448342	Hs.178551	ribosomal protein L8
122554	AA451886	Hs.154654	cytochrome P450, subfamily I (dioxin-ind
122857	AA463879	Hs.99606	EST, Weakly similar to STK2_HUMAN SERIN
122889	AA465704	Hs.287687	Homo sapiens cDNA: FLJ21960 fis, clone H
123399	AA521274	Hs.105516	EST
123662	AA609385	Hs.112703	ESTs, Moderately similar to AF171102 1 r
123762	AA610013		gb:af18d04.s1 Soares_testis_NHT Homo sap
123792	AA620333	Hs.112857	ESTs
123900	AA621223	Hs.112953	EST
123981	C20797	Hs.95481	ESTs
124126	H18517	Hs.164568	fibroblast growth factor 7 (keratinocyte
124404	N31998	Hs.164256	hypothetical protein FLJ20657
124557	N66025	Hs.141604	ESTs, Moderately similar to ALU1_HUMAN A
124703	R07294	Hs.300076	solute carrier family 22 (organic cation
124867	R68971	Hs.168500	ESTs
125092	T92544	Hs.137548	CD84 antigen (leukocyte antigen)
125111	T96240	Hs.178658	RAD23 (S. cerevisiae) homolog B
125331	AI422996	Hs.161378	ESTs
125349	T87826	Hs.164480	ESTs, Weakly similar to T50609 hypotheti
125426	R43963	Hs.184029	hypothetical protein DKFZp761A052
125436	R64472	Hs.16131	hypothetical protein FLJ12876
125465	AI375276	Hs.158732	ESTs
125515	R13353		gb:yf76c04.r1 Soares infant brain 1NIB H
125626	AI038854	Hs.180789	S164 protein
125656	AA040118	Hs.78687	neutral sphingomyelinase (N-SMase) activ
125743	H17151		gb:ym37a05.r1 Soares infant brain 1NIB H
125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass
125760	W03020	Hs.40300	calpain 3, (p94)
125804	R79519	Hs.16899	ESTs
125967	AI341206	Hs.173770	ESTs
126068	AI190171	Hs.144413	ESTs
126081	AI346024	Hs.227835	KIAA1049 protein
126150	AA018427	Hs.64616	chromosome 12 open reading frame 3
126171	AA704771	Hs.191942	ESTs
126198	AI469355	Hs.127310	ESTs
126224	AI097280	Hs.44493	Human DNA sequence from clone 462O23 on
126289	AA194603	Hs.73451	ESTs, Weakly similar to S55024 nebulin,
126343	AA628890	Hs.158701	ESTs
126406	AA034096		gb:yv41h02.r1 Soares fetal liver spleen
126419	AA451775	Hs.129064	Homo sapiens chromosome 19, cosmid F2216
126479	T78141	Hs.12285	ESTs, Weakly similar to I55214 salivary
126500	AA885306	Hs.184376	synaptosomal-associated protein, 23kD
126520	AA292988	Hs.72071	hypothetical protein FLJ20038
126701	AA515212	Hs.339670	ESTs, Weakly similar to AF147790 1 trans
126718	AA322718	Hs.309435	ESTs, Weakly similar to KIAA0927 protein
126739	AI160709	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE
126745	AA057506		gb:zf49g04.r1 Soares retina N2b4HR Homo
126846	AA663527	Hs.116910	ESTs
126872	AA136653		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
126952	AA195575	Hs.85962	hyaluronan synthase 3
127036	AI468598	Hs.276916	nuclear receptor subfamily 1, group D, m
127039	AA233366	Hs.168103	prp28, U5 snRNP 100 kd protein
127067	F06732		gb:HSC1JA051 normalized infant brain cDN
127083	Z44079	Hs.91608	otoferlin

127116	AA278492	Hs.288304	Homo sapiens cDNA FLJ11529 fis, clone HE
127282	AA347547	Hs.185780	ESTs
127349	AA412108	Hs.269350	ESTs
127352	AA416577	Hs.189105	ESTs, Weakly similar to NBR13 [H.sapiens
127482	AI337294	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I
127543	AI364367	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO
127553	AA282433		gb:aa63g02.r1 NCI_CGAP_GCB1 Homo sapiens
127556	AA679831	Hs.190228	ESTs
127859	AA806837	Hs.291559	ESTs
127993	AA847856	Hs.124565	ESTs
128277	AI018275	Hs.269791	ESTs
128285	AA634569	Hs.13351	LanC (bacterial lantibiotic synthetase c
128317	AI051960	Hs.303754	ESTs
128334	AI080130	Hs.134207	ESTs
128428	AI185718	Hs.143900	ESTs
128582	U22963	Hs.101840	major histocompatibility complex, class
128592	AA470056	Hs.113994	Homo sapiens cDNA FLJ20796 fis, clone CO
128751	AA442274	Hs.183176	ESTs
129105	AA224351	Hs.108681	Homo sapiens brain tumor associated prot
129161	N27334	Hs.181780	hypothetical protein FLJ20241
129246	N99174	Hs.206063	ESTs
129361	X64229	Hs.110713	DEK oncogene (DNA binding)
129577	AA424952	Hs.82906	CDC20 (cell division cycle 20, S. cerevi
129600	N78980	Hs.271599	hypothetical protein MGC10500
129989	AF005887	Hs.247433	activating transcription factor 6
130024	U15197	Hs.113271	ABO blood group (transferase A, alpha 1-
130292	U70136	Hs.218791	proteoglycan 4, (megakaryocyte stimulati
130589	AA234308	Hs.16441	DKFZP434H204 protein
130736	T99385		gb:ow89g07.s1 Soares_fetal_liver_spleen_
131238	R82327	Hs.24625	ESTs
131378	AA463886	Hs.203910	small glutamine-rich tetratricopeptide r
131601	M31165	Hs.29352	tumor necrosis factor, alpha-induced pro
131605	AA256220	Hs.29383	Homo sapiens mRNA; cDNA DKFZp434E2321 (f
131676	C20785	Hs.30514	ESTs
131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea
131873	H39997	Hs.166852	KIAA1683 protein
132023	F01927	Hs.3743	matrix metalloproteinase 24 (membrane-in
132273	AA489716	Hs.43658	DKFZP586L151 protein
132770	AA425647	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL
132859	D20925	Hs.69235	transportin-SR
133052	R40166	Hs.106826	KIAA1695 protein
133373	S72487	Hs.73946	endothelial cell growth factor 1 (platel
133446	M25322	Hs.73800	selectin P (granule membrane protein 140
134693	N70361	Hs.8854	Human transcription unit PVT gene, exons
134733	U03644	Hs.89421	CBF1 interacting corepressor
134965	J05480	Hs.272458	protein phosphatase 3 (formerly 2B), cat
135327	AA477989	Hs.98800	ESTs
135377	C21382	Hs.99766	Homo sapiens mRNA; cDNA DKFZp564J0323 (f
135398	AA194075	Hs.287270	ret proto-oncogene (multiple endocrine

TABLE 44B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108497	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
107897	91776_1	AA604872 AA026240
130736	611414_1	AI168326 T99385
108710	133560_1	AA121959 AA121960
100943	45976_1	AW864944 L07517 AW869606
124575	1666649_1	N68168 N69188 N90450
125439	465590_1	AW835829 AA826305 R01759
117697	499877_1	N40976 AA902795
125515	181_2	R13353 R13890 H11359
118387	65081_-5	N64579
126292	327512_1	AA491328 N42312
102798	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
126378	244444_1	N58924 AA347842
125743	5025_5	H17151 H11956
126406	95703_1	N76683 AA034096 AA034082

	127067	1534978_1	F06732 Z43705
	119243	1774795_1	T12603 T12604
	111443	31528_18	AF072503 AF208161 AA613238 H12439 N76991 D78692 BE019603 AA776439 R37932 T93615 AF072508 R00744 R01948 R68685 AI128496 AA865193 AI797629 H13302 AF072506 NM_014590 AF072505 R00743 T93661 T39519 R68740 H13097 N58614 N77302 H01372 N41878 H04136 AA426511 AW971553 AW900030 R76136 T52094 AI598135 AA781423 R76086 R77278 AI393478 AA837267 AI570707 R01901 R27412 N53177 AI379210 AI128526 AA250958 R79323 R27389 H01325 N55091 T69704 AA868777 T47345 R27591 AA860368 AA729556 H04137 T87297 C17420 AA293243 AA419144
	127278	240640_1	AA342715 AA367634
	103751	118557_1	AA131367 AA082824
	126636	80804_1	AA057531 AA001527
	127331	379388_1	F20186 AA622352
	127357	288073_1	AA424107 AA452788
	126745	104479_1	AA047854 AA057506 AA053841
	126762	110350_1	AA064613 AA064671
	126783	113388_1	AA083531 AA126047 AA074915 AA148649
	112309	1576900_1	R55021 H26613
	126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE158945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
	120284	158963_1	AA179656 AA182626 AA182603
	111829	46636_1	AF074991 R36070
	104668	82752_1	AW964385 AA007312 AI081711 AA318253 AW891655 T99192
	127553	202308_2	AA505046 AW969109 AA505047
	120379	34624_3	AL042725 BE063316 AW975610 AA457591 BE062092 AI655202 AA714296 AI267264 AI075321 AA223286 AA071122 AA227849 AA216700 AI696002 AA101867 AA099426 AA135997 AL041698 T02815 T51824 AA207189 T59230 T51868 AA663341 BE165757 AW818104 AW392686 AA584918 AA099408 AW856396 AW861859 AA053045
	127701	405284_1	AA679064 AA935466
	128410	288073_1	AA424107 AA452788
	114625	111686_1	AA081507 AA070071 AA070840 AA084362
	109026	150431_1	AA157811 AA836869
	108409	113869_1	AA075631 AA075578
	100687	tigr_HT3291	L18862
	109326	genbank_AA210719	AA210719
	123762	genbank_AA610013	AA610013
	116548	genbank_D20433	D20433
	125145	entrez_W38001	W38001
	125153	entrez_W38294	W38294
	116995	genbank_H83928	H83928
	102649	genbank_U68133	U68133
	118456	genbank_N66580	N66580
	102860	entrez_X00368	X00368
	120715	genbank_AA292700	AA292700
	120749	genbank_AA303235	AA303235
	113663	genbank_T95909	T95909
	113889	genbank_W72720	W72720
	108258	genbank_AA063269	AA063269
	101046	entrez_K01160	K01160
	129990	genbank_N30316	N30316
	122746	genbank_AA458791	AA458791
	124046	genbank_F10243	F10243
	108436	genbank_AA078801	AA078801
	124197	genbank_H52921	H52921
	101447	entrez_M21305	M21305
	108852	genbank_AA133131	AA133131
	101697	entrez_M64358	M64358
	108931	genbank_AA147186	AA147186
	101909	entrez_S69265	S69265
	117816	genbank_N48872	N48872
	119154	genbank_R61293	R61293
	119241	genbank_T12559	T12559
	119310	genbank_T40427	T40427
	119347	genbank_T64349	T64349
	119529	entrez_W38053	W38053
	112467	genbank_R65706	R65706
	112533	genbank_R69886	R69886
	112588	genbank_R77302	R77302
	121082	genbank_AA398722	AA398722
	123305	genbank_AA496133	AA496133
	123328	genbank_AA496968	AA496968
	100547	tigr_HT2219	M57417
	123490	genbank_AA599723	AA599723

TABLE 45A: 90 GENES DOWN-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 45A lists about 90 genes down-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	ExAccn	UnigeneID	Unigene Title
100137	D13627	Hs.15071	chaperonin containing TCP1, subunit 8 (t
100240	D31767	Hs.75416	DAZ associated protein 2
100289	D45248	Hs.179774	proteasome (prosome, macropain) activato
100658	HG2855-HT2995	Hs.75452	heat shock 70kD protein 2
100763	HG3597-HT3800		gb:Human major histocompatibility comple
100779	HG3731-HT4001	Hs.302063	immunoglobulin heavy constant mu
101091	L06132	Hs.149155	voltage-dependent anion channel 1
101155	L13972	Hs.301698	sialyltransferase 4A (beta-galactosidase
102223	U24685		gb:Homo sapiens immunoglobulin heavy cha
102282	U31383	Hs.79126	guanine nucleotide binding protein 10
102378	U40369	Hs.28491	spermidine/spermine N1-acetyltransferase
102386	U40998	Hs.81728	unc119 (C.elegans) homolog
102389	U41371	Hs.75916	splicing factor 3b, subunit 2, 145kD
102480	U50327	Hs.1432	protein kinase C substrate 80K-H
102566	U59752	Hs.303091	pleckstrin homology, Sec7 and coiled/coi
102605	U64444	Hs.181369	ubiquitin fusion degradation 1-like
102693	U73824	Hs.183684	eukaryotic translation initiation factor
102710	U77827	Hs.113207	G protein-coupled receptor 30
102920	X12451	Hs.78056	cathepsin L
102929	X13238	Hs.74649	cytochrome c oxidase subunit VIc
103166	X67951	Hs.180909	peroxiredoxin 1
103283	X80199	Hs.83422	MLN51 protein
103463	Y00281	Hs.2280	ribophorin I
103835	AA172215	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT
104796	AA029368	Hs.33026	hypothetical protein PP2447
105714	AA291429	Hs.12211	GDP-fucose transporter 1
105927	AA402968	Hs.332040	hypothetical protein MGC13010
105945	AA404512	Hs.14453	interferon consensus sequence binding pr
106001	AA410986	Hs.8963	Homo sapiens mRNA full length insert cDN
106027	AA412119	Hs.234799	breakpoint cluster region
106227	AA429262	Hs.19613	ESTs
106295	AA435664	Hs.8583	similar to APOBEC1
106417	AA448008	Hs.261828	G protein-coupled receptor kinase 7
107391	W02877	Hs.284294	Breakpoint cluster region protein, uteri
109107	AA169180	Hs.269280	ESTs
109685	F09325	Hs.28102	ESTs
110021	H11252	Hs.31037	ESTs
110738	H99370	Hs.139648	kinesin family member 1C
112746	R93237	Hs.74170	metallothionein 1E (functional)
113059	T26925	Hs.172684	vesicle-associated membrane protein 8 (e
113822	W47350	Hs.17466	retinoic acid receptor responder (tazaro
113859	W67225	Hs.13273	KIAA0592 protein
113909	W78127	Hs.9956	hypothetical protein FLJ20259
114693	AA122158	Hs.300683	Homo sapiens cDNA FLJ12825 fis, clone NT
115399	AA283182	Hs.92023	core histone macroH2A2.2
116606	D80217	Hs.259842	protein kinase, AMP-activated, gamma 2 n
116633	F02702	Hs.268726	ESTs, Highly similar to ZN91_HUMAN ZINC
119254	T15837	Hs.279009	matrix Gla protein
119493	W35384	Hs.50477	RAB27A, member RAS oncogene family
120108	W95696	Hs.16803	LUC7 (S. cerevisiae)-like
120886	AA365566	Hs.301342	hypothetical protein MGC4342
120953	AA397911	Hs.97499	ESTs, Weakly similar to unknown [H.sapie
121303	AA402441	Hs.303197	B-cell CLL/lymphoma 7C
121547	AA412448	Hs.104777	ESTs
123495	AA599650	Hs.106747	serine carboxypeptidase 1 precursor prot
123608	AA609144	Hs.112651	ESTs
123749	AA609949	Hs.112790	EST
124763	R39610	Hs.76288	calpain 2, (m/II) large subunit
125366	H60192	Hs.76853	Homo sapiens mRNA; cDNA DKFZp434N1728 (f
125657	AA481719	Hs.150540	Homo sapiens, clone IMAGE:3954961, mRNA,
125670	AI432621	Hs.82685	CD47 antigen (Rh-related antigen, integr
125882	H45538	Hs.101448	metastasis associated 1
126541	AA204913	Hs.7854	zinc/iron regulated transporter-like
126715	R70160	Hs.241552	KIAA0268 protein
126817	AA478642	Hs.291623	ESTs, Weakly similar to unnamed protein
127112	AI143906	Hs.125103	ESTs
127273	AA335263	Hs.144950	ESTs
127615	AA718919		gb:zv88a04.s1 Soares_NhHMPu_S1 Homo sapi
127635	AA766903	Hs.116346	ESTs, Highly similar to A46297 beta-1,6-
128528	R39234	Hs.251699	ESTs, Weakly similar to IDN4-GGTR14 [H.s
129398	AA437374	Hs.234573	Homo sapiens mRNA for TL132
129621	AA489459	Hs.301005	purine-rich element binding protein B
131037	AA256171	Hs.22391	chromosome 20open reading frame 3
131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
131631	AA486868	Hs.29802	slit (Drosophila) homolog 2
132079	H67964	Hs.38694	ESTs
132455	T15774	Hs.4892	Homo sapiens clone 24841 mRNA sequence
132582	AA318547	Hs.278712	eukaryotic translation initiation factor
132610	AA443114	Hs.5326	amino acid system N transporter 2; porcu
132755	AA609201	Hs.182635	ESTs
133192	AA393804	Hs.67052	vacuolar protein sorting 26 (yeast homol

133437	R57419	Hs.7370	phosphotidylinositol transfer protein, b
133449	AA094989	Hs.7381	voltage-dependent anion channel 3
133649	AA479139	Hs.75393	acid phosphatase 1, soluble
133814	M33882	Hs.76391	myxovirus (influenza) resistance 1, homo
134378	AF006088	Hs.82425	actin related protein 2/3 complex, subun
134419	L08044	Hs.82961	trefoil factor 3 (intestinal)
134548	U41515	Hs.333495	Deleted in split-hand/split-foot 1 regio
134776	J05582	Hs.89603	mucin 1, transmembrane
135032	AA243497	Hs.173685	hypothetical protein FLJ12619

TABLE 45B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
127615	380951_1	AA626215 AA718919
100763	tigr_HT3800	X12432 Y08693
102223	221_265	AF013616 AA300945 X65907 AF062264 AF062250 Z47228 Z75389 Z75374 AF062152 AF062146 Z75398 X64153 AF062101 AF062218 S59161 Z75392 AF062196 AF062192 X65904 U24685 AF062181 Z47241 Z75376 AF062217 Z47234 X64152 AF062187 AF062173 AF062158 Z47229 M74018 M74021 X54441 M84512 L29115 M84508 Z75384 AJ244983 AJ245240 AJ245030 AJ245042 M26998 L03635 S64473 AJ244997 AJ245013 AJ279535 U89766 AF174049 AF174085 AF174086 U97246 AJ245011 AJ245017 AJ245028 AJ245041 AJ245051 AJ245065 AJ245236 U22391 Z49143 Z74665 AF087428 S66098 Z70650 AJ244929 AF006528 AF022004 AF021983 U00556 AJ245035 Z70617 Z70605 AJ245052 AJ245046 AF087424 AF174054 S67110 U21257 U21267 U21268 Z35492 U71103 AF021991 L23518 Z70644 AJ245036 Z49141 AF089001 Z74695 Z46304 AF021957 AF021990 AF022005 AF052527 AF021947 Z70604 Z70610 AF062104 Z49135 X64235 Z46341 Z46305 Z46307 Z49136 AJ244996 Z46342 AJ244931 AJ244935 AJ244937 AJ244938 L12192 AJ244939 AJ244940 AJ244941 Z46308 AJ244962 AF062234 AJ244973 AJ244984 AJ244985 AF174088 AJ279519 AJ279521 AJ279526 AJ245009 AJ279531 AJ245008 AJ244994 AJ244991 AJ244990 AJ244988 AJ244987 X87440 AJ245238 Z70625 Z70626 Z70641 Z70640 Z70643 AJ244975 Z70616 Z70637 AJ244982 AJ244967 AJ239377 AJ245057 AF021948 AF107239 AJ245040 L34163 AF062231 Z70627 AF062113 AF006527 AF174041 AJ279537 Z70642 U00497 Z70639 AJ245054 AJ244960 AJ279524 AJ244943 AJ249631 AF035041 AJ245039 AJ245050 AF107233 AJ239362 AJ244969 Z46278 Z46290 Z46274 Z46281 AJ239351 L25293 AJ244944 AJ244951 Z46280 Z46270 AJ245043 Z46276 AF107241 Z46271 Z46277 AJ245034 Z46273 AJ244992 Z46282 Z70638 Z46275 AJ244972 Z46272 Z46279 Z46269 AF087422 M74469 X64159 AF103243 X64156 AJ244942 Z46316 AJ222547 Z46322 Z46324 Z46326 Z46327 AJ222556 Z46329 Z46330 Z46302 AJ222561 AJ222549 AJ222568 AJ222570 AJ222571 Z49139 AJ222578 AJ222562 AJ222577 Z46323 AJ222576 AJ222566 Z46315 AJ222557 AJ222564 AJ222559 AJ222573 AJ222575 Z46318 AJ222548 Z46319 AJ222552 AJ222550 AJ222567 AJ222558 AJ222563 Z46317 X87438 AJ222555 AJ240581 AF103161 AJ240580 AJ240594 Y17929 AJ240553 AJ240573 AJ240558 AJ240555 Y17927 Y17949 AJ240561 Y17948 Y17933 Y17947 Y17944 Y17928 Y17931 Y17934 AJ240595 Y17943 Y17932 Y17930 AJ240590 AJ240560 Y17945 AJ240556 S79918 AF103278 AW364256 AF103299 AF103122 X75022 AF004937 Z30557 Z30677 Z30573 Z30576 Z30561 Z30674 Z30562 Z30675 AW403129 AI203192 AW404253 AW237246 AI654630 H61354

Table 46A lists about 714 genes upregulated in esophageal cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 47A lists about 113 genes upregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 48A lists about 162 genes downregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

TABLE 46A:

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of esophageal tumor AIs divided by the 70th percentile of normal tissue AIs, where the 15th percentile of the normal tissue AIs was subtracted from both the numerator and denominator.

Pkey	ExAccn	UnigeneID	Unigene Title	R1
413608	J00267		Homo sapiens mRNA for caldesmon, 3' UTR	31.57
411243	AB039886	Hs.69319	CA11	26.06
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	25.65
401761			Target Exon	23.23
424098	AF077374	Hs.139322	small proline-rich protein 3	21.35
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	20.37
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	20.33
401780			NM_005557*:Homo sapiens keratin 16 (foca	18.94
421948	L42583	Hs.334309	keratin 6A	18.13
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	18.01
429538	BE182592	Hs.11261	small proline-rich protein 2A	17.31
400666			NM_002425:Homo sapiens matrix metallopro	17.28
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	16.96

	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	16.35
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	16.22
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	15.64
	421582	AI910275		trefoil factor 1 (breast cancer, estroge	14.86
5	425679	X05997	Hs.159177	lipase, gastric	14.53
	421773	W69233	Hs.112457	ESTs	14.26
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	14.26
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	13.93
	444325	AW152618	Hs.16757	ESTs	13.24
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	13.19
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	11.98
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.99
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	10.77
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	10.31
15	446292	AF081497	Hs.279682	Rh type C glycoprotein	9.69
	421978	AJ243662	Hs.110196	NICE-1 protein	9.68
	448811	AI590371	Hs.199460	ESTs	9.38
	453331	AI240665		ESTs	9.37
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	9.28
20	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	9.18
	406687	M31126		matrix metalloproteinase 11 (stromelysin	9.13
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	9.04
	450701	H39960	Hs.288467	hypothetical protein XP_098151	8.77
	418686	Z36830	Hs.87268	annexin A8	8.76
25	421110	AJ250717	Hs.1355	cathepsin E	8.42
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.42
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.38
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	8.18
	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	8.11
30	450375	AA009647		a disintegrin and metalloproteinase doma	8.03
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	7.97
	445891	AW391342	Hs.199460	DPCR1 protein	7.95
	437053	AU077018	Hs.3235	keratin 4	7.93
	423271	W47225	Hs.126256	interleukin 1, beta	7.80
35	409757	NM_001898	Hs.123114	cystatin SN	7.74
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	7.64
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	7.55
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.26
40	448045	AJ297436	Hs.20166	prostate stem cell antigen	7.14
	408243	Y00787	Hs.624	interleukin 8	7.13
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	7.08
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	7.04
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	7.04
45	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.98
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	6.89
	414774	X02419	Hs.77274	plasminogen activator, urokinase	6.85
	439926	AW014875	Hs.137007	ESTs	6.84
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.82
50	429259	AA420450	Hs.292911	Plakophilin	6.77
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	6.71
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	6.67
	429228	AI553633	Hs.326447	ESTs	6.61
	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	6.60
55	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.58
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.55
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	6.54
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.53
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.51
60	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.49
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.48
	428471	X57348	Hs.184510	stratifin	6.46
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	6.45
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.44
65	401747			Homo sapiens keratin 17 (KRT17)	6.42
	421508	NM_004833	Hs.105115	absent in melanoma 2	6.42
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	6.42
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.41
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	6.38
70	422596	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	6.38
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	6.36
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	6.35
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	6.33
	425415	M13903	Hs.157091	involucrin	6.32
75	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	415989	AI267700		ESTs	6.23
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.21
	449228	AJ403107	Hs.148590	protein related with psoriasis	6.21
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	6.18
80	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	6.06
	418663	AK001100	Hs.41690	desmocollin 3	6.04
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.98
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	5.96

	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	5.93
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	5.92
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.92
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	5.84
5	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.76
	400665			NM_002425:Homo sapiens matrix metallopro	5.75
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.72
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	5.72
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.71
10	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	5.70
	439606	W79123	Hs.58561	G protein-coupled receptor 87	5.70
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	5.68
	433447	U29195	Hs.3281	neuronal pentraxin II	5.67
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.64
15	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	5.62
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	5.60
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.53
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.50
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	5.48
20	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	5.47
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	5.44
	439223	AW238299	Hs.250618	UL16 binding protein 2	5.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	5.42
	402994			NM_002463*:Homo sapiens myxovirus (influ	5.40
25	447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	5.40
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	5.36
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	5.33
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	5.32
	449722	BE280074	Hs.23960	cyclin B1	5.31
30	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.30
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	5.29
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	5.29
	417720	AA205625	Hs.208067	ESTs	5.29
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.28
35	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	5.27
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	5.26
	430280	AA361258	Hs.237668	interleukin 7 receptor	5.25
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	5.24
	402075			ENSP00000251056*:Plasma membrane calcium	5.24
40	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	5.24
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	5.22
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.22
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domai	5.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	5.20
45	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epider	5.20
	406663	U24683	Hs.293441	immunoglobulin heavy constant mu	5.19
	409178	BE393948	Hs.50915	kallikrein 5	5.15
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.14
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	5.10
50	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	5.09
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.09
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	5.08
	411274	NM_002776	Hs.69423	kallikrein 10	5.07
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	5.03
55	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	5.03
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	5.02
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	5.02
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.02
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	5.00
60	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	5.00
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.97
	405770			NM_002362:Homo sapiens melanoma antigen,	4.96
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.94
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.94
65	426866	U02330	Hs.172816	neuregulin 1	4.93
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	4.92
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	4.91
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.90
	427786	BE407863	Hs.256871	ESTs	4.87
70	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	4.86
	444371	BE540274	Hs.239	forkhead box M1	4.86
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	4.85
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.84
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	4.83
75	409402	AF208234	Hs.695	cystatin B (stefin B)	4.81
	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.79
	401994			Target Exon	4.77
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.74
	421574	AJ000152	Hs.105924	defensin, beta 2	4.69
80	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.69
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.68
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.68
	407944	R34008	Hs.239727	desmocollin 2	4.67

	411296	BE207307	Hs.10114	growth suppressor 1	4.65
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	4.65
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.61
	421335	X99977	Hs.103505	ARS component B	4.60
5	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.59
	453779	N35187	Hs.43388	28kD interferon responsive protein	4.59
	423575	C18863	Hs.163443	periostin (OSF-2os)	4.59
	417308	H60720	Hs.81892	KIAA0101 gene product	4.58
	428651	AF196478	Hs.188401	annexin A10	4.58
10	424354	NM_014314	Hs.145612	RNA helicase	4.58
	404996			Target Exon	4.56
	404240			NM_018950:Homo sapiens major histocompat	4.56
	453095	AW295660	Hs.252756	ESTs	4.55
	410407	X66839	Hs.63287	carbonic anhydrase IX	4.55
15	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	4.55
	450685	L15533	Hs.423	pancreatitis-associated protein	4.54
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	4.53
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.52
	408380	AF123050	Hs.44532	diubiquitin	4.47
20	443859	NM_013409	Hs.9914	follistatin	4.46
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	4.44
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	4.44
	421777	BE562088	Hs.108196	HSPC037 protein	4.44
	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.43
25	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	4.42
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	4.42
	400419	AF084545		Target	4.42
	452571	W31518	Hs.34665	ESTs	4.41
	430044	AA464510	Hs.152812	ESTs	4.41
30	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	4.39
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	4.39
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.39
	453884	AA355925	Hs.36232	KIAA0186 gene product	4.38
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	4.37
35	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	4.37
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.37
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	4.36
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	4.36
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.34
40	439999	AA115811	Hs.6838	ras homolog gene family, member E	4.34
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.34
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	4.32
	402447			C1000201:gi|204416|gb|AAA02627.1| (L0519	4.31
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	4.28
45	432731	R31178	Hs.287820	fibronectin 1	4.27
	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	4.27
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	4.25
	425580	L11144	Hs.1907	galanin	4.25
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	4.23
50	409433	AA074382	Hs.135255	ESTs	4.23
	430630	AW269920	Hs.2621	cystatin A (stefin A)	4.22
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	4.21
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	4.20
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	4.20
55	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.19
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.19
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	4.18
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	4.17
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	4.16
60	448844	AI581519	Hs.177164	ESTs	4.16
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	4.16
	417599	AA204688	Hs.62954	ESTs	4.16
	402992			Target Exon	4.15
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	4.14
65	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	4.13
	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.12
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.10
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	4.10
70	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.10
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.09
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	4.08
	417933	X02308	Hs.82962	thymidylate synthetase	4.08
	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	4.06
75	417678	X06560	Hs.82396	2',5'-oligoadenylate synthetase 1 (40-46	4.06
	451541	BE279383	Hs.26557	plakophilin 3	4.06
	433848	AF095719	Hs.93764	carboxypeptidase A4	4.06
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.04
	429599	AA806106	Hs.123664	ESTs	4.03
80	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	4.02
	423787	AJ295745	Hs.236204	nuclear pore complex protein	4.00
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	4.00
	416091	AF295370	Hs.283082	defensin, beta 3	3.97

	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.97
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.97
	402408			NM_030920*:Homo sapiens hypothetical pro	3.97
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.95
5	414907	X90725	Hs.77597	polo (Drosophia)-like kinase	3.95
	452888	AW955454	Hs.30942	ephrin-B2	3.95
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.95
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.94
	419693	AA133749	Hs.301350	FXYD domain-containing ion transport reg	3.94
10	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.94
	422094	AF129535	Hs.272027	F-box only protein 5	3.94
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	3.93
	404286			C6001909:gi|704441|dbj|BAA18909.1| (D298	3.93
	423961	D13666	Hs.136348	periostin (OSF-2os)	3.92
15	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	3.91
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	3.91
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	3.91
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	3.91
	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	3.90
20	441553	AA281219	Hs.121296	ESTs	3.90
	428093	AW594506	Hs.104830	ESTs	3.90
	441020	W79283	Hs.35962	ESTs	3.89
	447078	AW885727	Hs.9914	ESTs	3.89
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	3.89
25	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	3.87
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	3.87
	426059	BE292842	Hs.166120	interferon regulatory factor 7	3.86
	419833	AA251131	Hs.220697	ESTs	3.85
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	3.85
30	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.83
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.83
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	3.83
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	3.83
	442599	AF078037	Hs.324051	RelA-associated inhibitor	3.82
35	405387			NM_022170*:Homo sapiens Williams-Beuren	3.82
	449539	W80363	Hs.58446	ESTs	3.82
	419079	AW014836	Hs.18644	ESTs	3.81
	410434	AF051152	Hs.63668	toll-like receptor 2	3.81
	408660	AA525775		ESTs, Moderately similar to PC4259 fem	3.80
40	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.80
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.80
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.79
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	3.79
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.78
45	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.78
	414561	AI064813	Hs.195155	Homo sapiens amino acid transport system	3.78
	411789	AF245505	Hs.72157	Adlican	3.77
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.77
	449378	AW664026	Hs.59892	ESTs	3.76
50	449961	AW265634	Hs.133100	ESTs	3.76
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.75
	407242	M18728		gb:Human nonspecific crossreacting antig	3.75
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.75
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.75
55	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	3.74
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	3.74
	441954	AI744935	Hs.8047	Fanconi anemia, complementation group G	3.74
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	3.73
	422648	D86983	Hs.118893	Melanoma associated gene	3.72
60	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfami	3.71
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	3.71
	428728	NM_016625	Hs.191381	hypothetical protein	3.71
	400245			Eos Control	3.71
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.70
65	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.70
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.70
	440659	AF134160	Hs.7327	claudin 1	3.69
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.67
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67
70	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	3.66
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	3.65
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	3.63
	414883	AA926960		CDC28 protein kinase 1	3.63
	428398	AI249368	Hs.98558	ESTs	3.63
75	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	3.63
	408482	NM_000676	Hs.45743	adenosine A2b receptor	3.63
	404287			C6001909:gi|704441|dbj|BAA18909.1| (D298	3.63
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.61
	414110	BE251752		gb:601112444F1 NIH_MGC_16 Homo sapiens c	3.61
80	427857	AL133017	Hs.2210	hypothetical protein FLJ22865	3.61
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	3.61
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.60
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	3.60

433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.60
430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, com	3.60
456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.59
437340	AL353935	Hs.135917	hypothetical protein DKFZp761D1823	3.59
435793	AB037734	Hs.4993	KIAA1313 protein	3.59
437016	AU076916	Hs.5398	guanine monphosphate synthetase	3.59
420247	AA256930	Hs.44680	hypothetical protein FLJ20979	3.58
424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	3.57
422282	AF019225	Hs.114309	apolipoprotein L	3.57
424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.57
421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.57
408015	AW136771	Hs.244349	epidermal differentiation complex protei	3.56
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	3.56
449039	AI962602	Hs.74284	hypothetical protein MGC2714	3.56
446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.55
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.55
428977	AK001404	Hs.194698	cyclin B2	3.55
402995			NM_002463*:Homo sapiens myxovirus (influ	3.55
416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.54
432917	NM_014125	Hs.241517	PRO0327 protein	3.54
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	3.53
445411	AL137255	Hs.12646	hypothetical protein FLJ22693	3.52
438113	AI467908	Hs.8882	ESTs	3.52
414420	AA043424	Hs.76095	immediate early response 3	3.51
419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.50
447208	BE315291	Hs.237971	hypothetical protein MGC5627	3.50
432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	3.49
442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.49
426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	3.49
429249	X81479	Hs.2375	egf-like module containing, mucin-like,	3.48
413900	AW409747	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/H	3.48
424242	AA337476	Hs.347408	hypothetical protein MGC13102	3.48
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.47
446480	NM_014578	Hs.15114	ras homolog gene family, member	3.46
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.46
428865	BE544095	Hs.164960	BarH-like homeobox 1	3.46
449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.46
450506	NM_004460		fibroblast activation protein, alpha	3.46
421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	3.45
422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.45
405545			Target Exon	3.45
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.44
441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.44
417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.44
417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	3.44
431228	AB006746	Hs.198282	phospholipid scramblase 1	3.44
422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.43
440502	AI824113	Hs.78281	regulator of G-protein signalling 12	3.43
448741	BE614567	Hs.19574	hypothetical protein MGC5469	3.43
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.43
406646	M33600	Hs.308026	major histocompatibility complex, class	3.42
413281	AA861271	Hs.222024	transcription factor BMAL2	3.42
449101	AA205847	Hs.23016	G protein-coupled receptor	3.42
430890	X54232	Hs.2699	glypican 1	3.41
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.41
412429	AV650262	Hs.75765	GRO2 oncogene	3.41
443211	AI128388	Hs.143655	ESTs	3.41
422209	AF005210	Hs.113222	chemokine (C-C motif) receptor 8	3.40
428303	AW974476	Hs.183601	regulator of G-protein signalling 16	3.39
421817	AF146074	Hs.108660	ATP-binding casselte, sub-family C (CFTR	3.39
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.39
422101	AW404176	Hs.111611	ribosomal protein L27	3.39
457670	AF119666	Hs.23449	insulin receptor tyrosine kinase substra	3.38
437033	AW248364	Hs.5409	RNA polymerase I subunit	3.37
425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.37
417059	AL037672	Hs.81071	extracellular matrix protein 1	3.37
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	3.36
414812	X72755	Hs.77367	monokine induced by gamma interferon	3.36
436748	BE159107	Hs.159263	collagen, type VI, alpha 2	3.36
401797			Target Exon	3.36
426309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	3.35
421563	NM_006433	Hs.105806	granulysin	3.35
402294			Target Exon	3.34
414024	AA134712	Hs.22410	gb:zm79g08.r1 Stratagene neuroepithelium	3.34
401961			NM_021626:Homo sapiens serine carboxypep	3.33
418462	BE001596	Hs.85266	integrin, beta 4	3.33
418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	3.33
424800	AL035588	Hs.153203	MyoD family inhibitor	3.33
412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.33
404440			NM_021048:Homo sapiens melanoma antigen,	3.33
432398	AA307808	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	3.33
421677	H64092	Hs.38282	ESTs	3.33
407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.32

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.32
	417197	AW994561	Hs.151777	eukaryotic translation initiation factor	3.32
	429669	BE185499	Hs.2471	KIAA0020 gene product	3.32
	409636	AA305729	Hs.18272	amino acid transporter system A1	3.32
5	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.32
	405386			Target Exon	3.32
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.31
	448275	BE514434	Hs.20830	kinesin-like 2	3.31
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.31
10	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.31
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.31
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	3.31
	404171			NM_000636*:Homo sapiens superoxide dismu	3.31
	418464	R87580	Hs.144531	gb:ym89h07.r1 Soares adult brain N2b4HB5	3.31
15	425566	AW162943	Hs.250618	UL16 binding protein 2	3.31
	410226	AI831958	Hs.61053	hypothetical protein	3.30
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.30
	443247	BE614387	Hs.333893	c-Myc target JPO1	3.30
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	3.30
20	428336	AA503115	Hs.183752	microseminoprotein, beta-	3.29
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	3.29
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.28
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.28
	405778			NM_005361:Homo sapiens melanoma antigen,	3.26
25	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.27
	421150	AI913562	Hs.189902	ESTs	3.27
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	3.27
	455813	BE141577		gb:QV2-HT0083-071299-018-a11 HT0083 Homo	3.27
	426064	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3	3.27
30	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.27
	456791	BE615453	Hs.346509	dedicator of cyto-kinesis 1	3.27
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	3.26
	429002	AW248439	Hs.2340	junction plakoglobin	3.26
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	3.25
35	407777	AA161071	Hs.71465	squalene epoxidase	3.25
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	3.25
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	3.24
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	3.24
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	3.24
40	447519	U46258	Hs.339665	ESTs	3.24
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	3.24
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.24
	423198	M81933	Hs.1634	cell division cycle 25A	3.23
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.23
45	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.22
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.22
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	3.22
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	3.22
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.22
50	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.21
	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	3.21
	412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	3.21
	413436	AF238083	Hs.68061	sphingosine kinase 1	3.21
	408636	BE294925	Hs.46680	CGI-12 protein	3.21
55	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	3.21
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.21
	411573	AB029000	Hs.70823	KIAA1077 protein	3.20
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.19
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.19
60	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	3.18
	401176			Target Exon	3.18
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.17
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.16
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.16
65	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	3.16
	452012	AA307703	Hs.279766	kinesin family member 4A	3.16
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.15
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	3.15
	433020	AI375726	Hs.279918	hypothetical protein	3.14
70	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	3.14
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.14
	420005	AW271106	Hs.133294	ESTs	3.14
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.13
	412270	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.13
75	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	3.13
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.12
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.11
	431722	AF161528	Hs.268049	hypothetical protein	3.11
	427239	BE270447	Hs.174070	ubiquitin carrier protein	3.11
80	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.10
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.10
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	3.10
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfami	3.10

	439755	AW748482	Hs.77873	B7 homolog 3	3.10
	404170			NM_000636*:Homo sapiens superoxide dismu	3.09
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	3.09
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.09
5	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.08
	421155	H87879	Hs.102267	lysyl oxidase	3.08
	441224	AU076964	Hs.7753	calumenin	3.08
	424326	NM_014479	Hs.145296	disintegrin protease	3.08
	429413	NM_014058	Hs.201877	DESC1 protein	3.08
10	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	3.08
	446510	H58306	Hs.15165	retinoic acid induced 14	3.08
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668 protein,	3.07
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	3.07
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.07
15	448853	NM_012204	Hs.22302	general transcription factor IIIC, polyp	3.07
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.07
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	3.06
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	3.06
	412577	Z22968	Hs.74076	CD163 antigen	3.06
20	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.06
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.05
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	3.05
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	3.04
	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	3.04
25	444726	NM_006147	Hs.84981	interferon regulatory factor 6	3.04
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	3.04
	437741	BE561610	Hs.5809	putative transmembrane protein; homolog	3.04
	442643	U82756	Hs.3991	PRP4/STK/WD splicing factor	3.04
	429358	AB037825	Hs.200317	KIAA1404 protein	3.03
30	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	3.03
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotat	3.03
	409154	U72882	Hs.50842	interferon-induced protein 35	3.02
	442173	N76101	Hs.8127	KIAA0144 gene product	3.02
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	3.01
35	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma autoantig	3.01
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	3.01
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	3.01
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	3.01
	459107	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo	3.00
40	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.00
	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	3.00
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	3.00
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.00
45	400200			NM_002788*:Homo sapiens proteasome (pros	3.00
	403330			Target Exon	2.99
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.99
	403416	AI744626		KIAA0564 protein	2.97
	403438			NM_031419*:Homo sapiens molecule possess	2.96
50	447942	F12628	Hs.155470	hypothetical protein MGC16040	2.96
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.95
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	2.94
	440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	2.94
	429547	AW009166	Hs.99376	ESTs	2.93
55	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	2.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.89
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.89
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.86
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	2.86
60	423425	AA375756	Hs.14449	KIAA1609 protein	2.86
	412851	AI826502	Hs.106149	ESTs	2.86
	400664			NM_002425:Homo sapiens matrix metallopro	2.86
	454140	AB040888	Hs.41793	hypothetical protein FLJ10474	2.85
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.85
65	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.84
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.83
	423767	H18283	Hs.132753	F-box only protein 2	2.82
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	2.82
	441801	AW242799	Hs.86366	ESTs	2.80
70	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	2.80
	416539	Y07909	Hs.79368	epithelial membrane protein 1	2.79
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.79
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.75
	417849	AW291587	Hs.82733	nidogen 2	2.74
75	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.73
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.72
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.71
	424874	AA347951	Hs.326413	Homo sapiens cDNA FLJ20812 fis, clone AD	2.71
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.71
80	447854	AW138454	Hs.11594	ESTs	2.71
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.70
	412636	NM_004415		desmoplakin (DPI, DPII)	2.69
	420576	AA297634	Hs.54925	KIAA1858 protein	2.68

	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.68
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.68
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.66
	428698	AA852773	Hs.334838	KIAA1866 protein	2.64
5	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	2.64
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	2.64
	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.63
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.63
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.62
10	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.59
	452620	AA436504	Hs.119286	ESTs	2.59
	420552	AK000492	Hs.98806	hypothetical protein	2.59
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.56
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.56
15	448454	NM_005879	Hs.21254	TRAF interacting protein	2.55
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	2.55
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.54
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	2.54
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.54
20	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.53
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	2.53
	452679	Z42387	Hs.83683	transmembrane, prostate androgen induced	2.51
	411908	L27943	Hs.72924	cytidine deaminase	2.49
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.48
25	430024	AI808780	Hs.227730	integrin, alpha 6	2.47
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.46
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.45
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	2.45
	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	2.45
30	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.44
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.42
	413048	M93221	Hs.75182	mannose receptor, C type 1	2.40
	403851			C5002154*:gi|7299015|gb|AAF54217.1| (AE0	2.39
	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	2.37
35	423903	M57765	Hs.1721	interleukin 11	2.37
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.36
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.32
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.31
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	2.31
40	406974	M57293		gb:Human parathyroid hormone-related pep	2.31
	401924			ENSP00000246632*:cDNA FLJ20261 fis, clon	2.30
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.29
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.29
	436608	AA628980		down syndrome critical region protein DS	2.28
45	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a l	2.27
	434398	AA121098	Hs.3638	serum-inducible kinase	2.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	2.26
	418030	BE207573	Hs.83321	neuromedin B	2.25
	404927			Target Exon	2.25
50	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.23
	411388	X72925	Hs.69752	desmocollin 1	2.21
	445757	AW449065	Hs.13264	KIAA0856 protein	2.18
	405069			NM_006212*:Homo sapiens 6-phosphofructo-	2.17
55	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.16
	443168	AI038653	Hs.50500	ESTs	2.15
	444301	AK000136	Hs.10760	asporin (LRR class 1)	2.13
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.11
	426471	M22440	Hs.170009	transforming growth factor, alpha	2.10
60	445019	AI205540	Hs.281295	ESTs	2.08
	402021			NM_031891:Homo sapiens cadherin 20, type	2.07
	431866	NM_012098	Hs.8025	angiopoietin-like 2	2.05
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.04
	409571	AA504249	Hs.187585	ESTs	2.03
65	450831	R37974	Hs.25255	ESTs	1.99
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.99
	445960	AI268399	Hs.140489	ESTs, Weakly similar to LIN1_HUMAN LINE-	1.98
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.97
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	1.91
70	426850	BE247670	Hs.172766	MAP/microtubule affinity-regulating kina	1.90
	427335	AA448542	Hs.251677	G antigen 7B	1.90
	450649	NM_001429	Hs.25272	E1A binding protein p300	1.88
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	1.88
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.88
75	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	1.86
	433226	AW503733	Hs.9414	KIAA1488 protein	1.86
	413129	AF292100	Hs.104613	RP42 homolog	1.85
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.85
	446620	AA126808	Hs.179902	transporter-like protein	1.81
80	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	1.79
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.78
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	1.77
	423482	BE280172	Hs.129228	galactokinase 2	1.77

	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.76
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.75
	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	1.74
	405102			C15001220*:gi|4469558|gb|AAD21311.1| (AF	1.74
5	433201	AB040896	Hs.21104	KIAA1463 protein	1.73
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.65
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.62
	414961	U27266	Hs.927	myosin-binding protein H	1.61
	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	1.61
10	422170	AI791949	Hs.112432	anti-Mullerian hormone	1.61
	431846	BE019924	Hs.271580	uroplakin 1B	1.58
	404468			C3000442*:gi|11120696|ref|NP_068518.1| c	1.57
	405779			NM_005367:Homo sapiens melanoma antigen,	1.55
	441129	AA074904	Hs.296420	ESTs, Weakly similar to T18651 hypotheti	1.55
15	427244	AA402400	Hs.178045	ESTs	1.52
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	1.52
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	1.51
	418367	AA326035	Hs.59236	hypothetical protein DKFZp434L0718	1.51
	440340	AW895503	Hs.125276	ESTs	1.48
20	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	1.47
	424750	D29956	Hs.152818	ubiquitin specific protease 8	1.46
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	1.44
	406374			C16001364:gi|11067373|ref|NP_067689.1| C	1.43
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	1.40
25	404405			Target Exon	1.39
	401258			NM_030932*:Homo sapiens diaphanous (Dros	1.38
	433323	AA805132	Hs.159142	ESTs	1.36
	427441	AA412605	Hs.343879	SPANX family, member C	1.33
	444707	AI188613	Hs.41690	desmocollin 3	1.31
30	409103	AF251237	Hs.112208	XAGE-1 protein	1.27
	451106	BE382701	Hs.25960	N-MYC oncogene	1.27
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	1.23
	430686	NM_001942	Hs.2633	desmoglein 1	1.21
	429325	AW086739	Hs.243770	ESTs	1.19
35	406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	1.03
	418827	BE327311	Hs.47166	HT021	1.01
	404104			C6001378*:gi|1171748|sp|P46530|NOTC_BRAR	1.00

40 TABLE 46B

Pkey: Unique Eos probeset Identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
413808	2905_1	AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580678 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T26354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767
421582	13358_1	X00474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
406687	0_0	M31126
450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758
415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM466657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
454241	685806_1	BE184942 BE184946 AW238414 BE144666

452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564544 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300555 AW170777 AA586956 AL571889 AL555850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804869 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
408660	105529_1	AW975281 AA664986 AA525775 AA056342 AI538978
400245	12188_1	X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 AI074589 AI523475 BE890249 AW406263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 AI460106 AA740411 AI499168 AI078223 AI682923 BE696559 AW375385 AA788739 BG984978 Z40874 T17054 F09669 AW844043 U10439 BI711870 AW245957 AU158567 AA679305 AA679316 W72510 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172 AW192891 AI707980 AI094937 AI042115 AI200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826 AI422774 AW873114 AW073597 AW664483 AI218710 AW020550 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655 AI554424 AI274187 BE465703 AW512940 AW241366 AI923954 AA576649 AW168294 AA813181 AA912168 AI049736 AW514073 AA548255 AI569630 BE710031 AA244182 AI341697 AA563904 AI537990 AW517908 AW172943 Z39498 AI750294 AW150414 AI253293 BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 BI021048 BM048783 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 BI919250 BI253018 AW130996 BE074249 BE895428 BI034862 BE083277 BF952166
414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
414110	1634167_1	BE253764 BE250764 BE255757 BE251752 BE251925
450506	1529_1	U09278 NM_004460 U76833 AF007822 AL550894 BG203919 AL575714 AI478772 AW022667 AW613820 AI435793 AI051768 AI200109 AA436611 BG208151 AI446661 BG215551 BM449645 AW630055 BG620125 AL550932 AW471133 AU136648 BE925603 BF826688
455813	1515590_1	BE141577 BE141585 BE141587
439780	49082_1	AL109688 R23665 R26578
400200	3806_1	BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA869528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI707743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473
412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487
436608	32229_2	BC015981 AJ301615 AA628980 AI126603 BF184719

TABLE 46C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423

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401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
400666	8118496	Plus	17982-18115,20297-20456
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
400665	8118496	Plus	16879-17023
402994	2996643	Minus	4727-4969
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
405770	2735037	Plus	61057-62075
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
404240	5002624	Minus	116132-116407,116653-116922
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
402992	7767907	Minus	42137-42515
402408	9796239	Minus	110326-110491
404286	2326514	Plus	51086-51301
405387	6587915	Minus	3769-3833,5708-5895
404287	2326514	Plus	53134-53261
402995	2996643	Minus	5962-6216
405545	1054740	Plus	118677-118807,119091-119296,121626-12182
401797	6730720	Plus	6973-7118
402294	2282012	Minus	2575-3000
401961	4581193	Minus	124054-124209
404440	7528051	Plus	80430-81581
405386	6579238	Minus	40959-41297
404171	9930793	Plus	173667-173783,176876-177055
405778	7280331	Plus	18748-19757
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
401176	9438469	Minus	20475-20734
404170	9930793	Plus	168836-169248

TABLE 47A:

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Maximum of esophageal tumor AIs divided by the 98th percentile of the normal esophagus AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	31.70
411243	AB039886	Hs.69319	CA11	30.12
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	18.46
444325	AW152618	Hs.16757	ESTs	18.22
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	17.52
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	16.28
400666			NM_002425:Homo sapiens matrix metallopro	15.59
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	15.22
425679	X05997	Hs.159177	lipase, gastric	14.60
432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	13.14
431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	12.60
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.00
453331	AI240665		ESTs	11.20
431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	10.77
408380	AF123050	Hs.44532	diubiquitin	10.32
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.32
412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	10.22
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	10.18
408243	Y00787	Hs.624	interleukin 8	9.80
414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	9.75
450375	AA009647		a disintegrin and metalloproteinase doma	9.12
407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	8.88
433447	U29195	Hs.3281	neuronal pentraxin II	8.64
421508	NM_004833	Hs.105115	absent in melanoma 2	8.46
452862	AW378065	Hs.8687	ESTs	8.34
432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	7.92
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	7.86
409757	NM_001898	Hs.123114	cystatin SN	7.62
452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.60
413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	7.58
452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	7.46
437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.44
406687	M31126		matrix metalloproteinase 11 (stromelysin	7.24
430280	AA361258	Hs.237868	interleukin 7 receptor	7.18
439343	AF086161	Hs.114611	hypothetical protein FLJ11808	7.13
429228	AI553633	Hs.326447	ESTs	7.04
421110	AJ250717	Hs.1355	cathepsin E	6.98
414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	6.88
424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	6.88
406673	M34996	Hs.198253	major histocompatibility complex, class	6.72
421582	AI910275		trefoil factor 1 (breast cancer, estroge	6.52

	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	6.40
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	6.32
	439926	AW014875	Hs.137007	ESTs	6.32
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.12
5	411296	BE207307	Hs.10114	growth suppressor 1	6.03
	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	5.86
	413441	AI929374	Hs.75367	Src-like-adapter	5.86
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	5.81
	417715	AW969587	Hs.86366	ESTs	5.76
10	413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	5.63
	400665			NM_002425:Homo sapiens matrix metallopro	5.60
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.53
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	5.44
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.42
15	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.40
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	5.38
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	5.08
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a l	5.08
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	5.04
20	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.92
	436856	AI469355	Hs.127310	ESTs	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.60
	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	4.53
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.48
25	404240			NM_018950:Homo sapiens major histocompat	4.36
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	4.34
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.29
	425139	AW630488	Hs.25338	protease, serine, 23	4.24
	415989	AI267700		ESTs	4.20
30	406202	AA227710	Hs.43658	DKFZP586L151 protein	4.11
	450701	H39960	Hs.288467	hypothetical protein XP_098151	4.06
	423271	W47225	Hs.126256	interleukin 1, beta	4.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.96
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	3.90
35	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.86
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.86
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	3.76
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	3.49
	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	3.44
40	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	3.37
	435370	AI964074	Hs.225838	ESTs	3.29
	443378	AW392550	Hs.9260	proteasome (prosome, macropain) subunit,	3.19
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.18
	409154	U72882	Hs.50842	interferon-induced protein 35	3.13
45	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	3.12
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.00
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.76
	402992			Target Exon	2.57
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.54
50	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	2.52
	413945	NM_000591	Hs.75627	CD14 antigen	2.51
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	2.50
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	2.48
	415149	X12451	Hs.78056	cathepsin L	2.47
55	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	2.46
	410422	AL042014	Hs.53348	Homo sapiens, clone MGC:15203, mRNA, com	2.45
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.45
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.39
	422562	AI962060	Hs.118397	AE-binding protein 1	2.35
60	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	2.28
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	2.19
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	2.19
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	2.03
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.03
65	428981	BE313077	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.83
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	1.79
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (fr	1.70
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	1.69
	412773	H15785	Hs.74573	similar to vaccinia virus HindIII K4L OR	1.66
70	414024	AA134712	Hs.22410	gb:zm79g08.r1 Stratagene neuroepithelium	1.65
	426530	U24578	Hs.278625	complement component 4A	1.58
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.52

75 TABLE 47B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993

			H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58761 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
	450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758
	452410	59661_1	AL133619 AI435410 AA622747 AW272464 AI215594 AI673758 AI476447 AI804128 AI581345 AI026826 AI300820 AW513621 AA256162 AI559724 AI493388 AA614641 AI125754 AI214351 AI567080 AI200813 AI476629 AI685732 AA602400 AA730140 AI565082 AI269603 AI807095 AA905453 AA505909 AI204595 AI582930 AI686077 AA757863 AA730154 AA664048 BI831663 AI734138 AI734130 AI732734 AW043563 AI741241 AI732741 BF111446 BE677727 AA437369 AA426284 AA433997 AA425820
	406687	0_0	M31126
	421582	13358_1	X00474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418
	413808	2905_1	AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI691151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580678 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236

TABLE 47C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
400665	8118496	Plus	16879-17023
404240	5002624	Minus	116132-116407,116653-116922
402992	7767907	Minus	42137-42515

TABLE 48A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of normal esophagus AIs divided by the 90th percentile of esophageal tumor AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1
407245	X90568	Hs.172004	titin	37.43
426752	X69490	Hs.172004	titin	30.23
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	23.69
407013	U35637		gb:Human nebulin mRNA, partial cds	17.09
400440	X83957	Hs.83870	nebulin	15.56
406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	14.21
428087	AA100573	Hs.182421	troponin C2, fast	13.03
417070	Z19077	Hs.172004	titin	13.02
406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	12.61
405001	U58196		interleukin enhancer binding factor 1	12.53
418391	NM_003281	Hs.84673	troponin I, skeletal, slow	12.46
418205	L21715	Hs.83760	troponin I, skeletal, fast	12.40
422633	X55832	Hs.118804	enolase 3, (beta, muscle)	12.21
400499			C10001858:gi|6679124|ref|NP_032759.1| ne	11.99
418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	10.53
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	10.21
417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	10.14
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	10.13
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	10.00
416373	AA195845	Hs.73680	ESTs, Weakly similar to S12658 cysteine-	9.65
415672	N53097	Hs.193579	ESTs	9.57
409096	AA194412	Hs.50550	sarcomeric muscle protein	9.48

431360	NM_000427	Hs.251680	loricrin	9.42
416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	9.20
426429	X73114	Hs.169849	myosin-binding protein C, slow-type	9.15
422069	AJ010063	Hs.343603	titin-cap (telethonin)	8.96
409028	AB014513	Hs.49998	Z-band alternatively spliced PDZ-motif	8.64
437206	AW975934	Hs.283382	ESTs, Weakly similar to I38344 titin, ca	8.48
421296	NM_002666	Hs.103253	perilipin	8.47
412129	M21984	Hs.73454	troponin T3, skeletal, fast	8.39
434352	AF129505	Hs.86492	small muscle protein, X-linked	8.28
418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	7.93
408591	AF015224	Hs.46452	mammaglobin 1	7.88
435124	AA725362	Hs.120456	ESTs	7.76
430681	AW969675	Hs.291232	ESTs	7.70
454229	AW957744	Hs.278469	lacrimal proline rich protein	7.68
424734	AI217685	Hs.96844	ESTs	7.59
428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.57
431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	7.41
443727	Z25389	Hs.18459	ESTs	7.21
408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	7.04
413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	6.98
424485	AI685069	Hs.272556	peptidylarginine deiminase type I	6.93
403805			Target Exon	6.87
429997	NM_006789	Hs.227457	apolipoprotein B mRNA editing enzyme, ca	6.72
416532	F00797	Hs.85844	neurotrophic tyrosine kinase, receptor,	6.70
419711	C02621	Hs.159282	ESTs	6.70
422640	M37984	Hs.118845	troponin C, slow	6.68
433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.55
406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	6.34
451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.27
446962	AI351421	Hs.279709	muscle specific ring finger protein 1	6.20
411102	AA401295	Hs.23926	triadin	6.17
411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.15
454059	NM_003154	Hs.37048	statherin	5.95
451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	5.85
434360	AW015415	Hs.127780	ESTs	5.57
420813	X51501	Hs.99949	prolactin-induced protein	5.52
417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	5.46
424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	5.42
446523	NM_003063	Hs.334629	sarcolipin	5.41
402270			Target Exon	5.25
437846	AA773866	Hs.244569	esophagus cancer-related gene-2	5.24
424982	U94777		phosphorylase, glycogen; muscle (McArdle	5.17
414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	5.14
410621	AA194329	Hs.172004	filin	5.10
429134	AA446953	Hs.99004	ESTs	5.06
436519	AJ278124	Hs.238756	myozenin	5.04
447023	AA356764	Hs.17109	integral membrane protein 2A	5.03
427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	5.02
426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	5.00
433635	AI074502	Hs.134292	hypothetical protein MGC12921	4.98
429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	4.96
411021	F00055	Hs.172004	titin	4.95
416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	4.93
424897	D63216	Hs.153684	frizzled-related protein	4.92
406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.92
428824	W23624	Hs.173059	ESTs	4.78
418692	AK000268	Hs.87383	hypothetical protein	4.74
448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	4.73
432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.66
424049	AB014524	Hs.136380	KIAA0624 protein	4.65
439609	AW971945	Hs.293236	ESTs	4.65
433122	AB019391	Hs.58049	ESTs	4.62
415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	4.59
415655	W05433		ESTs	4.59
442376	W95588	Hs.129982	Homo sapiens cDNA FLJ12228 fis, clone MA	4.58
452308	AI167560	Hs.61297	ESTs	4.57
418072	F35210	Hs.86507	Human DNA sequence from clone RP3-353C17	4.56
429413	NM_014058	Hs.201877	DESC1 protein	4.53
423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.53
438704	AI435060	Hs.32825	ESTs	4.50
413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	4.49
430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	4.48
419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	4.46
422313	AF045941	Hs.115166	sciellin	4.43
417045	F01180	Hs.332030	Homo sapiens ORF1	4.41
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.39
435101	AI743156	Hs.131064	ESTs	4.37
432408	N39127		ESTs, Weakly similar to A46010 X-linked	4.35
439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	4.35
429930	AI580809	Hs.99569	ESTs	4.30
429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	4.26
429454	AL039940	Hs.202949	KIAA1102 protein	4.20
411000	N40449	Hs.201619	ESTs, Weakly similar to S38383 SEB4B pro	4.11

	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.99
	428560	AI243209	Hs.98669	ESTs, Weakly similar to B47411 ADPribosy	3.95
	438328	AI492261	Hs.32450	ESTs	3.84
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.84
5	453876	AW021748	Hs.110406	ESTs, Weakly similar to I38022 hypotheti	3.83
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	3.82
	430171	AF086289	Hs.234766	skin-specific protein	3.80
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	3.75
	446082	AI274139	Hs.156452	ESTs	3.74
10	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.70
	431205	AA194560	Hs.250763	tropomodulin 4 (muscle)	3.68
	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.68
	424747	AA346241	Hs.231887	EST	3.67
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	3.63
15	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.62
	453817	AW755253	Hs.61920	ESTs	3.57
	416431	AW384459	Hs.172004	titin	3.52
	425971	AF135024	Hs.165296	kallikrein 13	3.49
	412452	AA215731	Hs.79265	suppression of tumorigenicity 5	3.48
20	421512	AB007923	Hs.265848	myomegalin	3.41
	413922	AI535895	Hs.221024	ESTs	3.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.36
	418067	AI127958	Hs.83393	cystatin E/M	3.32
	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.29
25	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	3.26
	420197	AW139647	Hs.88134	ESTs, Weakly similar to A57291 cytokine	3.23
	425869	AA524547	Hs.160318	FXYD domain-containing ion transport reg	3.21
	404270			NM_006061:Homo sapiens specific granule	3.21
	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	3.17
30	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.13
	452023	AB032999	Hs.27566	KIAA1173 protein	3.08
	417713	D42047	Hs.82432	KIAA0089 protein	2.99
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	2.97
	450300	AL041440	Hs.58210	ESTs, Highly similar to ITH4_HUMAN INTER	2.97
35	451814	AA847992	Hs.137003	ESTs	2.83
	452360	AI742082	Hs.98539	ESTs	2.67
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	2.57
	408104	AW972927	Hs.293968	ESTs	2.57
	444329	W73753	Hs.209637	hypothetical protein FLJ12921	2.54
40	439652	W67826	Hs.55412	ESTs, Weakly similar to K1CJ_HUMAN KERAT	2.50
	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon(Ita	2.33
	425855	AF135025	Hs.159679	kallikrein 12	2.32
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	2.28
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.25
45	411388	X72925	Hs.69752	desmocollin 1	2.25
	425721	AC002115	Hs.159309	uroplakin 1A	2.12
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	2.10
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	2.02
	417405	W28657	Hs.5307	ESTs	2.01
50	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	1.95
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.79
	430513	AJ012008	Hs.241586	G6C protein	1.68
	454478	AW805749	Hs.318885	superoxide dismutase 2, mitochondrial	1.68
	416559	AI039195	Hs.128060	ESTs	1.66
55	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	1.64
	415780	U75898	Hs.78846	heat shock 27kD protein 2	1.55
	409702	AI752244		eukaryotic translation elongation factor	1.50

60 TABLE 48B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
407013	2073_7	U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376
424982	25362_1	AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967 F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F28742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311 F32380 F25216 F19679 F18656 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940 F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W80691 F16457 F24094 F16783 AA180319 F28443 F17763 F17448 F00542 AA197179 AA193012
415655	15499_1	AJ276240 N70563 F37502 F29200 F27903 F18577 F19683 F20867 Z28857 F30994 F31752 F17375 F15601 F17543 F17411
432408	2061_18	AV724258 AA247153 BF736219 BF513744 AW058048 AI082691 AA865520 N39127 AV724549 F20776 AA249747 AW970392 AA535433 F36964 F33894
409702	38388_1	AK056951 AK026458 BI439120 BM021106 F30243 BM055214 BM054962 BM069667 F37401 AA563621 AI752243 AI720773 AI933014 F18964 F35317 F35258 F27772 H39537 AW445222 F19408 H28557 F30608 F31797 F30960 BF837737 BF837688 AL551046 BI758668 BI765038 BI837440 BE392882 BI438601 AI093511 AI752244 AI784111 BG490221 BF338840 BF338974 BG896472 AL576843 AW966769 F25388 F37436 H28558 AI025548 AA782333 F30929 F36002 F21229 AI720539 AA719449 F21231 F18924 AA626886 F30774 F27704 F31411 F31127 F33381 F36153 F31793 F31138 F31956 F33901 AA298244 BI757347 AI810201 AI692843 F29441 H51409 F21804 AW973249 F18440 F17572 F32499 AA327152 AA534140 AI188088 F18893 F23362 AA010888 F18143 Z28500 H27651 AI720790 F22425 H13178 H28677 F21098 F37777 F21466 F16598 F23420 AL574723 R75610 F34035 F17845 F18560 F25902 R79117 F35534 F15713 AI612800 F16563 F15645 F33609 F29995 BG939623 F17385 F17384 F18660 F17922 F15523 AI093253 F18359 F31452 F00232 AI583430 BM021353 AA284108 H27650 H29935 BE708208 AA010737 H51451

Z19399 AI678418 AI952535 F17265 F17826 F37939 F35639 F17367 W75962 R70189 Z28755 R72106 AA335915 R75700 R79116 W72887 AI581552 R71403 F23388 C03913 BI756149 BI116109 BF790727 AL553994 R82966 W47487 AA456066 AW984608 BE708220 BG490537 W47419

TABLE 48C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405001	6015406	Minus	104646-104819
400499	9796071	Minus	148495-148806
403805	8140491	Minus	51483-51742,53429-53511
402270	3108020	Plus	117656-117822
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965

Table 49A. 1562 genes upregulated in lung cancer relative to normal body tissues

Table 49A shows 1562 genes upregulated in lung cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar accession number, GenBank accession number

UniGeneID: UniGene number

Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).

UniGene Title: UniGene gene title

R1 90th percentile of lung tumor AIs divided by the 50th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from the numerator and denominator.

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1

421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphate), member 2; Ribosomal_L20,Na_Pi_cotrans;TM=Y;; 24.06
439335; AA742697; Hs.62492; ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]; none;SS=M; 21.70
406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;; 19.36
421341; AJ243212; Hs.279611; deleted in malignant brain tumors 1; zona_pellucida,CUB,SRCR;SS=M; 16.99
452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine proteinase [H.sapiens]; none,none; 16.67
429259; AA420450; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none,none; 16.50
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member A1; aldedh;; 16.24
408000; L11690; Hs.620; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FliD,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M;; 14.75
421798; N74880; Hs.29877; N-acylsphingosine amidohydrolase (acid ceramidase)-like; SAPA,Surfactant_B,none; 14.18
439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 [H.sapiens]; none,none; 13.94
431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 13.54
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 12.97
444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothetical protein YGL050w - yeast (Saccharomyces cerevisiae) [S.cerevisiae]; Collagen;TM=M;SS=M; 12.92
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;; 12.76
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP;TM=M;SS=M; 12.50
414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;; 12.12
436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;; 12.00
418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none,none; 11.99
419693; AA133749; Hs.301350; FXYD domain-containing ion transport regulator 3; ATP1G1_PLM_MAT8;TM=Y;SS=M; 11.88
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 11.38
414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin-like) receptor 1; lectin_c;TM=Y;SS=M; 11.21
428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3;TM=Y;SS=M; 11.08
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member B2; aldedh;TM=M;SS=M; 11.01
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisoIV,HATPase_c;SS=M; 10.69
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4); ank;; 10.65
439223; AW238299; Hs.250618; UL16 binding protein 2; Idl_recept_a,PKD,MHC_I;TM=M;SS=Y; 10.52
441835; AB036432; Hs.184; advanced glycosylation end product-specific receptor; homeobox,Acyltransferase,notch,EGF,ank,Acyltransferase; 10.47
451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ABC_tran,SRP54;TM=Y;SS=M; 10.33
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;; 10.21
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 10.14
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); PTN_MK;TM=M;SS=Y; 10.13
433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recp;TM=M;SS=Y; 10.12
454098; W27953; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none,none; 10.05
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 9.98
430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]; none,none; 9.79
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; none,pkinase,fn3,ig; 9.60
414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 9.54
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;; 9.52
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 9.48

423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); Kunitz_BPTI,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 9.44
418882; NM_004996; Hs.89433; ATP-binding cassette, sub-family C (CFTR/MRP), member 1; ABC_membrane,ABC_tran;TM=Y;SS=M; 9.32
435472; AW972330; Hs.283022; triggering receptor expressed on myeloid cells 1; ig;TM=M;SS=M; 9.26
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens]; none,none; 9.18
419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR/MRP), member 3; ABC_tran,ABC_membrane;TM=Y;SS=M; 9.06
441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone HRC00953; 7tm_3,none; 8.98
446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 8.74
436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 8.71
421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 8.71
423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; vwa,Cache;TM=M;; 8.66
439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 8.63
438091; AW373062; ; nuclear receptor subfamily 1, group I, member 3; hormone_rec,zf-C4,none; 8.60
421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;; 8.57
413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;SS=M; 8.56
408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;SS=M; 8.52
414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;SS=M; 8.49
430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;; 8.42
413011; AW068115; Hs.821; biglycan; LRR,LRRNT;SS=M; 8.40
446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 8.39
411089; AA456454; ; cell division cycle 2-like 1 (PITSLRE proteins); none,none; 8.37
422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); BIR;TM=M;; 8.34
453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; none;SS=M; 8.25
449019; AI949095; Hs.67776; ESTs, Weakly similar to T22341 hypothetical protein F47B8.5 - Caenorhabditis elegans [C.elegans]; none,none; 8.24
409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;; 8.22
416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 8.19
451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M;; 8.16
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 8.16
429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M;; 8.14
445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank;; 8.14
421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase;SS=Y; 8.10
414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); ig;TM=Y;SS=M; 8.03
439285; AL133916; ; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 7.97
439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B; Sema,PSI,integrin_B;TM=Y;; 7.86
424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2; pkinase;TM=M;; 7.85
424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 7.85
409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;; 7.84
415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); SH3,TPR;TM=M;; 7.73
427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, receptor for (CD16); ig;TM=Y;SS=M; 7.72
430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily, member 17; IL2;SS=M; 7.71
451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 7.70
435575; AF213457; Hs.44234; triggering receptor expressed on myeloid cells 2; ig;TM=Y;SS=M; 7.70
427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;; 7.70
426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; ig,ICAM_N;TM=M;SS=M; 7.67
422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB;TM=Y;SS=M; 7.64
413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; SAM_PNT,none; 7.54
424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding protein; 7tm_1;TM=Y;SS=M; 7.52
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); Y_phosphatase,DSPc;TM=M;; 7.46
421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen alpha 1(XI) chain precursor [H.sapiens]; none;TM=Y;SS=M; 7.40
421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 7.39
438089; W05391; ; nuclear receptor subfamily 1, group I, member 3; hormone_rec,zf-C4,none; 7.38
428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;; 7.36
448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor, epsilon; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 7.36
416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; none;TM=M;; 7.31
418506; AA084248; Hs.85339; G protein-coupled receptor 39; none,none; 7.25
441553; AA281219; Hs.121295; ESTs; none,FG-GAP,integrin_A; 7.25
422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3;TM=M;; 7.21
415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-type, Z polypeptide 1; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 7.20
438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; transferrin,Guanylate_kin,PDZ,SH3; 7.20
412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M;; 7.14
418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 7.14
428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 7.12
418462; BE001595; Hs.85266; integrin, beta 4; fn3,integrin_B,Calx-beta,EGF;TM=M;SS=M; 7.08
420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 7.02
428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;; 7.00
449230; BE613348; Hs.211579; melanoma cell adhesion molecule; ig,isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 6.98
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; Furin-like,pkinase,Recep_L_domain,YLP,none; 6.97
421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M;; 6.96
410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; ITAM;TM=Y;SS=M; 6.93
428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 6.93
421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT;TM=M;; 6.91
451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin_N;SS=M; 6.86
432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;, mRNA sequence; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPc,tsp_1,Ribosomal_S21,rvp;TM=M;; 6.84
442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;; 6.77
448243; AW369771; Hs.52620; integrin, beta 8; integrin_B,none; 6.76
427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh;SS=M; 6.75
418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.74
426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; sugar_tr;TM=Y;SS=M; 6.73

430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; HCO3_cotransp;TM=Y;; 6.71
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 6.71
431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor); FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 6.70
410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 6.69
424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation antigen; PAAD_DAPIN,HIN;; 6.69
431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor); vwa,integrin_A,FG-GAP;TM=Y;SS=M; 6.65
428157; AI738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 6.64
430770; AA765694; Hs.123296; ESTs; none,none; 6.63
412270; AC005262; Hs.73797; guanine nucleotide binding protein (G protein), alpha 15 (Gq class); G-alpha,arf;TM=M;; 6.59
439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005735; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 6.59
427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M;; 6.59
413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 6.58
429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 6.58
416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 6.58
418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 6.57
426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); Pribosyltran,OMPdecase;TM=M;; 6.57
402260; ; ; NM_001436*:Homo sapiens fibrillarin (FBL), mRNA. transcript) (F8A), mRNA.; pkinase,Fibrillarin,none; 6.56
456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide); none;TM=Y;; 6.53
444006; BE395085; Hs.10086; type I transmembrane protein Fn14; tdl_recepl_a,PKD,MHC_I;TM=M;SS=Y; 6.53
411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; inositol_P,ig;TM=M;; 6.52
435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;TM=Y;SS=M; 6.52
432920; U37689; Hs.3128; polymerase (RNA) II (DNA directed) polypeptide H; none;TM=M;; 6.48
412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; PLDc;TM=M;; 6.48
409208; Y00093; Hs.51077; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); vwa,FG-GAP,integrin_A,vwa,integrin_A,FG-GAP; 6.43
424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF;; 6.43
418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; ig;TM=Y;SS=M; 6.41
413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PLACE2000103; HLH,death,TNFR_c6,Acyl-CoA_hydro; 6.41
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;; 6.39
453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPase;TM=M;; 6.37
424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 6.37
428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;SS=M; 6.36
432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 6.34
409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.34
451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate, RC3); IQ,7tm_1;TM=M;; 6.34
443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; none;TM=M;SS=Y; 6.34
401027; ; ; Target Exon; none,none; 6.26
418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin_B,EGF,PSI;TM=Y;SS=M; 6.22
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); SH2;SS=M; 6.21
408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone ADKA02377; 7tm_3,none; 6.20
408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3; efhand,ion_trans,K_tetra,none; 6.19
456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudogene; LIM,PDZ,pkinase;SS=M; 6.18
408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 6.17
426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 6.17
445019; AI205540; Hs.281295; ESTs; none,none; 6.16
438552; AJ245820; Hs.6314; type I transmembrane receptor (seizure-related protein); none,none; 6.16
414907; X90725; Hs.77597; polo (Drosophia)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M;; 6.14
425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; PI3_PI4_kinase,FAT,FATC;TM=M;; 6.13
417421; AL138201; Hs.82120; nuclear receptor subfamily 4, group A, member 2; hormone_rec,zf-C4;SS=M; 6.13
425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 6.12
422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 6.12
427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M;; 6.12
421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.11
444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 thromboxane A-2 receptor, endothelial [H.sapiens]; Bcl-2,none; 6.10
423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y;; 6.10
409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y;; 6.09
411020; NM_005770; Hs.67726; macrophage receptor with collagenous structure; SRCR,Collagen;TM=Y;SS=M; 6.09
425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 6.08
439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD); PAF-AH_Ib,Lipase_GDSL;TM=M;; 6.07
421753; BE314828; Hs.107911; ATP-binding cassette, sub-family B (MDR/TAP), member 6; ABC_tran,ABC_membrane;TM=Y;SS=M; 6.07
406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gene, complete CDS.; none,none; 6.07
425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase,pkinase_C;TM=M;SS=M; 6.06
452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; C1q,Collagen;SS=M; 6.05
414883; AA926960; ; CDC28 protein kinase 1; CKS;; 6.05
414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPc,tsp_1,Ribosomal_S21,rvp;TM=M;; 6.03
452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 6.03
448782; AL050295; Hs.22039; KIAA0758 protein; 7tm_2,ig,GPS,SEA;TM=Y;; 6.03
449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 6.01
445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 6.00
424381; AA285249; Hs.146329; protein kinase Chk2; pkinase,FHA,DnaJ;TM=M;; 6.00
420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M;; 5.99
439310; AF086120; Hs.102793; ESTs; casein_kappa,pkinase,ig,none; 5.97
414972; BE263782; Hs.77695; KIAA0008 gene product; GKAP;TM=M;; 5.97
425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 5.94
444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 5.93
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin;TM=M;; 5.93
421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 5.92
426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586I2022 (from clone DKFZp586I2022); none;TM=Y;SS=M; 5.92
407792; AI077715; Hs.39384; putative secreted ligand homologous to fjx1; none;TM=M;SS=Y; 5.91
428771; AB028992; Hs.193143; KIAA1069 protein; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 5.91
438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; ig,MHC_II_alpha,none; 5.91

440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 5.90
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M;; 5.90
408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, receptor, type 2; ig,pkinase,LRR,LRRNT,LRRCT;TM=Y;SS=M; 5.89
413186; AU077141; Hs.75231; solute carrier family 16 (monocarboxylic acid transporters), member 1; sugar_tr;TM=Y;SS=M; 5.89
430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.88
422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 5.88
425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; none;TM=M;SS=Y; 5.88
429619; AL120751; Hs.211568; eukaryotic translation initiation factor 4 gamma, 1; none,none; 5.86
437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222); SH2,SH3,BTB; 5.86
436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 5.85
429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, calcium-dependent); C2,PLA2_B;TM=M;; 5.85
419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 5.83
428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily, member 6b, decoy; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD;; 5.83
414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 5.82
451320; AW118072; ; diacylglycerol kinase, zeta (104kD); none;TM=M;; 5.82
400991; ; ; Target Exon; Armadillo_seg,lectin_c,none; 5.81
456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral transforming sequence c; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M;; 5.81
434263; N34695; Hs.44648; ESTs; ig,none; 5.81
428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino acid transporter), member 5; eIF6,SDF;TM=M;; 5.78
421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; p450;TM=Y;SS=M; 5.78
449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain,none; 5.77
409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 5.77
412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); MIF,sugar_tr,none; 5.75
409533; AW969543; Hs.21291; mitogen-activated protein kinase kinase kinase 13; Peptidase_C48,none; 5.73
457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) receptor; hormone_rec,zf-C4,Metallothio_5;TM=M;; 5.73
416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); none,none; 5.72
448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; SH2,STAT,STAT_bind,STAT_prot;TM=M;; 5.72
452295; BE379936; Hs.28866; programmed cell death 10; serpin,none; 5.72
448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; NUDIX;TM=M;SS=M; 5.72
448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitter transporter, creatine), member 8; SNF;TM=Y;; 5.71
417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr_redox;TM=Y;SS=M; 5.69
453323; AF034102; Hs.32951; solute carrier family 29 (nucleoside transporters), member 2; Nucleoside_tran;TM=Y;SS=M; 5.69
410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 5.69
412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 46kD; rrm,hormone_rec,zf-C4,sugar_tr;; 5.69
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; none;TM=Y;SS=M; 5.66
447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; PP2C;TM=M;; 5.65
438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 5.65
421391; AW304350; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig,none; 5.64
417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; Sm,pkinase;; 5.64
406137; ; ; NM_000179*:Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM_000178.1 GI; MutS_C,PWWP,MutS_N;TM=M;; 5.63
421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_PI4_kinase,PI3Ka;TM=M;; 5.62
445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; PABP,rrm,pkinase,14-3-3; 5.62
447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; SH3,PH,RhoGEF;TM=M;; 5.61
446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein coupled, 6; 7tm_1;TM=Y;SS=M; 5.59
433662; W07162; Hs.150826; CATX-8 protein; ras,ABC_tran,arf;TM=M;SS=M; 5.59
449029; N28989; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; aa_permeases;TM=Y;SS=M; 5.58
431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 5.57
430508; AI015435; Hs.104637; ESTs; SDF;TM=Y;SS=M; 5.56
426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; 7tm_1;TM=Y;SS=M; 5.55
421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.54
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;; 5.54
429563; BE619413; Hs.2437; eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD); hexapep,W2,hormone2,DUF29;TM=M;; 5.52
412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subunit, non-ATPase, 2; PC_rep;TM=M;; 5.51
45229; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; pkinase;TM=M;; 5.51
437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (from clone DKFZp547C136); ABC_tran,GTP_EFTU,ABC_membrane,none; 5.50
423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 5.48
422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); SH3,PX;TM=M;; 5.48
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304; Nucleoside_tra2,none; 5.48
426691; NM_006201; Hs.171834; PCTAIRE protein kinase 1; pkinase;TM=M;; 5.48
453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M;; 5.48
412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; none,none; 5.44
430486; BE062109; Hs.241551; chloride channel, calcium activated, family member 2; none;TM=Y;SS=M; 5.43
430066; AI929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR_synt; 5.40
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; kinesin,fn3,Y_phosphatase;TM=M;; 5.40
411825; AK000334; Hs.72289; hypothetical protein FLJ20327; SNF,Zip;TM=Y;; 5.36
400205; ; ; NM_006265*:Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA.(APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA.; DUF173;SS=M; 5.35
410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 5.34
407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 5.34
425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M;; 5.32
400210; ; ; Eos Control; Adap_comp_sub,Clat_adaptor_s;TM=M;; 5.32
414825; X06370; Hs.77432; epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 5.31
414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2; serpin;SS=M; 5.30
416000; R82342; Hs.79856; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; none,sugar_tr; 5.30
414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 5.29
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; SH2,SH3,pkinase;TM=M;; 5.29
450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; none,none; 5.29
456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, complete cds; none,PK,PK_C,myosin_head,RhoGAP; 5.28
410068; AI633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3;TM=M;; 5.28
456629; AW891965; Hs.279789; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 5.27
417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); pkinase,Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 5.26
444051; N48373; Hs.10247; activated leucocyte cell adhesion molecule; none,none; 5.26

404083; ; ; C6002159*:gi|628027|pir||A53593 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor ty; none;SS=M; 5.26
422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1; mito_carr;TM=M;; 5.26
419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;; 5.26
427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 5.25
425921; NM_007231; Hs.162211; solute carrier family 6 (neurotransmitter transporter), member 14; SNF;TM=Y;SS=M; 5.25
448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A, member 4A; none;TM=Y;SS=M; 5.24
441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,ig;TM=M;; 5.23
446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 5.23
422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;; 5.23
447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazarotene induced) 3; none;TM=Y;; 5.21
446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; SH3,HS1_rep;TM=M;; 5.20
450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;; 5.19
425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; Troponin,Exo_endo_phos,IQ;TM=M;; 5.19
446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonine kinase 21); CNH,DAG_PE-bind,PH,Involucrin,M;TM=M;; 5.19
434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.19
447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, subfamily J, member 15; IRK;TM=Y;; 5.19
407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; Ribosomal_S14,ank,pkinase,death,none; 5.18
442200; AW590572; Hs.235768; ESTs; none,none; 5.18
446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A, member 6A; none;TM=Y;SS=M; 5.18
452690; AI536070; Hs.15085; ESTs; pou,homeobox,ig_chan,ANF_receptor; 5.18
419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR_ITPR,RyR,MIR;TM=Y;; 5.17
431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;; 5.16
418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M;; 5.16
407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta (Liddle syndrome); ASC;TM=Y;SS=M; 5.15
429500; X78565; Hs.289114; hexabrachion (tenascin C, cytotactin); EGF,fn3,fibrinogen_C,toxin_2,Keratin_B2;TM=M;SS=Y; 5.15
411984; NM_005419; Hs.72988; signal transducer and activator of transcription 2, 113kD; SH2,STAT,STAT_bind,STAT_prot;TM=M;; 5.15
433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 5.14
452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M;; 5.14
453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.14
427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; SRP14,TNFR_c6;SS=M; 5.14
430563; AA481269; ; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; ABC_tran,GTP_EFTU,ABC_membrane,none; 5.13
431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr;TM=Y;; 5.12
431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3; ER_lumen_recept;TM=M;SS=M; 5.12
417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarotene induced) 1; none,none; 5.11
418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase kinase 1; pkinase,CNH;TM=M;; 5.11
409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfamily, member 13; TNF;TM=Y;SS=M; 5.11
436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;; 5.09
411296; BE207307; Hs.10114; growth suppressor 1; 2OG-FeII_Oxy;TM=M;SS=M; 5.09
410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rrm;TM=M;; 5.09
404440; ; ; NM_021048:Homo sapiens melanoma antigen, family A, 10 (MAGEA10), mRNA. VERSION NM_021049.1 GI; MAGE;TM=M;; 5.08
424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none,none; 5.08
422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; arf,ras;TM=M;; 5.07
452222; AW806287; Hs.21432; SEX gene; Sema,TIG,PSI,GDI; 5.07
430300; U60805; Hs.238648; oncostatin M receptor; fn3;TM=Y;SS=M; 5.07
408369; R38438; Hs.182575; solute carrier family 15 (H??? transporter), member 2; PTR2;TM=Y;; 5.07
422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;SS=M; 5.06
449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain,none; 5.06
430024; AI808780; Hs.227730; integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 5.06
412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; HSP90,HATPase_c;TM=M;; 5.05
437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase,RIO1,none; 5.05
400296; AA305627; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y;; 5.04
446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3,none; 5.04
425262; D87119; Hs.155418; GS3955 protein; pkinase;SS=M; 5.04
414703; BE243877; Hs.76941; ATPase, Na? transporting, beta 3 polypeptide; Na_K-ATPase;TM=Y;SS=M; 5.03
434808; AF155108; Hs.256150; Homo sapiens, Similar to RIKEN cDNA 2810027O19 gene, clone MGC:14827, mRNA, complete cds; none;TM=M;; 5.03
425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member 21; death,TNFR_c6;TM=Y;SS=M; 5.03
449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none,none; 5.03
448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;; 5.02
413441; AI929374; Hs.75367; Src-like-adapter; SH2,SH3;TM=M;; 5.02
427618; NM_000760; Hs.2175; colony stimulating factor 3 receptor (granulocyte); fn3;TM=M;SS=M; 5.02
417666; AI345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M;; 5.02
429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); CDK5_activator,none; 5.01
445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; ras,arf,TK;SS=M; 5.01
426285; U20620; Hs.343581; karyopherin alpha 1 (importin alpha 5); Armadillo_seg,IBB;TM=M;; 5.01
421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4;TM=Y;SS=M; 5.01
424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; SH2,STAT,STAT_bind,STAT_prot,none; 5.00
425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-receptor type 1; Y_phosphatase,DSPc;TM=M;SS=M; 5.00
446946; AI878932; Hs.317; topoisomerase (DNA) I; Topoisomerase_I,Topoisomer_I_N,RrnaAD,Hanta_nucleocap;TM=M;; 4.99
413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); TPR,PDZ,WW,Guanylate_kin;TM=M;; 4.98
412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor); 7tm_1;TM=Y;SS=M; 4.98
400792; AA635062; ; Homo sapiens mRNA; cDNA DKFZp434O0515 (from clone DKFZp434O0515); zf-C3HC4,CARD,BIR;TM=M;; 4.98
417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related oncogene homolog; SH2,SH3,pkinase;TM=M;; 4.98
427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); vwa,integrin_A,FG-GAP;TM=Y;SS=M; 4.98
442080; AW444761; Hs.44565; ESTs; ank;; 4.97
454042; H22570; ; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 4.97
452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 4.96
416276; U41060; Hs.79136; LIV-1 protein, estrogen regulated; Peptidase_C4,Osteopontin,Zip;TM=Y;SS=M; 4.96
408847; AW290997; Hs.30348; ESTs; pkinase,ig,none; 4.96
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 4.95
450737; AW007152; Hs.203330; ESTs; trypsin,ldl_recept_a,none; 4.95
443354; AW970672; Hs.9247; protein kinase, AMP-activated, alpha 1 catalytic subunit; pkinase,RIO1;TM=M;; 4.94

414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M;; 4.94
424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD_Synth,Idh,Idh_C,pkinase;SS=M; 4.94
434206; AW136973; Hs.180479; ESTs, Weakly similar to S69890 mitogen inducible gene mig-2 [H.sapiens]; PH;TM=M;; 4.93
418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); 7tm_1,7tm_2;TM=Y;SS=M; 4.93
408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, partial cds; UvrD-helicase,RNB,Runt;TM=M;; 4.93
426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 4.92
424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; Ets,SAM_PNT;TM=M;; 4.92
414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; fn2,CIMR;TM=M;SS=M; 4.92
407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; ig;TM=Y;SS=M; 4.92
409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; DEAD,helicase_C,CARD;TM=M;; 4.91
416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); ig,ITAM,Zn_clus;TM=Y;SS=M; 4.91
404289; ; ; NM_002944*:Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA.; fn3,pkinase,DUF139;TM=Y;SS=M; 4.90
428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; Nramp;TM=Y;; 4.90
407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 4.89
432179; X75208; Hs.2913; EphB3; EPH_lbd,fn3,pkinase,SAM;TM=Y;SS=M; 4.89
401083; ; ; NM_016582*:Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM_016579.1 GI; PTR2;TM=Y;SS=M; 4.89
402211; AA811738; ; KIAA0430 gene product; ion_trans,K_tetra;TM=Y;; 4.88
421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polypeptide 4; pkinase,pkinase_C;TM=M;; 4.87
431810; X67155; Hs.270845; kinesin-like 5 (mitotic kinesin-like protein 1); kinesin;TM=M;; 4.86
425295; AA431366; Hs.37251; ESTs; pkinase,none; 4.86
424439; AA579535; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase;; 4.86
419168; AI336132; Hs.33718; Homo sapiens cDNA FLJ12641 fis, clone NT2RM4001953; none,none; 4.86
442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequence; K_tetra,DUF51,none; 4.86
425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;; 4.86
410293; AK000047; Hs.61960; hypothetical protein; K_tetra;TM=M;; 4.86
443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; C1q,Collagen;SS=M; 4.85
445903; AI347487; Hs.132781; class I cytokine receptor; fn3;TM=Y;; 4.85
427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a ligand); 7tm_1;TM=Y;SS=M; 4.85
428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); vwa,integrin_A,FG-GAP;TM=Y;SS=M; 4.84
445143; U29171; Hs.75852; casein kinase 1, delta; zf-C3HC4,Filamin,zf-B_box,NHL,pkinase,zf-MIZ;TM=M;; 4.82
427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;; 4.81
427857; AL133017; Hs.2210; hypothetical protein FLJ22865; myosin_head,IQ,zf-MYND;TM=M;SS=M; 4.81
422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); aldedh,aakinase;TM=M;; 4.81
414280; BE410769; Hs.75873; zyxin; LIM,ig,pkinase;TM=M;SS=M; 4.81
424570; AA343306; Hs.133511; ESTs; SH3,ank,none; 4.80
451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c,none; 4.80
402705; AA214618; ; activator of S phase kinase; AhpC-TSA;TM=M;SS=M; 4.80
410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3;TM=M;; 4.80
419972; AL041465; Hs.182982; golgin-67; none,none; 4.80
427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 4.80
413476; U25849; Hs.75393; acid phosphatase 1, soluble; LMWPc;TM=M;SS=M; 4.80
415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, receptor for (CD32); ig;TM=Y;; 4.79
402233; ; ; NM_030760*:Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA.; 7tm_1;TM=Y;SS=M; 4.79
448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; NusG;SS=M; 4.79
407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; pfkB;TM=M;; 4.79
405370; ; ; NM_005569*:Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA.; pkinase,LIM,PDZ;SS=M; 4.79
416498; U33632; Hs.79351; potassium channel, subfamily K, member 1 (TWIK-1); ion_trans;TM=Y;SS=M; 4.78
429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 4.78
424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase;TM=M;; 4.78
433133; AB027249; Hs.104741; PDZ-binding kinase; T-cell originated protein kinase; pkinase;TM=M;; 4.78
431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); none;TM=M;SS=Y; 4.78
417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; ig,abhydrolase; 4.78
450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 4.78
447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase;SS=M; 4.77
409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321); none;NA;NA; 4.77
446196; AI744888; Hs.149470; ESTs; zf-C3HC4,Sulfate_transp,STAS; 4.77
429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4;TM=Y;SS=M; 4.77
426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chloride transporters), member 7; none;TM=Y;; 4.77
425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); Armadillo_seg,IBB,DEAD,helicase_C,Sec63,DDT,PHD,bromodomain;TM=M;; 4.77
444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; DSPc;TM=M;; 4.77
452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702; GDI,7tm_1,none; 4.76
447207; AA442233; Hs.17731; hypothetical protein FLJ12892; none;TM=M;; 4.76
400846; ; ; sortilin-related receptor, L(DLR class) A repeats-containing (SORL1); EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.76
452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1,OATP_C;TM=Y;; 4.75
406809; AF000574; Hs.22405; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2; ig,Gemini_mov;TM=M;SS=M; 4.75
427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE;TM=M;; 4.75
444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHITE), member 1; ABC_tran,PRK,GBP;TM=Y;; 4.74
410406; AI969703; Hs.1466; glycerol kinase; FGGY,FGGY_C;TM=M;; 4.73
411653; AF070578; Hs.71168; Homo sapiens clone 24674 mRNA sequence; none;NA;NA; 4.73
437667; BE616412; Hs.286218; junctional adhesion molecule 1; none,HLH; 4.73
417781; BE279380; Hs.82563; KIAA0153 protein; TTL,Acyl_transf; 4.73
453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,ldl_recept_a,none; 4.73
412228; AW503785; Hs.73792; complement component (3d/Epstein Barr virus) receptor 2; sushi;TM=Y;SS=M; 4.73
418255; AW135405; Hs.37251; ESTs; pkinase,none; 4.73
413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; SDF;TM=Y;SS=M; 4.73
406906; Z25424; ; gb:H.sapiens protein-serine/threonine kinase gene, complete CDS.; none,none; 4.73
432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; Metallophos;TM=M;; 4.72
424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;SS=M; 4.72
422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; NDK,PH,Oxysterol_BP;SS=M; 4.71
426136; AW957239; ; gb:EST369309 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence; PP2C,none; 4.71
446203; Z47553; Hs.14286; flavin containing monooxygenase 5; FMO-like,pyr_redox;TM=Y;SS=M; 4.71
451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.71

424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y;; 4.70
424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; Idh,Idh_C,SH3,pkinase,UBA;TM=M;; 4.70
427206; NM_004586; Hs.173965; ribosomal protein S6 kinase, 90kD, polypeptide 3; none,none; 4.70
421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; EGF,F5_F8_type_C,laminin_G,Sulfate_transp,STAS,7tm_3,xan_ur_permease;TM=Y;SS=M; 4.70
413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); UQ_con;TM=M;; 4.70
405484; ; ; C3002124*:gi|12737280|ref|XP_006682.2| keratin 18 [Homo sapiens]||6633; none;SS=M; 4.70
401345; M83738; ; protein tyrosine phosphatase, non-receptor type 9; none;TM=M;; 4.70
416602; NM_006159; Hs.79389; nel (chicken)-like 2; EGF,vwc,TSPN;SS=Y; 4.69
412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 4.69
437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 4.69
432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;; 4.69
400843; ; ; NM_003105*:Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.68
433409; AI278802; Hs.25661; ESTs; pkinase,pkinase; 4.68
413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 4.68
430259; BE550182; Hs.127826; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 4.68
425761; AW664214; Hs.196729; ESTs; SH3,Ribosomal_S3Ae; 4.68
431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone COL04544; pkinase,Furin-like,Recep_L_domain,none; 4.68
419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subunit, non-ATPase, 11; CDK5_activator,PCI,none; 4.67
425966; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C;TM=M;; 4.67
408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 4.67
453476; AI640500; Hs.24633; SAM domain, SH3 domain and nuclear localisation signals, 1; SH3,SAM;SS=M; 4.67
412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; MARCKS;SS=M; 4.67
424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 fis, clone PLACE1001076; pkinase,Furin-like,Recep_L_domain,none; 4.66
446051; BE048061; Hs.37054; ephrin-A3; Ephrin,A_deamin,dsrm,z-alpha; 4.66
436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.66
408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, member 3; Y_phosphatase;TM=M;; 4.66
435542; AA687376; ; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.66
429682; NM_006306; Hs.211602; SMC1 (structural maintenance of chromosomes 1, yeast)-like 1; ABC_tran,SMC_N,SMC_C,KID;TM=M;; 4.66
417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 4.66
418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_C,AT_hook,SNF2_N;TM=M;; 4.65
415117; AF120499; Hs.78016; polynucleolide kinase 3'-phosphatase; Viral_helicase1;TM=M;; 4.65
418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA;SS=M; 4.65
426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;; 4.64
429263; AA019004; Hs.198396; ATP-binding cassette, sub-family A (ABC1), member 4; ABC_tran,SRP54;TM=Y;SS=M; 4.64
431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;; 4.63
435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none;TM=M;; 4.63
437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor); TIMP,pkinase,DAG_PE-bind,RBD; 4.63
413436; AF238083; Hs.68061; sphingosine kinase 1; DAGKc;TM=M;; 4.63
421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; efhand,ldl_recept_a;SS=M; 4.62
442590; AI002686; Hs.130313; ESTs; none,Y_phosphatase,Band_41,connexin; 4.62
416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding domain; efhand;SS=M; 4.62
423740; Y07701; Hs.293007; aminopeptidase puromycin sensitive; Peptidase_M1,Armadillo_seg; 4.61
429300; AB011108; Hs.198891; serine/threonine-protein kinase PRP4 homolog; pkinase;TM=M;; 4.60
447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.60
412942; AL120344; Hs.75074; mitogen-activated protein kinase-activated protein kinase 2; pkinase;TM=M;; 4.60
419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc;; 4.59
417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); EGF,lectin_c,sushi;TM=M;SS=M; 4.59
411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 4.59
434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;SS=M; 4.58
447312; AI434345; Hs.36908; activating transcription factor 1; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;; 4.58
435254; AW194689; Hs.30778; ESTs; pkinase,Bacterial_PQQ,none; 4.58
426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone HRC06741; Esterase,enolase,Peptidase_S9;TM=M;; 4.58
421685; AF189723; Hs.106778; ATPase, Ca transporting, type 2C, member 1; Cation_ATPase_C,Cation_ATPase_N,E1-E2_ATPase,Hydrolase,XPG_N;TM=Y;; 4.58
447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; fn3,ig,Y_phosphatase,MAM;TM=Y;SS=M; 4.58
427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 4.57
441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200; none,none; 4.57
409581; U66243; Hs.55039; mitogen-activated protein kinase 12; pkinase;SS=M; 4.57
423184; NM_004428; Hs.1624; ephrin-A1; Ephrin;TM=M;SS=M; 4.56
443920; AL037764; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 4.56
422627; BE336857; Hs.118787; transforming growth factor, beta-induced, 68kD; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.56
418869; AW516565; ; gb:xq01d05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone 3' similar to contains Alu repetitive element ;contains element MER11 repetitive element ;, mRNA sequence; none,RasGAP,WW,IQ; 4.56
430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus receptor; SPX,EXS;TM=Y;; 4.56
437157; BE048860; Hs.120655; ESTs; IRK,none; 4.55
422769; AA938905; Hs.120017; olfactory receptor, family 7, subfamily E, member 38 pseudogene; none,none; 4.55
457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDc;TM=M;; 4.55
434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PLACE1002962; 7tm_1,none; 4.55
421140; AA298741; Hs.102135; signal sequence receptor, delta (translocon-associated protein delta); none;TM=Y;SS=M; 4.55
406364; ; ; Target Exon; hexapep;TM=M;; 4.55
434682; AA827165; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig,none; 4.54
438939; H21012; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COL01963; F5_F8_type_C,pkinase,Ets,none; 4.54
433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; EF_TS,UBA;; 4.54
411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;SS=M; 4.54
408956; AK001868; Hs.49344; hypothetical protein FLJ11006; ion_trans;TM=Y;; 4.54
416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related); SH3;TM=M;; 4.53
410226; AI831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;; 4.53
422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); Sm;SS=M; 4.52
418355; L42563; Hs.1165; ATPase, H? transporting, nongastric, alpha polypeptide; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase;TM=Y;; 4.52
400261; ; ; Eos Control; ig,MHC_II_beta;TM=Y;SS=M; 4.52
444633; AF111713; Hs.286218; junctional adhesion molecule 1; ig;TM=Y;SS=M; 4.52
422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo sapiens cDNA, mRNA sequence; Sec7,PH,ANF_receptor,lig_chan,WD40,IRK; 4.52

400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 4.51
412604; AW978324; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;; 4.51
448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin;TM=M;; 4.51
457906; AW975939; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,pkinase; 4.51
456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 4.51
429690; AW956329; Hs.23721; ESTs; none,sugar_tr,Ribosomal_S25; 4.50
424618; L29472; Hs.1802; major histocompatibility complex, class II, DO beta; ig,MHC_II_beta;TM=Y;SS=M; 4.50
444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 4.50
405490; ; ; NM_031414:Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA.; pkinase,TUDOR;TM=M;; 4.50
424494; U78575; Hs.149255; phosphatidylinositol-4-phosphate 5-kinase, type I, alpha; PIP5K;SS=M; 4.50
441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 4.50
443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22_Claudin,none; 4.50
410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; SH2,Y_phosphatase,DSPc;TM=M;; 4.50
429556; AW139399; Hs.98988; ESTs; none;TM=M;; 4.50
458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 4.49
425209; AL049761; Hs.155140; caseln kinase 2, alpha 1 polypeptide; pkinase,ABC1;TM=M;; 4.49
425695; NM_005401; Hs.159238; protein tyrosine phosphatase, non-receptor type 14; Y_phosphatase,Band_41,DSPc;TM=M;; 4.49
424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;; 4.49
412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPc;SS=M; 4.48
400755; AA635062; ; Homo sapiens mRNA; cDNA DKFZp434O0515 (from clone DKFZp434O0515); zf-C3HC4,CARD,BIR;TM=M;; 4.48
425566; AW162943; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 4.48
410151; X15723; Hs.59242; paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein); Peptidase_S8,P;TM=Y;SS=M; 4.48
423536; L22075; Hs.1666; guanine nucleotide binding protein (G protein), alpha 13; UCR_hinge,G-alpha,arf;TM=M;; 4.48
424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2,HRM;TM=Y;SS=M; 4.48
427878; C05766; Hs.181022; CGI-07 protein; none,zf-C2H2; 4.48
443991; NM_002250; Hs.10082; potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4; CaMBD,SK_channel,Ion_trans;TM=Y;SS=M; 4.48
422605; H16646; Hs.118666; hypothetical protein PP591; PAPS_reduct,MoCF_biosynth;; 4.47
410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]; SH3,PDZ,Guanylate_kin,none; 4.47
434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M;; 4.47
410032; BE065985; ; gb:RC3-BT0319-120200-014-a09 BT0319 Homo sapiens cDNA, mRNA sequence; abhydrolase_2,none; 4.46
423078; M35198; Hs.123125; integrin, beta 6; integrin_B,EGF,pp-binding;TM=Y;SS=M; 4.46
400263; ; ; Eos Control; GTP_EFTU,EFG_C,GTP_EFTU_D2,serpin;TM=M;; 4.46
441406; Z45957; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M;; 4.45
434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; none;TM=M;; 4.45
413227; M79082; ; ESTs; none,none; 4.45
441321; H17182; Hs.7771; B-cell associated protein; Band_7;TM=M;; 4.45
457194; H20669; Hs.35406; ESTs, Highly similar to unnamed protein product [H.sapiens]; none,pkinase,PBD; 4.45
414745; AA160511; Hs.5326; amino acid system N transporter 2; porcupine; none,none; 4.45
404276; ; ; NM_002944*:Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA.; fn3,pkinase,DUF139;TM=Y;SS=M; 4.45
426966; AI493134; ; sclerostin; DAN;TM=M;SS=M; 4.45
408873; AL046017; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none,none; 4.44
426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (from clone DKFZp586B0220); pkinase,none; 4.44
432798; AA565309; Hs.194015; ESTs; Integrin_B,Sema,PSI,TIG,none; 4.44
439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.44
417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor,none; 4.43
452098; AI858183; ; gb:wi46a12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone 3' similar to contains Alu repetitive element;, mRNA sequence; SH3,none; 4.43
426874; N67325; Hs.347487; ESTs; SH3,TonB_boxC,none; 4.43
422714; AB018335; Hs.119387; KIAA0792 gene product; DUF221;TM=Y;SS=M; 4.42
410741; Z11695; Hs.324473; mitogen-activated protein kinase 1; pkinase,none; 4.42
432193; AA372264; Hs.273193; hypothetical protein FLJ10706; pkinase;TM=M;; 4.41
409506; NM_006153; Hs.54589; NCK adaptor protein 1; SH2,SH3;TM=M;; 4.41
429390; AB040942; Hs.201500; KIAA1509 protein; none;TM=M;; 4.41
421859; AA356620; Hs.108947; KIAA0050 gene product; ank,PH,ArfGap;SS=M; 4.41
451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none,none; 4.41
421748; NM_014718; Hs.107809; KIAA0726 gene product; cadherin;TM=Y;; 4.40
410416; BE410072; Hs.63304; protein phosphatase methylesterase-1; none;TM=M;; 4.40
450457; AA367701; Hs.6639; KIAA1624 protein; none;TM=M;SS=M; 4.40
433029; NM_014322; Hs.279926; opsin 3 (encephalopsin); 7tm_1,Monooxygenase;TM=Y;SS=M; 4.40
408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;; 4.40
421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1;TM=Y;SS=M; 4.40
440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; SPRY,BAG,UPF0001; 4.40
451154; AA015879; Hs.33536; ESTs; TIMP,none; 4.40
433895; AI287912; Hs.3628; mitogen-activated protein kinase kinase kinase kinase 4; pkinase,zf-C4,CNH,ERM;TM=M;; 4.40
422034; AC006486; Hs.333069; Ets2 repressor factor; Ets;TM=M;; 4.39
444009; AI380792; Hs.135104; ESTs; TNFR_c6,TIL,none; 4.39
420020; BE295866; Hs.94382; adenosine kinase; pfkB;SS=M; 4.39
416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, complete cds; none;TM=Y;SS=M; 4.39
417655; AA780791; Hs.14014; hypothetical protein FLJ14813; pkinase,pkinase_C;TM=M;; 4.39
402915; ; ; ENSP00000202587*:Bicarbonate transporter-related protein BTR1.; HCO3_cotransp;TM=Y;; 4.39
453199; AI336266; Hs.32353; mitogen-activated protein kinase kinase kinase 4; pkinase;TM=M;; 4.38
416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 4.38
453672; U73531; Hs.34526; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 4.38
437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365O12.1 [H.sapiens]; GPS,7tm_2;TM=Y;; 4.38
420039; NM_004605; Hs.94581; sulfotransferase family, cytosolic, 2B, member 1; Sulfotransfer;SS=M; 4.38
412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm_1,none; 4.38
452203; X57522; ; transporter 1, ATP-binding cassette, sub-family B (MDR/TAP); ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 4.37
425317; AW205118; Hs.210546; interleukin 21 receptor; none;TM=Y;SS=M; 4.37
432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.37
424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y79AA1001384, highly similar to Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA; none,none; 4.37
434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;; 4.37
412596; AA161219; Hs.799; diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor); EGF;TM=Y;SS=M; 4.36
440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; fn3;SS=M; 4.36

432987; AI864771; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none;TM=Y;SS=M; 4.36
436943; AA773838; Hs.5353; caspase 10, apoptosis-related cysteine protease; ICE_p10,ICE_p20,DED;TM=M;; 4.36
457897; AI356125; Hs.345168; ESTs, Weakly similar to HXA2_HUMAN HOMEOBOX PROTEIN HOX-A2 [H.sapiens]; homeobox;NA;NA; 4.36
406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); Sema,pkinase,TIG,PSI,none; 4.36
413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylinositol-specific); SH2,SH3,C2,PH.PI-PLC-Y,PI-PLC-X,PDGF;SS=M; 4.35
408101; AW968504; Hs.123073; CDC2-related protein kinase 7; none,none; 4.35
414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); Man-6-P_recep;TM=M;SS=M; 4.35
425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; aldo_ket_red,none; 4.35
438937; AW952654; Hs.244624; ESTs; EPH_lbd,pkinase,fn3,SAM,none; 4.35
412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; none,lectin_c; 4.35
436540; BE397032; Hs.14468; hypothetical protein MGC14226; rrm,7tm_1,SNF;TM=M;; 4.34
435267; N23797; Hs.110114; ESTs; none,Syja_N,Exo_endo_phos; 4.34
405616; ; ; Target Exon; none,SH3,BAR; 4.34
432141; BE410964; Hs.272736; nuclear receptor binding protein; pkinase;TM=M;; 4.33
417927; R73095; Hs.24122; ESTs; none,pkinase; 4.33
429849; U33053; Hs.2499; protein kinase C-like 1; pkinase,pkinase_C,HR1;TM=M;; 4.33
425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;; 4.33
453863; X02544; Hs.572; orosomucoid 1; lipocalin,aldedh,ubiquitin,IRK;SS=M; 4.33
400847; ; ; NM_003105*:Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.33
414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_PI4_kinase;TM=M;; 4.33
413858; NM_001610; Hs.75589; acid phosphatase 2, lysosomal; acid_phosphat;TM=Y;SS=M; 4.33
442539; AL119506; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP,adenylatekinase; 4.33
419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4;TM=M;; 4.32
436703; AW880614; Hs.146381; RNA binding motif protein, X chromosome; rrm,SH3,PH,CH,RhoGEF; 4.32
414899; AW975433; Hs.36288; ESTs; pkinase,SH2,SH3,none; 4.32
444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; ASC,death,TNFR_c6; 4.31
415135; AW673559; Hs.78040; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; ER_lumen_recept,none; 4.31
444070; NM_015367; Hs.10267; MIL1 protein; Bcl-2;TM=Y;; 4.31
422611; AA158177; Hs.118722; fucosyltransferase 8 (alpha (1,6) fucosyltransferase); SH3,K-box;TM=M;SS=Y; 4.31
437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; bromodomain;TM=M;; 4.30
440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; sugar_tr;TM=Y;SS=M; 4.30
414080; AA135257; Hs.47783; B aggressive lymphoma gene; A1pp;TM=M;; 4.30
415072; BE253687; Hs.77876; Homo sapiens, clone IMAGE:3461982, mRNA, partial cds; Metallophos,Armadillo_seg;TM=M;; 4.30
442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 4.30
432328; AI572739; Hs.195471; 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; PGAM,6PF2K;TM=M;; 4.29
439490; AW249197; Hs.100043; ESTs, Weakly similar to A46302 PTB-associated splicing factor, long form [H.sapiens]; none;TM=M;; 4.29
422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (from clone DKFZp761E212); none,Na_H_Exchanger; 4.29
415214; AI445236; Hs.125124; EphB2; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 4.29
430316; NM_000875; Hs.239176; insulin-like growth factor 1 receptor; fn3,Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 4.29
429099; BE439952; Hs.196177; phosphorylase kinase, gamma 2 (testis); pkinase,Bac_DNA_binding;TM=M;; 4.29
425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding,PAH,BAH,bromodomain,PHD,SET;TM=M;; 4.28
437603; AW979259; Hs.293673; ESTs; death,none; 4.28
439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triphosphate pyrophosphatase); Ham1p_like;TM=M;; 4.28
424512; X53002; Hs.149846; integrin, beta 5; integrin_B,EGF;TM=Y;SS=M; 4.28
442980; AA857025; Hs.8878; kinesin-like 1; kinesin,Luteo_ORF3,DUF164;TM=M;; 4.28
420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetraspan NET-7); transmembrane4;TM=Y;SS=M; 4.27
409582; R27430; Hs.271565; ESTs; none,Neur_chan_LBD,Neur_chan_memb; 4.27
439096; AA830185; ; ESTs; ras,none; 4.27
414561; AI064813; Hs.195155; Homo sapiens amino acid transport system N2 (SN2) mRNA, complete cds; Aa_trans;TM=Y;; 4.27
411835; U29343; Hs.72550; hyaluronan-mediated motility receptor (RHAMM); bZIP;SS=M; 4.27
428781; AF164799; Hs.193384; putative 28 kDa protein; pkinase,DAG_PE-bind,pkinase_C,OPR;SS=M; 4.27
430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4,zf-RanBP,pkinase; 4.27
415149; X12451; Hs.78056; cathepsin L; Peptidase_C1;SS=M; 4.26
444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 4.26
402328; ; ; Target Exon; pkinase;TM=M;; 4.26
416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none,none; 4.26
420942; H03514; Hs.15589; ESTs; none,pkinase; 4.26
453902; BE502341; Hs.3402; ESTs; none,none; 4.26
425505; AL036456; ; gb:DKFZp564D2062_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564D2062 5', mRNA sequence; arf,G-alpha,none; 4.26
427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor 3A; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 4.26
432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met-related tyrosine kinase); pkinase,Sema,PSI,TIG,A4_EXTRA;TM=M;SS=M; 4.26
417007; AF224741; Hs.80768; chloride channel 7; CBS,voltage_CLC;TM=Y;; 4.26
447960; AW954377; Hs.26412; ring finger protein 26; zf-C3HC4;TM=Y;SS=M; 4.26
442300; AI765908; Hs.129166; ESTs; none;SS=M; 4.25
421856; NM_016447; Hs.108931; MAGUK protein p55T; Protein Associated with Lins 2; SH3,PDZ,Guanylate_kin,L27;TM=M;; 4.25
452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PLACE1010076; pkinase,Activin_recp,none; 4.25
422451; AA310753; Hs.42491; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; PDZ,SH2,STAT,STAT_bind,STAT_prot,none; 4.25
453955; AW579207; Hs.304666; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; fn3,ig,MAM,none; 4.25
457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substrate; SH3;TM=M;; 4.25
419133; U46116; Hs.89627; protein tyrosine phosphatase, receptor type, G; fn3,Y_phosphatase,carb_anhydrase,DSPc;TM=Y;SS=M; 4.25
419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; aa_permeases;TM=Y;SS=M; 4.25
415198; AW009480; Hs.943; natural killer cell transcript 4; none;TM=M;; 4.24
416440; AI823912; Hs.79335; Homo sapiens, Similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1, clone MGC:15280, mRNA, complete cds; SWIB;TM=M;; 4.24
419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothetical protein [H.sapiens]; none,spectrin,SH3,PH,CH; 4.24
449444; AW818436; Hs.23590; solute carrier family 16 (monocarboxylic acid transporters), member 4; none;TM=Y;SS=M; 4.24
433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carbOpept,Propep_M14;SS=M; 4.24
442213; N36110; Hs.305971; solute carrier family 2 (facilitated glucose transporter), member 10; sugar_tr;TM=Y;SS=M; 4.24
412681; AW983655; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M;; 4.24
424653; AW977534; Hs.151469; calcium/calmodulin-dependent serine protein kinase (MAGUK family); none,none; 4.24
421066; AU076725; Hs.101408; branched chain aminotransferase 2, mitochondrial; aminotran_4;; 4.23

428338; AF147765; Hs.232093; ESTs; fn2,CIMR;TM=M;SS=M; 4.23
443329; BE262943; Hs.9234; hypothetical protein MGC1936; none;TM=Y;SS=M; 4.23
432314; AA533447; Hs.312989; ESTs; Xlink,none; 4.23
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 4.23
454166; AW993356; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 4.23
442596; AI457102; Hs.347970; Human glucose transporter pseudogene; none,none; 4.23
442549; AI751601; Hs.8375; TNF receptor-associated factor 4; MATH,zf-TRAF,zf-C3HC4;SS=M; 4.22
424154; AF026004; Hs.141660; chloride channel 2; voltage_CLC,CBS,EPO_TPO,PC_rep; 4.22
433419; AI830342; Hs.211272; ESTs; transmembrane4,none; 4.22
421921; H83363; Hs.6820; translocase of inner mitochondrial membrane 10 (yeast) homolog; zf-Tim10_DDP,efhand,CH,spectrin,serpin;TM=M;; 4.22
445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK,none; 4.22
424812; AF059252; Hs.153299; DOM-3 (C. elegans) homolog Z; none;TM=M;; 4.22
410668; BE379794; Hs.65403; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 4.22
416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic acid transporters), member 6; none,none; 4.22
418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;; 4.21
447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; none,none; 4.21
400208; ; ; Eos Control; FCH,RhoGAP,SH3;TM=M;; 4.21
405369; ; ; NM_005569*:Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA.; pkinase,LIM,PDZ;SS=M; 4.21
445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M;; 4.21
441208; AI339704; Hs.150401; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ion_trans,RYDR_ITPR,MIR,none; 4.21
427217; AA399272; Hs.144341; ESTs; ANP,GHMP_kinases,none; 4.21
400845; ; ; NM_003105*:Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.21
422667; H25642; ; ESTs; FMO-like,FMO-like; 4.21
450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus]; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.20
448950; AF288687; Hs.9275; CGI-152 protein; E1-E2_ATPase,Hydrolase;TM=Y;; 4.20
408634; AW407254; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none,none; 4.20
422335; AA375957; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none,none; 4.20
426754; NM_014264; Hs.172052; serine/threonine kinase 18; pkinase;TM=M;; 4.20
435810; BE349853; Hs.2785; keratin 17; zf-Tim10_DDP,SH2,SH3,pkinase,PH,BTK,Ribosomal_L44; 4.20
446143; BE245342; Hs.306079; sec61 homolog; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 4.20
426626; AI124572; Hs.323879; inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; zf-C2H2;TM=M;; 4.20
403716; ; ; Target Exon; Adap_comp_sub,PDZ,DEP,DIX,Dishevelled,hexapep,W2,ABC_tran; 4.19
415749; BE262529; Hs.78771; phosphoglycerate kinase 1; PGK,none; 4.19
434599; AB002313; Hs.3989; plexin B2; PSI,Sema,TIG;NA;NA; 4.19
412600; L28824; Hs.74101; spleen tyrosine kinase; SH2,pkinase;; 4.19
416738; N29218; Hs.40290; ESTs; ABC_tran,ABC_membrane,none; 4.19
410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD,helicase_C,PRK,AIP3;TM=M;; 4.19
431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none,none; 4.19
407305; AA715284; ; gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens cDNA clone similar to contains Alu repetitive element;, mRNA sequence; pkinase,integrin_B,Sema,PSI,TIG,none; 4.18
452880; AA029332; Hs.87549; ESTs; none,integrin_B; 4.18
428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (yeast APC11 homolog); none;SS=M; 4.18
421964; X73079; Hs.288579; polymeric immunoglobulin receptor; ig,Cobalamin_bind;TM=M;SS=M; 4.18
409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;; 4.18
421790; AW896201; Hs.22654; sodium channel, voltage-gated, type I, alpha polypeptide; ion_trans,IQ,PEP-utilizers_C;TM=Y;; 4.18
429668; AA626142; Hs.179991; ESTs, Weakly similar to S28942 protein kinase C [H.sapiens]; none,none; 4.18
443068; AI188710; ; ESTs; Endonuclease,pkinase,Activin_recp,none; 4.18
418827; BE327311; Hs.47166; HT021; none;TM=M;; 4.18
447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine protease; ICE_p10,ICE_p20,DED;TM=M;; 4.18
429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M;; 4.18
422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; none,none; 4.18
438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ;SS=M; 4.18
413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like 1; SH2,SAM,Exo_endo_phos;SS=M; 4.18
424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,IRK;TM=M;; 4.17
421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none,none; 4.17
431544; AK000770; Hs.299329; Homo sapiens cDNA FLJ20763 fis, clone COL09911; none,none; 4.17
413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; CBS,IMPDH_C,IMPDH_N,NPD;TM=M;; 4.17
452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA_topoisoIV,K-box;TM=M;; 4.17
425606; U52112; Hs.158331; renin-binding protein; none;; 4.16
416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recep_L_domain,fn3,none; 4.16
402447; ; ; C1000201:gi|204416|gb|AAA02627.1| (L05195) fructose transporter [Rattus norvegicus] gi|44; none;TM=Y;SS=M; 4.16
452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; Euk_porin;TM=M;SS=M; 4.15
426395; BE151985; Hs.5722; hypothetical protein FLJ23316; pkinase,none; 4.15
404140; ; ; NM_006510:Homo sapiens ret finger protein (RFP), transcript variant alpha, mRNA.; zf-C3HC4,SPRY,zf-B_box;SS=M; 4.15
432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate synthase 2; APS_kinase,ATP-sulfurylase;TM=M;; 4.15
405516; ; ; ENSP00000200457*:Thyroid receptor interacting protein 6 (TRIP6) (OPA-interactingprotein 1) (Zyxin related protein 1) (ZRP-1).; LIM;TM=M;; 4.15
448390; AL035414; Hs.21068; hypothetical protein; FGGY_C;TM=M;; 4.15
435732; AF229178; Hs.123136; leucine rich repeat and death domain containing protein; none,none; 4.15
414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;; 4.15
411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor, pi; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 4.14
424339; BE257148; Hs.145416; endoglycan; none;TM=Y;SS=M; 4.14
427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog; ig,pkinase;TM=Y;SS=M; 4.14
440524; R71264; Hs.16798; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.14
436115; AW512033; Hs.102004; ESTs; pkinase,none; 4.14
447050; NM_016314; Hs.17200; STAM-like protein containing SH3 and ITAM domains 2; SH3,VHS,UIM;SS=M; 4.14
418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 4.14
420727; H75701; Hs.99886; complement component 4-binding protein, beta; sushi;SS=M; 4.14
433075; NM_002959; ; sortilin 1; Exo_endo_phos,Atrophin-1,BNR,Kelch;TM=M;; 4.14
422783; AA598956; Hs.120439; ethanolamine kinase; Choline_kinase;TM=Y;; 4.14
410726; AI623859; Hs.15936; ESTs; pkinase,pro_isomerase,none; 4.14

417903; NM_002342; Hs.1116; lymphotoxin beta receptor (TNFR superfamily, member 3); TNFR_c6;TM=M;SS=M; 4.14
428307; W27393; Hs.183648; protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1; SAM,SH3,HS1_rep; 4.14
442434; AA995787; Hs.129583; ESTs; IRK,none; 4.13
438361; AA805666; Hs.146217; Homo sapiens cDNA: FLJ23077 fis, clone LNG05840; pkinase,pkinase_C,none; 4.13
445580; AF167572; Hs.12912; skb1 (S. pombe) homolog; none;SS=M; 4.13
421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm_1;TM=M;; 4.13
400252; ; ; NM_004651*:Homo sapiens ubiquitin specific protease 11 (USP11), mRNA. substrate 1 (PTPNS1), mRNA.; UCH-1,UCH-2;TM=M;; 4.13
446641; AL049229; Hs.15787; Homo sapiens mRNA; cDNA DKFZp564O1016 (from clone DKFZp564O1016); none,pkinase,PBD; 4.13
400209; ; ; NM_001666:Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA. VERSION NM_006083.2 GI; FCH,RhoGAP,SH3;TM=M;; 4.13
429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm,BAG;SS=M; 4.13
411826; AW947946; Hs.26706; CGI-121 protein; none,DSPc; 4.13
423189; M59371; Hs.171596; EphA2; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 4.12
413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; integrin_B,Glyco_hydro_56;SS=M; 4.12
414874; D26351; Hs.77515; inositol 1,4,5-triphosphate receptor, type 3; ion_trans,MIR,RYDR_ITPR;TM=Y;; 4.12
432047; NM_016247; Hs.272380; interphotoreceptor matrix proteoglycan 200; EGF,SEA;TM=Y;SS=M; 4.12
451820; AW058357; Hs.199248; ESTs; 7tm_1;TM=Y;SS=M; 4.12
445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; zf-C2H2,BTB,K_tetra,WD40,Syntaxin; 4.12
424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK-2); pkinase,Activin_recp;TM=M;SS=M; 4.12
405110; ; ; C7000199:gi|12643960|sp|Q9Y6T7|KDGB_HUMAN DIACYLGLYCEROL KINASE, BETA (DIGLYCERIDE KINASE :; none,none; 4.12
441026; AW179058; Hs.99858; ribosomal protein L7a; pkinase,LRR,LRRCT,Ribosomal_L7Ae,none; 4.11
443142; AI696513; Hs.108705; protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform; HEAT,Vitellogenin_N,HEAT_PBS;SS=M; 4.11
450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg;TM=M;; 4.11
459601; AL044470; Hs.270604; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none,SH3,PGAM,UBA; 4.10
417300; AI765227; Hs.55610; solute carrier family 30 (zinc transporter), member 1; Cation_efflux;TM=Y;SS=M; 4.10
427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (from clone DKFZp564N0763); none,spectrin,SH3,PH,CH; 4.10
416239; AL038450; Hs.48948; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,none; 4.10
429311; AF080157; Hs.198998; conserved helix-loop-helix ubiquitous kinase; pkinase,none; 4.10
412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); Exo_endo_phos,Atrophin-1,BNR,Kelch;TM=M;; 4.10
418420; AW604405; Hs.324874; hypothetical protein MGC3079; Phosphodiest;TM=Y;; 4.10
434396; AA632270; Hs.162851; Homo sapiens cDNA FLJ14317 fis, clone PLACE3000401; pkinase,none; 4.10
454438; AA224053; Hs.172405; cell division cycle 27; SPRY,7tm_3,ANF_receptor; 4.10
439578; AW263124; Hs.315111; nuclear receptor co-repressor/HDAC3 complex subunit; WD40;TM=M;; 4.10
451995; AI827431; Hs.224645; ESTs, Weakly similar to IF16_HUMAN GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 [H.sapiens]; none,PAAD_DAPIN,HIN; 4.10
420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TiT3 complex); ITAM;TM=M;SS=M; 4.10
442942; AW167087; Hs.131562; ESTs; pkinase,none; 4.09
428187; AI687303; Hs.285529; G protein-coupled receptor 49; 7tm_1,none; 4.09
418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function); Phosphodiest;TM=Y;SS=M; 4.09
416445; AL043004; Hs.79337; KIAA0135 protein; pkinase,PAS;TM=M;; 4.08
427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2; pkinase;TM=M;; 4.08
403608; ; ; C3001199:gi|7494834|pir||T15308 hypothetical protein B0286.2 - Caenorhabditis elegans||41; 7tm_1,7tm_2,GPS,WIF;TM=Y;SS=M; 4.08
427177; AB006537; Hs.173880; interleukin 1 receptor accessory protein; ig,TIR;TM=Y;SS=M; 4.08
401241; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 4.07
444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase Rsp5; potential epithelial sodium channel regulator; WW,HECT,RNA_pol_A,none; 4.07
448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;; 4.06
426006; R49031; Hs.22627; ESTs; pkinase,TBC; 4.06
434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;; 4.06
408761; AA057264; Hs.238936; ESTs, Weakly similar to (defline not available 7496841) [C.elegans]; 7tm_1,none; 4.05
425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;SS=M; 4.05
413109; AW389845; Hs.110855; ESTs; PHO4,none; 4.05
426457; AW894667; Hs.169965; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2;TM=M;; 4.05
435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-Hacid_DH_C;TM=M;; 4.04
429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase); CARD,ICE_p10,ICE_p20;SS=M; 4.04
444378; R41339; Hs.12569; ESTs; ig,pkinase,LRR,LRRNT,LRRCT,none; 4.04
449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; none;TM=Y;SS=M; 4.04
427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm_1,none; 4.04
413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-related family, member 3; none,START; 4.04
418540; AI821597; Hs.90877; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ank,CAP_GLY,7tm_1; 4.03
442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rrm,IRK;SS=M; 4.02
448659; AF191838; Hs.21712; TANK-binding kinase 1; pkinase;TM=M;; 4.02
412935; BE267045; Hs.75064; tubulin-specific chaperone c; none;; 4.02
414844; AA296874; Hs.77494; deoxyguanosine kinase; dNK;; 4.02
445817; NM_003642; Hs.13340; histone acetyltransferase 1; none;TM=M;; 4.02
426728; NM_007118; Hs.171957; triple functional domain (PTPRF interacting); SH3,ig,pkinase,PH,spectrin,RhoGEF;TM=M;; 4.02
420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 4.02
405102; ; ; C15001220*:gi|4469558|gb|AAD21311.1| (AF126008) breast cancer nuclear receptor-binding auxi; DAG_PE-bind,PH,RhoGEF,DC1;SS=M; 4.02
439964; AI732902; Hs.124652; Homo sapiens cDNA FLJ12376 fis, clone MAMMA1002494; pkinase,none; 4.01
429680; AL035754; Hs.2474; toll-like receptor 1; LRR,LRRCT,TIR;TM=M;SS=M; 4.01
453891; AB037751; Hs.36353; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1035904; none,none; 4.01
426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 3.99
424232; AB015982; Hs.143460; protein kinase C, nu; pkinase,DAG_PE-bind,PH;TM=M;; 3.99
408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none,none; 3.98
449517; AW500106; Hs.23643; serine/threonine protein kinase MASK; pkinase;TM=M;; 3.98
404185; ; ; Target Exon; sugar_tr;TM=Y;SS=M; 3.98
441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; none;TM=M;; 3.98
429638; AI916662; Hs.211577; kinectin 1 (kinesin receptor); bZIP,Tropomyosin,spectrin,LBP_BPI_CETP,B56,M;TM=Y;SS=M; 3.97
417386; AL037228; Hs.82043; D123 gene product; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 3.97
452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; MORN,sugar_tr;TM=Y;SS=M; 3.96
417183; R52089; Hs.172717; ESTs; pkinase,LRRCT,ig,LRR,LRRNT,none; 3.95
439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; none;TM=M;; 3.94
424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;; 3.94
422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, subfamily J, member 2; IRK;TM=Y;; 3.94

450746; D82673; Hs.278589; general transcription factor II, i; none,SH3_PX; 3.94
418516; NM_006218; Hs.85701; phosphoinositide-3-kinase, catalytic, alpha polypeptide; PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B,none; 3.94
414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone LNG09846; none;NA;NA; 3.93
416537; T99086; Hs.144904; nuclear receptor co-repressor 1; myb_DNA-binding,RNA_pol_A,none; 3.93
450747; AI064821; Hs.318535; ESTs, Highly similar to 1818357A EWS gene [H.sapiens]; rrm,zf-RanBP,GAS2; 3.93
444825; AW167613; ; mitogen-activated protein kinase kinase kinase 8; pkinase;TM=M;; 3.93
408354; AI382803; Hs.159235; ESTs; none,none; 3.93
453945; NM_005171; Hs.36908; activating transcription factor 1; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;; 3.93
428532; AF157326; Hs.184786; TBP-interacting protein; Armadillo_seg,VHS,HEAT;TM=M;; 3.92
413967; AW204431; Hs.117853; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Armadillo_seg,IBB,PHD,DDT,none; 3.91
415906; AI751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone HRC02860; Ephrin,none; 3.91
450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 3.91
440255; AI932285; Hs.160569; ESTs; none,pkinase; 3.90
421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;; 3.90
433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1;SS=M; 3.90
433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M;; 3.90
419609; U46415; Hs.270379; gb:HSU46415 Human pancreatic cancer cell line Patu 8988t Homo sapiens cDNA clone xs476, mRNA sequence; PWWP,none; 3.90
433198; AA992841; Hs.27263; KIAA1458 protein; none,none; 3.89
407721; Y12735; Hs.38018; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3; pkinase;TM=M;; 3.89
427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none;TM=M;; 3.89
453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; none,none; 3.89
446329; NM_013272; Hs.14805; solute carrier family 21 (organic anion transporter), member 11; kazal,OATP_N,OATP_C;TM=Y;SS=M; 3.89
429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;; 3.88
432074; AA525248; Hs.149723; ESTs; Y_phosphatase,none; 3.88
435143; R12375; Hs.194600; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 3.87
423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 3.87
428474; AB023182; Hs.184523; KIAA0965 protein; pkinase;TM=M;; 3.87
419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT2RP2002066, highly similar to Rattus norvegicus transmembrane receptor Unc5H2 mRNA; death,ZU5;SS=M; 3.86
415457; AW081710; Hs.7369; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; MORN,sugar_tr;TM=Y;SS=M; 3.86
447061; D86964; Hs.17211; dedicator of cyto-kinesis 2; SH3;TM=M;; 3.86
426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M;; 3.86
451961; NM_003800; Hs.27345; RNA guanylyltransferase and 5'-phosphatase; mRNA_cap_enzyme,DSPc,DNA_ligase,mRNA_cap_C;TM=M;; 3.86
417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-receptor type 2; Y_phosphatase;TM=Y;; 3.86
446874; AW968304; Hs.56156; ESTs; none,RGS; 3.85
418630; AI351311; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; pkinase,none; 3.85
416140; AI918035; Hs.301198; roundabout (axon guidance receptor, Drosophila) homolog 1; none,none; 3.85
425474; Z48054; Hs.158084; peroxisome receptor 1; TPR;TM=M;; 3.85
413073; AL038165; Hs.75187; translocase of outer mitochondrial membrane 20 (yeast) homolog; MAS20,zf-A20,VPS9;TM=M;SS=M; 3.85
411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;; 3.84
428782; X12830; Hs.193400; interleukin 6 receptor; fn3,ig;TM=Y;SS=M; 3.84
450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig;TM=Y;SS=M; 3.84
433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine protease; CARD,ICE_p10,ICE_p20;SS=M; 3.83
440332; AI218517; Hs.188051; ESTs; fn3,pkinase,SAM,EPH_lbd,none; 3.83
445803; AV655264; Hs.4283; ESTs; pkinase,RGS,PH,myosin_head,Myosin_tail; 3.83
435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;; 3.83
414991; C17898; ; gb:C17898 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-554E10 5', mRNA sequence; Zip,none; 3.83
423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage); fn3;TM=Y;SS=M; 3.82
419088; AI538323; Hs.52620; integrin, beta 8; integrin_B,none; 3.82
411704; AI499220; Hs.71573; hypothetical protein FLJ10074; pkinase;TM=M;; 3.82
459346; AW510557; Hs.258016; EST; none;TM=M;; 3.82
445330; R52656; Hs.21691; ESTs; 7tm_1,none; 3.82
451452; BE560065; Hs.26433; dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase); Glycos_transf_4;TM=Y;SS=M; 3.81
405545; ; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.81
448165; NM_005591; Hs.20555; meiotic recombination (S. cerevisiae) 11 homolog B; Metallophos,Ribosomal_L15e;SS=M; 3.81
416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 3.80
415444; BE247295; Hs.78452; solute carrier family 20 (phosphate transporter), member 1; PHO4,LIM;TM=M;; 3.80
421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg;SS=M; 3.80
438581; AW977766; Hs.292133; ESTs, Moderately similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,RIO1,none; 3.79
439199; R40373; Hs.26299; ESTs; ion_trans,none; 3.78
450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; TNFR_c6;TM=Y;SS=M; 3.78
417691; AU076610; Hs.82399; low density lipoprotein receptor defect C complementing; none;SS=M; 3.78
430355; NM_006219; Hs.239818; phosphoinositide-3-kinase, catalytic, beta polypeptide; PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B;TM=M;; 3.78
448119; H38587; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 3.78
442013; AA506476; Hs.10600; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for cysteine desulfurase, two genes for novel proteins and the gene for the splicing factor CC1.3 with a second isoform (CC1.; none,none; 3.77
425481; AW978162; Hs.18571; ESTs; none,Oxysterol_BP; 3.77
411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA1330 protein [H.sapiens]; RNA_pol_A,ig,MHCK_EF2_kinase;SS=M; 3.77
426866; U02330; Hs.172816; neuregulin 1; Peptidase_M49,EGF,ig,Neuregulin;TM=M;; 3.77
430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 3.77
434398; AA121098; Hs.3838; serum-inducible kinase; pkinase,POLO_box;TM=M;; 3.77
415485; AW272990; Hs.18571; ESTs; none,Oxysterol_BP; 3.76
453226; AA641926; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c,none; 3.76
418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;; 3.76
424842; AA034127; Hs.153487; signal transducing adaptor molecule (SH3 domain and ITAM motif) 1; SH3,VHS,UIM;TM=M;; 3.75
426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;; 3.75
419952; AK000967; Hs.93872; KIAA1682 protein; none;TM=M;; 3.75
425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;; 3.75
431696; AA259068; Hs.267819; protein phosphatase 1, regulatory (inhibitor) subunit 2; none;SS=M; 3.75

444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1. Contains part of a gene for a novel protein similar to membrane transport proteins, the 5' end of a novel gene, ESTs, STSs, GSSs and three CpG islands; pkinase,RIO1,APH,KOW;TM=M;; 3.75
405411; ; ; ENSP00000252213:SODIUM BICARBONATE COTRANSPORTER.; none;TM=Y;SS=M; 3.75
405602; ; ; Target Exon; pkinase;SS=M; 3.75
429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadillo_seg,none; 3.75
430153; AW968128; Hs.336679; ESTs; pkinase,none; 3.74
414180; AI863304; Hs.120905; Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391; PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B,none; 3.74
432236; AA531132; ; gb:nj47h06.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone, mRNA sequence; pkinase,none; 3.74
433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds; none,spectrin,SH3,PH,CH; 3.74
426485; NM_006207; Hs.170040; platelet-derived growth factor receptor-like; ig;SS=M; 3.74
408414; AI114688; Hs.17998; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; fn3,ig;TM=Y;SS=M; 3.73
409793; AI825463; Hs.147996; protein kinase, X-linked; pkinase,pkinase_C;TM=M;; 3.73
412456; T32689; Hs.7859; ESTs; BAG,none; 3.73
407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase C-beta 1; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 3.73
442229; AI885776; Hs.8164; Multibrey nanism; MATH,DENN,GRAM,zf-B_box,dDENN,uDENN;SS=M; 3.73
450151; AI088196; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig,pkinase,none; 3.72
408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc;TM=M;; 3.72
417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF;SS=M; 3.72
403391; ; ; C3001164*:gi|1730196|sp|P50573|GAR3_RAT GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 SUBUNIT PRE; none;TM=Y;; 3.72
417527; AA203524; ; gb:zx56e10.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone 5', mRNA sequence; SH3;SS=M; 3.71
428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase); pkinase;TM=M;; 3.71
428180; AI129767; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; G-alpha,arf;TM=M;; 3.71
422127; AW504286; Hs.112049; SET binding factor 1; dDENN,DENN,GRAM,PH;SS=M; 3.70
430570; AI417881; Hs.292464; ESTs; 7tm_2,Fz,Frizzled,none; 3.70
452561; AI692181; Hs.49169; KIAA1634 protein; TPR,PDZ,WW,Guanylate_kin;TM=M;; 3.69
432336; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm,pkinase;TM=M;; 3.69
419945; AW290975; Hs.118923; ESTs; SH3,PDZ,Guanylate_kin,transferrin; 3.69
426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate_kin;TM=M;; 3.68
436534; AA721628; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig;TM=Y;SS=M; 3.68
407202; N58172; Hs.109370; ESTs; F5_F8_type_C,pkinase,Ets,none; 3.67
420297; AI628272; Hs.88323; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase,TUDOR,none; 3.67
417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase;TM=M;; 3.67
425304; AA463844; Hs.31339; fibroblast growth factor 11; FGF,Neur_chan_LBD,Neur_chan_memb,none; 3.67
418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 3.67
419511; AA429750; Hs.75113; general transcription factor IIIA; Glypican,none; 3.66
424315; AW614850; Hs.193384; putatative 28 kDa protein; none,none; 3.66
413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;; 3.66
425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; peroxisome proliferator-activated receptor interacting protein; thyroid hormone receptor binding protein; none;TM=M;; 3.65
446983; AA157484; Hs.97199; complement component C1q receptor; EGF,lectin_c,Tissue_fac,Xlink,TIL;TM=Y;SS=M; 3.65
434350; AL042940; Hs.93872; KIAA1682 protein; none,none; 3.65
457317; AA683016; Hs.12210; hypothetical protein FLJ13732 similar to tensin; SH2;TM=M;; 3.65
434416; AA805903; Hs.59498; cell division cycle 2-like 5 (cholinesterase-related cell division controller); pkinase,none; 3.65
410174; AA306007; Hs.59461; DKFZP434C245 protein; none,DSPc; 3.65
423598; BE247600; Hs.155538; ESTs; 7tm_1;TM=Y;SS=M; 3.65
440861; BE244115; Hs.7482; KIAA0682 gene product; rrm,Guanylate_kin;TM=M;; 3.64
454954; AW993013; Hs.49169; KIAA1634 protein; TPR,PDZ,WW,Guanylate_kin;TM=M;; 3.64
430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;; 3.64
450587; AI828854; Hs.258538; striatin, calmodulin-binding protein; pkinase,WD40;TM=Y;; 3.64
424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OVARC1001372, highly similar to Homo sapiens liprin-alpha4 mRNA; SAM;SS=M; 3.64
425645; AA361027; ; gb:EST70242 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence; HMG_box,DNA_mis_repair,HATPase_c,none; 3.64
417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;SS=M; 3.63
451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;; 3.63
412314; AA825247; Hs.250899; heat shock factor binding protein 1; 7tm_1;TM=Y;SS=M; 3.63
418303; AA215701; Hs.186541; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; eIF5_eIF2B,W2,pkinase,UBA,KA1; 3.63
452716; AI914925; Hs.222240; ESTs; SH2,STAT,STAT_bind,STAT_prot,none; 3.63
403869; ; ; NM_004520*:Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA. member 3 (KCNQ3), mRNA.; kinesin;TM=M;; 3.63
450377; AB033091; Hs.74313; KIAA1265 protein; Zip;TM=M;SS=M; 3.63
417793; AW405434; Hs.82575; small nuclear ribonucleoprotein polypeptide B''; rrm;TM=M;; 3.63
404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36;TM=Y;SS=M; 3.63
429554; NM_012275; Hs.207224; interleukin 1, delta; IL1;TM=M;; 3.63
417871; AA521368; Hs.24252; ESTs; IBB,Armadillo_seg,none; 3.62
437672; AW748265; Hs.5741; flavohemoprotein b5?; heme_1,NAD_binding,lipoxygenase,FAD_binding_6;TM=M;; 3.62
438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; lipoxygenase,PLAT,none; 3.62
447217; BE465754; Hs.17776; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 3.61
407961; AW672939; Hs.41694; origin recognition complex, subunit 2 (yeast homolog)-like; none,pkinase,pro_isomerase; 3.61
428640; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1; SH2,SH3,pkinase;SS=M; 3.61
455608; BE011437; ; gb:CM4-BN0220-080500-170-f03 BN0220 Homo sapiens cDNA, mRNA sequence; none,CDK5_activator; 3.61
407748; AL079409; Hs.38176; KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP); PP2C,LRR,PH;TM=M;; 3.60
421474; U76362; Hs.104637; solute carrier family 1 (glutamate transporter), member 7; SDF;TM=Y;SS=M; 3.60
449987; AW079749; Hs.184719; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ABC_tran,ABC_membrane,Ion_trans; 3.60
403142; ; ; NM_002706*:Homo sapiens protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform (PPM1B), mRNA.; PP2C;TM=M;; 3.60
400844; ; ; NM_003105*:Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 3.59
450152; AI138635; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig,pkinase,none; 3.59
429782; NM_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain-binding protein; rrm,NTF2;TM=M;; 3.59
436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;SS=M; 3.59
437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR_c6,laminin_EGF;TM=Y;; 3.58
426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf,Ca_channel_B,SH3; 3.58
431170; AW971246; Hs.291022; ESTs; LRR,CARD,none; 3.58
434542; AA769310; Hs.61260; hypothetical protein FLJ13164; PH,Oxysterol_BP;TM=M;SS=M; 3.58

420181; AI380089; Hs.158951; ESTs; none,Ig,pkinase,LRR,LRRCT; 3.57
450572; AI700863; Hs.202494; Homo sapiens cDNA FLJ13245 fis, clone OVARC1000681; Na_sulph_symp,none; 3.57
433618; AA602539; Hs.345494; ESTs; G-alpha,A_deaminase; 3.57
452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; pkinase,none; 3.57
418512; AW498974; ; diacylglycerol kinase, zeta (104kD); ras,none; 3.57
451752; AB032997; Hs.26966; KIAA1171 protein; ATP-synt_C,TBC;TM=Y;SS=M; 3.57
417129; AI381800; Hs.300684; calcitonin gene-related peptide-receptor component protein; none,none; 3.57
449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing); ThiF,UBACT,pkinase,UCH-2,UCH-1,rrm,zf-C2H2,zf-RanBP,G-patch; 3.57
412124; H43378; Hs.288550; Homo sapiens cDNA: FLJ23156 fis, clone LNG09609; none,none; 3.56
435021; AA922192; Hs.54709; ESTs; EPH_lbd,pkinase,fn3,SAM,none; 3.56
431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit, alpha type, 4; proteasome;TM=M;; 3.56
437387; AI198874; Hs.28847; AD026 protein; none,7tm_1,WD40; 3.56
422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha;TM=M;; 3.56
452102; U04343; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none;TM=Y;SS=M; 3.56
420112; NM_005109; Hs.95220; oxidative-stress responsive 1; pkinase;TM=M;; 3.55
437639; AA827712; Hs.291880; ESTs; SH3,none; 3.55
457500; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm,pkinase;TM=M;; 3.55
415660; AI909007; Hs.78563; ubiquitin-conjugating enzyme E2G 1 (homologous to C. elegans UBC7); UQ_con;TM=M;; 3.55
423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M;; 3.55
428727; AF078847; Hs.191356; general transcription factor IIH, polypeptide 2 (44kD subunit); PHO4,LIM;TM=M;; 3.55
411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;; 3.55
408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos;TM=M;; 3.55
412350; AI659306; Hs.73826; protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte); Y_phosphatase,Band_41,PDZ;TM=M;; 3.55
446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 3.55
427283; AL119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin); Sulfatase,Somatomedin_B,Phosphodiest,Endonuclease;TM=M;SS=Y; 3.55
414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17,none; 3.55
424848; AI263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin,none; 3.54
402704; ; ; C1001099*:gi|6005896|ref|NP_009101.1| testis-specific protein kinase 2 [Homo sapiens] gi|4; none,none; 3.54
444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; aa_permeases;TM=Y;SS=M; 3.54
429587; AI675749; Hs.211608; nucleoporin 153kD; zf-RanBP,integrin_B;TM=M;; 3.53
413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone HSI02313; none,none; 3.53
431045; AW968560; Hs.301957; nudix (nucleoside diphosphate linked moiety X)-type motif 5; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 3.53
423855; AA331761; Hs.254859; ESTs; none,pkinase,UQ_con,vwa,FG-GAP,integrin_A; 3.53
440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP;TM=M;; 3.52
410686; AI733735; Hs.114905; IRE1, S. cerevisiae, homolog of; pkinase,Bacterial_PQQ;TM=M;SS=M; 3.52
449810; AB008681; Hs.23994; activin A receptor, type IIB; pkinase,Activin_recp;TM=Y;SS=M; 3.52
418755; Y14443; Hs.88219; zinc finger protein 200; zf-C2H2,zf-BED;TM=M;; 3.52
448804; AW512213; Hs.342849; ADP-ribosylation factor-like 5; arf,Ca_channel_B,SH3; 3.52
438507; AA809052; Hs.182018; ESTs; none,none; 3.52
456559; AI336273; Hs.102548; glucocorticoid receptor DNA binding factor 1; none,PAS; 3.51
410054; AL120050; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP,adenylatekinase; 3.51
422321; AA906427; Hs.181035; hypothetical protein MGC11296; none;TM=M;; 3.51
445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2,PH;TM=M;; 3.50
407393; AB038237; ; gb:Homo sapiens mRNA for G protein-coupled receptor C5L2, complete cds.; 7tm_1;TM=Y;SS=M; 3.50
443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine protease; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 3.50
420673; AB008112; Hs.99847; peroxisome biogenesis factor 1; AAA,APS_kinase;TM=M;SS=M; 3.49
424663; NM_002351; Hs.151544; SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome); SH2;TM=M;; 3.49
429327; AA283981; Hs.199248; prostaglandin E receptor 4 (subtype EP4); 7tm_1;TM=Y;SS=M; 3.49
400178; ; ; Eos Control; none,Somatomedin_B; 3.49
439549; AW937885; Hs.137314; ESTs; SH2,none; 3.49
436345; AA873008; Hs.121572; ESTs; CARD,BIR,zf-C3HC4,CARD,BIR,zf-C3HC4; 3.49
427658; H61387; Hs.30868; nogo receptor; LRR,LRRNT,LRRCT;SS=M; 3.48
402833; ; ; C1002508:gi|6691937|emb|CAB65797.1| (AL096770) bA150A6.2 (novel 7 transmembrane receptor; none,none; 3.48
442363; AI337304; Hs.23120; PIST; fn3,pkinase,PDZ,DUF139;TM=Y;SS=M; 3.48
409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; none;TM=M;; 3.47
417971; Y08991; Hs.83050; phosphoinositide-3-kinase, regulatory subunit 4, p150; pkinase,WD40,HEAT;SS=M; 3.47
432169; Y00971; Hs.2910; phosphoribosyl pyrophosphate synthetase 2; Pribosyltran;; 3.47
447425; AI963747; Hs.18573; acylphosphatase 1, erythrocyte (common) type; Acylphosphatase;SS=M; 3.47
427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 3.46
401851; ; ; NM_002401*:Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA.; pkinase;SS=M; 3.46
407877; AW016811; Hs.234478; Homo sapiens cDNA: FLJ22648 fis, clone HSI07329; pkinase,pkinase_C,none; 3.45
432279; N95104; Hs.274260; ATP-binding cassette, sub-family C (CFTR/MRP), member 6; ABC_tran,ABC_membrane,none; 3.45
437103; AW139408; Hs.152940; ESTs; Choline_kinase,none; 3.45
420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339, mRNA, complete cds; 7tm_1;TM=Y;SS=M; 3.44
422209; AF005210; Hs.113222; chemokine (C-C motif) receptor 8; 7tm_1,7tm_2;TM=Y;SS=M; 3.44
410781; AI375672; Hs.165026; ESTs; pkinase,laminin_Nterm,laminin_EGF,cyclin,F-box,cyclin_C,serpin,ATP-synt_C; 3.44
437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSPc;TM=M;; 3.43
419855; AI935182; Hs.144139; ESTs; zf-C3HC4,UBA,Cbl_N,Cbl_N2,Cbl_N3,zf-C3HC4,UBA,Cbl_N,Cbl_N2,Cbl_N3; 3.43
433336; AF017986; Hs.31386; secreted frizzled-related protein 2; Fz,NTR;SS=M; 3.43
428483; AI908539; Hs.184592; KIAA0344 gene product; none,none; 3.43
445119; AF035121; Hs.12337; kinase insert domain receptor (a type III receptor tyrosine kinase); Ig,pkinase;TM=Y;SS=M; 3.42
454468; AI590319; Hs.19122; eukaryotic translation initiation factor 4E-like 3; none,Neur_chan_LBD,Neur_chan_memb,IF4E; 3.42
410386; W26187; Hs.3327; Homo sapiens cDNA: FLJ22219 fis, clone HRC01637; pkinase,Guanylate_kin,PDZ,SH3,L27,none; 3.42
422907; AI879263; Hs.77273; Human glucose transporter pseudogene; none,none; 3.42
449816; AI701457; Hs.38694; ESTs; SET,BAH,PK,PK_C; 3.42
440074; AA863045; Hs.10669; ESTs, Weakly similar to T00050 hypothetical protein KIAA0400 [H.sapiens]; SH3,ank,tubulin-binding,ArfGap,PH;TM=M;SS=M; 3.42
425475; W56339; Hs.107057; ESTs; pkinase,none; 3.42
401242; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 3.41
429276; AF056085; Hs.198612; G protein-coupled receptor 51; 7tm_3,ANF_receptor,bZIP;TM=Y;; 3.41
445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, type I, 107kD; none,none; 3.41
410908; AA121686; Hs.10592; ESTs; GTP_EFTU,GTP_EFTU_D3,GTP_EFTU_D2,none; 3.41

452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor type, E; Y_phosphatase,none; 3.40
447898; AW969638; Hs.112318; 6.2 kd protein; none,none; 3.40
450402; BE218027; Hs.89969; ESTs; SH3,none; 3.40
441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB,none; 3.40
408546; W49512; Hs.46348; bradykinin receptor B1; 7tm_1;TM=Y;SS=M; 3.40
410927; T77635; ; gb:yc91h06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone 5', mRNA sequence; none,none; 3.40
409646; AW161391; Hs.709; deoxycytidine kinase; dNK;SS=M; 3.39
417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone COL04162; Sulfate_transp,STAS,HMG_box; 3.39
449343; AI151418; ; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); none,none; 3.39
450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_tail,EGF; 3.39
414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;; 3.38
418428; Y12490; Hs.85092; thyroid hormone receptor interactor 11; bZIP,kinesin,GTP_cyclohydrol,M;TM=M;; 3.37
422369; AF005216; Hs.115541; Janus kinase 2 (a protein tyrosine kinase); SH2,pkinase;TM=M;; 3.37
456451; AI761180; Hs.94211; rod1 (required for cell differentiation, S.pombe) homolog 1; none;TM=M;; 3.37
438543; AA810141; Hs.192182; ESTs; SH2,pkinase,none; 3.37
401943; NM_012434; ; solute carrier family 17 (anion/sugar transporter), member 5; none;TM=M;; 3.36
415276; U88666; Hs.78353; SFRS protein kinase 2; pkinase;TM=M;; 3.36
447881; BE620886; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; pkinase,pkinase; 3.35
434533; AA639257; Hs.292549; ESTs; SH3,PDZ,Guanylate_kin,none; 3.35
432639; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence; none,IRK; 3.35
410678; BE540516; Hs.293732; hypothetical protein MGC3195; Armadillo_seg;TM=M;SS=Y; 3.35
402807; ; ; ENSP00000235229:SEMB.; integrin_B,Sema,PSI;TM=Y;; 3.35
420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank;; 3.34
437389; AL359587; Hs.271586; hypothetical protein DKFZp762M115; secY,E1_dehydrog,transket_pyr,none; 3.34
453423; NM_002647; Hs.32971; phosphoinositide-3-kinase, class 3; PI3_PI4_kinase,PI3Ka,PI3K_C2;TM=M;; 3.34
414270; L20852; Hs.347527; solute carrier family 20 (phosphate transporter), member 2; Enterotoxin_A,PHO4;TM=Y;SS=M; 3.33
417479; AI057052; ; ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]; LRR,CARD,none; 3.33
424946; M64572; Hs.153932; protein tyrosine phosphatase, non-receptor type 3; Band_41,PDZ,Y_phosphatase,none; 3.33
452681; AF153330; Hs.30246; solute carrier family 19 (thiamine transporter), member 2; Folate_carrier;TM=Y;SS=M; 3.33
426477; AA379464; ; gb:EST92386 Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence; DUF6,MATH,BTB; 3.33
438283; AI458931; Hs.37282; ESTs; none,transmembrane4; 3.33
421327; AA837295; Hs.188802; ESTs; none,IMP4,Y_phosphatase; 3.33
432481; AW451645; Hs.151504; Homo sapiens cDNA FLJ11973 fis, clone HEMBB1001221; laminin_G,Collagen,COLFI,CorA,TSPN,none; 3.33
452682; AA456193; Hs.9071; progesterone membrane binding protein; homeobox,none; 3.32
428997; AF065391; Hs.194718; zinc finger protein 265; zf-RanBP;TM=M;; 3.32
432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M;; 3.31
443601; AI078554; Hs.15682; ESTs; ank,pkinase,death,Ribosomal_S14; 3.31
430597; AF062006; Hs.285529; G protein-coupled receptor 49; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 3.31
419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (GEF) 4; SH3,PH,RhoGEF;TM=M;; 3.31
400380; NM_018485; Hs.283079; G protein-coupled receptor C5L2; 7tm_1;TM=Y;SS=M; 3.31
415983; AI436798; Hs.117078; Homo sapiens cDNA: FLJ23028 fis, clone LNG01852, highly similar to HSU08023 Human cellular proto-oncogene (c-mer) mRNA; fn3,ig,pkinase;TM=Y;SS=M; 3.31
441054; AA913591; Hs.126480; ESTs; none,7tm_1; 3.31
418342; BE002723; ; leptin receptor; ICE_p20,DED,ICE_p10,ICE_p20,DED; 3.31
446128; AW836779; Hs.113029; ribosomal protein S25; none,7tm_1; 3.31
425086; AW957571; Hs.12319; Homo sapiens cDNA FLJ12774 fis, clone NT2RP2001663, moderately similar to ENOLASE (EC 4.2.1.11); none,Guanylate_kin,PDZ,SH3; 3.31
425725; NM_012243; Hs.159322; solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3; DUF6;TM=Y;SS=M; 3.30
422608; AW160644; Hs.118695; potassium voltage-gated channel, subfamily G, member 1; ion_trans,K_tetra;TM=Y;; 3.30
429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M;; 3.30
433656; AW974941; Hs.292385; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,ABC1,none; 3.30
413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic) inhibitor alpha; PKI;SS=M; 3.30
402603; ; ; ENSP00000251206*:KIAA0778 PROTEIN (FRAGMENT).; none;TM=Y;; 3.30
418801; AA228366; Hs.115122; ESTs; integrin_A,FG-GAP,none; 3.30
400275; ; ; NM_006513*:Homo sapiens seryl-tRNA synthetase (SARS), mRNA. (SAM68), mRNA.; tRNA-synt_2b,Seryl_tRNA_N;TM=M;; 3.29
440286; U29589; Hs.7138; cholinergic receptor, muscarinic 3; 7tm_1;TM=Y;; 3.29
409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; G-alpha,none; 3.29
432736; AA788898; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.29
408738; NM_014785; Hs.47313; KIAA0258 gene product; none;TM=M;; 3.29
443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955; Aa_trans,none; 3.29
405328; ; ; NM_005391:Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3), mRNA.; HATPase_c;SS=M; 3.28
418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit 6; none,none; 3.28
408756; AA524743; Hs.44883; ESTs; Armadillo_seg,IBB,DEAD,helicase_C,Sec63,DDT,PHD,bromodomain;TM=M;; 3.28
415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15; mito_carr;TM=M;; 3.28
417805; U38545; Hs.82587; phospholipase D1, phosphatidylcholine-specific; PH,PLDc,PX;TM=M;; 3.28
410254; BE004131; Hs.318510; Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15; efhand,none; 3.28
443968; AA287702; Hs.10031; KIAA0955 protein; CARD;TM=M;SS=M; 3.28
438899; AF085833; Hs.135624; ESTs; none,PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 3.27
415663; AW296841; Hs.313332; ESTs; UQ_con,Neur_chan_LBD,Neur_chan_memb; 3.27
414087; W19712; ; gb:zb36d03.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 3.27
442833; AA328153; Hs.88201; ESTs, Weakly similar to A Chain A, Crystal Structure Of The Human Acyl Protein Thioesterase 1 At 1.5 A Resolution [H.sapiens]; abhydrolase_2;TM=M;; 3.27
444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 3.26
432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis repressor with CARD domain); CARD;TM=M;; 3.26
458943; AW249181; Hs.19954; ESTs, Weakly similar to T19873 hypothetical protein C41C4.2 - Caenorhabditis elegans [C.elegans]; none,pkinase,RGS; 3.26
411974; AW880414; Hs.84264; acidic protein rich in leucines; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,asp; 3.26
437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate cotransporter, member 4; HCO3_cotransp;TM=Y;; 3.26
423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 3.25
442643; U82756; Hs.3991; PRP4/STK/WD splicing factor; WD40;SS=M; 3.25
417525; R93355; Hs.192991; ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]; SH3,ig,pkinase,PH,spectrin,RhoGEF;SS=M; 3.25
412283; BE069084; ; gb:QV3-BT0379-140100-058-g12 BT0379 Homo sapiens cDNA, mRNA sequence; ion_trans,RYDR_ITPR,MIR,none; 3.25
411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 3.25
400352; AF227133; ; taste receptor, type 2, member 7; none;TM=Y;SS=M; 3.25

402974; ; ; Target Exon; Y_phosphatase,GnRH,hormone5,hormone4; 3.25
407644; D16815; Hs.37288; nuclear receptor subfamily 1, group D, member 2; hormone_rec,zf-C4;TM=M;SS=M; 3.25
421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; helicase_C;SS=M; 3.25
438022; AW517524; Hs.135201; NOD2 protein; LRR,CARD,GTP_CDC,Viral_helicase1;TM=M;; 3.24
449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase;TM=M;; 3.24
428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; EGF,sushi,trypsin,CUB,ABC_tran,ABC_membrane;SS=M; 3.24
427319; AW631495; Hs.27135; B-cell receptor-associated protein BAP29; filament;TM=Y;SS=M; 3.24
421970; AF227156; Hs.110103; RNA polymerase I transcription factor RRN3; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;; 3.24
411887; AW182924; Hs.128790; ESTs; pkinase;TM=M;; 3.24
430180; AA331406; Hs.75456; A kinase (PRKA) anchor protein 10; RGS;SS=M; 3.24
410267; AW978005; Hs.12600; N-ethylmaleimide-sensitive factor attachment protein, beta; none,NTF2; 3.23
410240; AL157424; Hs.61289; synaptojanin 2; Exo_endo_phos,Syja_N,rrm,Gram-ve_porins;TM=M;; 3.23
434510; AF143885; Hs.18190; EST; SH3,FCH,none; 3.22
422592; BE081857; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none,PI-PLC-X,PH,PI-PLC-Y,C2; 3.22
439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none,none; 3.22
448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX;TM=M;; 3.22
409245; AA361037; Hs.288036; tRNA isopentenylpyrophosphate transferase; Armadillo_seg;TM=M;; 3.22
458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 3.22
409048; H59990; Hs.37699; ESTs; Armadillo_seg,IBB,none; 3.22
420357; U94333; Hs.97199; complement component C1q receptor; EGF,lectin_c,Tissue_fac,Xlink,TIL;TM=Y;SS=M; 3.22
426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin,loxin_4;SS=M; 3.21
411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activating protein) 1; SH2,SH3,C2,PH,RasGAP;TM=M;SS=M; 3.21
438333; R39382; Hs.25283; cyclin-dependent kinase 8; pkinase,none; 3.20
414202; BE275653; Hs.270379; transmembrane 6 superfamily member 1; 7tm_5,none; 3.20
429651; D79248; Hs.279870; ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; MgtE,none; 3.20
400987; ; ; C11000939:gi|11464993|ref|NP_065260.1| gene for odorant receptor MOR83 [Mus musculus] gi|6; none;TM=Y;SS=M; 3.20
413760; Z25101; Hs.25127; Homo sapiens mRNA for KIAA1725 protein, partial cds; none,ank,ArfGap; 3.20
408468; AI909712; Hs.93837; phosphatidylinositol transfer protein, membrane-associated; PX,PH,PLDc,PH,PLDc,PX; 3.20
409463; AI458165; Hs.17296; hypothetical protein MGC2376; K_tetra;TM=M;; 3.20
425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none;TM=M;; 3.19
423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbonate cotransporter, member 7; HCO3_cotransp;TM=Y;SS=M; 3.19
407753; AL045916; Hs.293419; ESTs; Ephrin,none; 3.19
419355; AA428520; Hs.90061; progesterone binding protein; heme_1;TM=Y;SS=M; 3.19
454128; AL031259; Hs.41639; programmed cell death 2; zf-MYND;TM=M;; 3.19
421202; AF193339; Hs.102506; eukaryotic translation initiation factor 2-alpha kinase 3; pkinase;TM=Y;SS=M; 3.19
446360; N42553; Hs.267914; homolog of mouse transient receptor potential-phospholipase C-interacting kinase ChaK; hypothetical protein FLJ20117; ion_trans,MHCK_EF2_kinase;TM=M;; 3.18
458882; R34993; Hs.226666; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; CRAL_TRIO,PKI; 3.18
424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; pkinase,TBC; 3.18
444745; AF117754; Hs.11861; thyroid hormone receptor-associated protein, 240 kDa subunit; none;TM=M;; 3.18
426399; AA652588; Hs.301348; Homo sapiens cDNA FLJ13271 fis, clone OVARC1001000; SH3,HS1_rep,none; 3.18
425836; AW955696; Hs.90960; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 3.18
403335; ; ; NM_021815:Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA.; SSF;TM=Y;SS=M; 3.17
428788; AF082283; Hs.193516; B-cell CLL/lymphoma 10; CARD;TM=M;; 3.17
429558; AI391454; Hs.207251; nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein; none;SS=M; 3.17
440248; AA876138; Hs.153136; ESTs; SH2,none; 3.17
423706; U95216; Hs.131924; G protein-coupled receptor 65; 7tm_1;TM=Y;SS=M; 3.17
429752; H52348; Hs.36636; ESTs; pkinase,pkinase; 3.17
446163; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis, clone PLACE1010270; none;NA;NA; 3.17
456773; AI038192; Hs.129764; EGF-like repeats and discoidin I-like domains 3; rrm,SH3,myosin_head,IQ,MyTH4,EGF,F5_F8_type_C,Band_41;TM=M;; 3.17
434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone HRC12631; pkinase,none; 3.16
435972; W95088; Hs.114198; ESTs; pkinase,OPR,none; 3.16
441401; AI824338; Hs.126891; ESTs; Tissue_fac;TM=M;SS=M; 3.16
410497; AL157648; Hs.157078; Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033; none,none; 3.16
401113; H25530; ; solute carrier family 22 (organic cation transporter), member 1-like; none;SS=M; 3.16
424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS;SS=M; 3.15
453880; AI803166; Hs.28462; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; HSP70,none; 3.15
435391; AA704588; Hs.58934; ESTs; PIP5K,none; 3.15
428065; AI634046; Hs.157313; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 3.15
452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H.sapiens]; SH3,none; 3.15
426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affinity); none;TM=M;SS=M; 3.15
421247; BE391727; Hs.102910; general transcription factor IIH, polypeptide 4 (52kD subunit); none;TM=M;; 3.14
440249; AI246590; Hs.249175; ESTs; TatD_DNase,pkinase,death,none; 3.14
409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG;TM=M;; 3.13
446135; AW130288; Hs.170318; hypothetical protein FLJ10147; hormone_rec,zf-C4;SS=M; 3.13
400440; X83957; Hs.83870; nebulin; SH3,Nebulin;; 3.12
409099; AK000725; Hs.50579; hypothetical protein FLJ20718; Armadillo_seg;TM=M;; 3.12
434237; AF119908; Hs.235516; hypothetical protein PRO2955; none;SS=M; 3.12
428179; AI127772; Hs.279696; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; pkinase,PX,pkinase_C;SS=M; 3.12
422824; NM_012108; Hs.121128; BCR downstream signaling 1; SH2,PH;TM=M;; 3.11
409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14E12, mRNA sequence; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 3.11
435411; AW444619; Hs.138211; ESTs; none,pkinase; 3.11
424852; AI222779; Hs.144848; ESTs; adenylatekinase,SH2,pkinase,none; 3.11
441970; AW959918; Hs.155160; ESTs; rrm,zf-C2H2; 3.11
453370; AI470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y;; 3.11
413285; BE078405; ; gb:QV2-BT0617-080300-071-g03 BT0617 Homo sapiens cDNA, mRNA sequence; GCV_T;SS=M; 3.10
429458; BE161832; Hs.292689; ESTs; pkinase,bZIP,Armadillo_seg,none; 3.10
401185; ; ; NM_021625:Homo sapiens vanilloid receptor-related osmotically activated channel; OTRPC4 protein (OTRPC4), mRNA.; ank,Ion_trans;TM=Y;; 3.10
404537; Z25884; ; chloride channel 1 , skeletal muscle (Thomsen disease, autosomal dominant); none;TM=Y;; 3.10
417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone HEP03834; voltage_CLC,CBS,none; 3.09
450792; AA400323; Hs.183041; ESTs; none,ABC_tran; 3.09

420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP,7tm_1; 3.09
444040; AF204231; Hs.182982; golgin-67; SH3,C2,PH,RhoGEF,efhand;TM=M;; 3.09
416990; AF124145; Hs.80731; autocrine motility factor receptor; zf-C3HC4,CUE;TM=Y;; 3.09
442215; AI703172; Hs.129005; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; none,none; 3.09
424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK,none; 3.09
426623; AA382826; Hs.132793; ESTs; none;TM=M;; 3.08
419577; L36531; Hs.91296; integrin, alpha 8; integrin_A,FG-GAP;TM=Y;; 3.08
426618; AL036456; Hs.171374; smg GDS-ASSOCIATED PROTEIN; Armadillo_seg;TM=M;; 3.08
445133; AW157646; Hs.153506; ESTs; efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FliD,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M;; 3.08
423681; AB023215; Hs.131525; Homo sapiens mRNA; cDNA DKFZp434E199 (from clone DKFZp434E199); partial cds; TTL;TM=M;; 3.08
428730; AA625947; Hs.25750; ESTs; HECT,none; 3.08
427976; AW977808; Hs.80545; mitogen-activated protein kinase 8 interacting protein 2; Ribosomal_L37e,pkinase; 3.08
412448; L12964; Hs.73895; tumor necrosis factor receptor superfamily, member 9; TNFR_c6;TM=Y;SS=M; 3.08
416814; AW192307; Hs.80042; dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylglucosyltransferase; Alg6_Alg8,7tm_1;TM=Y;SS=M; 3.08
427395; AW298741; Hs.97861; ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]; none,aldedh,aakinase; 3.08
436267; AW450938; Hs.180115; ESTs; none,PFK; 3.07
422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic acid transporters), member 6; sugar_tr;TM=Y;SS=M; 3.07
439238; N47305; Hs.46668; ESTs; 7tm_1;TM=Y;SS=M; 3.07
458760; AI498631; Hs.111334; ferritin, light polypeptide; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.07
424236; AW058114; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M;; 3.06
427286; AW732802; Hs.2132; epidermal growth factor receptor pathway substrate 8; SH3,TonB_boxC;TM=M;; 3.06
423878; AI907090; Hs.52891; hypothetical protein PRO1853; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.06
419270; NM_005232; Hs.89839; EphA1; fn3,pkinase,SAM,EPH_lbd;TM=M;SS=M; 3.06
450407; NM_000810; Hs.24969; gamma-aminobutyric acid (GABA) A receptor, alpha 5; Neur_chan_LBD,Neur_chan_memb;TM=Y;; 3.06
456249; AI206144; Hs.82508; HRIHFB2206 protein; none;SS=M; 3.06
441560; F13386; Hs.7888; Homo sapiens clone 23736 mRNA sequence; pkinase,Recep_L_domain,Furin-like,YLP,none; 3.05
446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 3.05
447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); pyr_redox;TM=M;; 3.05
425390; AI092634; Hs.156114; protein tyrosine phosphatase, non-receptor type substrate 1; ig;TM=Y;SS=M; 3.04
409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF;SS=M; 3.04
413962; AA331563; Hs.24678; sphingosine-1-phosphatase; PAP2;TM=Y;; 3.04
426578; R23027; ; gb:yh27e07.r1 Soares placenta Nb2HP Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 3.04
438005; BE151746; ; gb:PM1-HT0305-061299-003-a06 HT0305 Homo sapiens cDNA, mRNA sequence; pkinase,UBA,KA1,none; 3.04
438316; AA789249; Hs.80042; gb:aj27g08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391582 3', mRNA sequence; none,none; 3.04
452850; H23230; Hs.22481; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; CBS,voltage_CLC,none; 3.03
405266; ; ; Target Exon; arf,G-alpha;SS=M; 3.03
402615; ; ; C1003844*:gi|6912550|ref|NP_036483.1| olfactory receptor, family 10, subfamily J, member 1; none;TM=Y;SS=M; 3.03
422803; W28669; Hs.139041; ESTs; transmembrane4,none; 3.02
439325; AF086139; Hs.150423; cyclin-dependent kinase 9 (CDC2-related kinase); pkinase,Mur_ligase,Mur_ligase_C; 3.02
416389; AA180072; Hs.149846; integrin, beta 5; integrin_B,none; 3.02
418836; AI655499; Hs.161712; ESTs; pkinase,Activin_recp,PDZ,ZU5,death; 3.02
438996; AW748336; Hs.110613; KIAA0421 protein; none;TM=M;; 3.02
422676; D28481; Hs.1570; histamine receptor H1; 7tm_1;TM=Y;SS=M; 3.02
450267; AW505538; Hs.243620; ESTs; pkinase,none; 3.01
400566; ; ; Target Exon; none;TM=Y;; 3.01
407816; AW500857; Hs.40137; anaphase-promoting complex 1; meiotic checkpoint regulator; PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN,none; 3.01
429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase); Y_phosphatase,Band_41,PDZ;SS=M; 3.01
417067; AJ001417; Hs.81086; solute carrier family 22 (extraneuronal monoamine transporter), member 3; sugar_tr;TM=Y;SS=M; 3.00
403212; ; ; NM_019595:Homo sapiens intersectin 2 (ITSN2), mRNA. (CHRNA9), mRNA.; SH3,efhand,C2,PH,RhoGEF;TM=M;; 3.00
410141; R07775; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COL01963; F5_F8_type_C,pkinase,Ets,none; 3.00
421059; AI654133; Hs.30212; thyroid receptor interacting protein 15; none,none; 3.00
452335; AW188944; Hs.61272; ESTs; none,IRK; 2.99
437644; AA748575; Hs.136748; lectin-like NK cell receptor; lectin_c;TM=Y;SS=M; 2.99
435876; AW612586; Hs.160271; G protein-coupled receptor 48; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 2.99
429177; AA447527; Hs.207429; ESTs; 7tm_1,none; 2.99
449289; BE466067; Hs.225660; ESTs; 3Beta_HSD,pkinase; 2.99
454701; AW854930; ; gb:PM0-CT0263-201099-003-f06 CT0263 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prot,none; 2.99
409995; AW960597; Hs.129206; ESTs; pkinase,none; 2.98
446860; AV660685; Hs.282953; ESTs; none,PP2C; 2.98
438684; AA830105; Hs.194976; SH2 domain-containing phosphatase anchor protein 1; ig;TM=Y;SS=M; 2.98
434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;; 2.98
403290; ; ; C10001011*:gi|4758212|ref|NP_004411.1| dual specificity phosphatase 8 [Homo sapiens] gi|601; none;TM=M;; 2.97
433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kinase (CaM kinase) II delta; pkinase,none; 2.97
421990; T31811; Hs.110480; DC12 protein; GKAP,DUF159;TM=M;; 2.97
428315; AA688152; Hs.98505; ESTs; pkinase,none; 2.97
411140; AW819463; ; gb:RC5-ST0293-061299-031-C07 ST0293 Homo sapiens cDNA, mRNA sequence; Choline_kinase,Carn_acyltransf,Sulfatase,Carn_acyltransf; 2.97
453998; H47802; Hs.7557; FK506-binding protein 5; none,none; 2.97
401342; ; ; Target Exon; none,none; 2.97
453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); dNK,none; 2.96
410976; R36207; Hs.25092; hypothetical protein MGC10744; none;TM=M;SS=M; 2.96
431074; BE072772; Hs.153279; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; none,serpin; 2.96
443829; AI087954; Hs.23348; S-phase kinase-associated protein 2 (p45); F-box,none; 2.96
400356; AF227137; ; taste receptor, type 2, member 13; none;TM=Y;SS=M; 2.95
422559; AW247696; Hs.155839; hypothetical protein MGC12934; adh_zinc,PGK,Semialdhyde_dh;SS=M; 2.95
423482; BE280172; Hs.129228; galactokinase 2; GHMP_kinases;TM=M;; 2.95
438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.95
414581; AA256213; Hs.72010; ESTs; none,Carn_acyltransf,Choline_kinase,SCO1-SenC,Glycos_transf_3,Glycos_trans_3N; 2.95
453058; AW612293; Hs.288684; Homo sapiens cDNA FLJ11750 fis, clone HEMBA1005568; SH2,SH3,C2,PH,RasGAP,none; 2.95
430556; AW967807; Hs.13797; ESTs; HECT,none; 2.94
400471; ; ; Target Exon; none;TM=M;; 2.94
419459; AW291128; Hs.278422; DKFZP586G1122 protein; Metallophos,7tm_1; 2.94
407013; U35637; ; gb:Human nebulin mRNA, partial cds; SH3,Nebulin;; 2.94
421476; AW953805; Hs.21887; ESTs; Piwi,PAZ,Piwi; 2.94

426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073;SS=M; 2.94
405588; ; ; NM_000299*:Homo sapiens plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) (PKP1), mRNA.; Armadillo_seg;TM=M;; 2.94
443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none,none; 2.94
416737; AF154335; Hs.79691; LIM domain protein; LIM,PDZ;TM=M;; 2.93
428522; R10184; Hs.191987; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none,ArfGap,PH,TNFR_c6; 2.93
447818; W79940; Hs.21906; Homo sapiens clone 24670 mRNA sequence; none,pkinase; 2.93
432925; AA878324; ; ESTs; none,none; 2.93
443670; AW178935; Hs.238707; ESTs; RmaAD,DENN,dDENN,uDENN;TM=M;; 2.93
447555; AI391662; Hs.160963; Homo sapiens, clone MGC:12318, mRNA, complete cds; none;TM=M;; 2.93
435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; none;TM=M;; 2.93
417670; R07785; ; gb:yf15c06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5' similar to contains Alu repetitive element;contains MSR1 repetitive element ;, mRNA sequence; XYPPX,ABC_membrane,ABC_tran; 2.93
424148; BE242274; Hs.1741; integrin, beta 7; integrin_B,EGF,metalthio,PSI;TM=Y;SS=M; 2.92
439090; H65724; Hs.347158; gb:yr76a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 2.92
408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmin;TM=M;; 2.92
428796; AU076734; Hs.193665; solute carrier family 28 (sodium-coupled nucleoside transporter), member 2; Nucleoside_tra2,BPD_transp_2;TM=Y;; 2.92
415272; AA164215; Hs.203186; ESTs; none,Exo_endo_phos,BNR,Atrophin-1,B56,pkinase,ig,TPR; 2.92
424775; AB014540; Hs.153026; SWAP-70 protein; efhand,PH,Neuregulin;TM=M;; 2.92
439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 2.92
441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg;TM=M;; 2.91
444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1; Somatomedin_B,Endonuclease,Phosphodiest;TM=Y;SS=M; 2.91
400398; AF137396; Hs.283879; ubiquilin 3; 7tm_1,Abi;TM=Y;SS=M; 2.91
435592; AI830490; Hs.1466; glycerol kinase; FGGY,FGGY_C;TM=M;; 2.90
400539; ; ; Target Exon; none;TM=M;; 2.90
403743; ; ; C1002604:gi|8393668|ref|NP_058989.1| kinase interacting with leukemia-associated gene (st; none;TM=M;; 2.90
418913; BE046745; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Y_phosphatase,IMP4,none; 2.90
428169; AI928984; Hs.182793; golgi phosphoprotein 2; photoRC,UPF0118;TM=Y;; 2.90
403912; ; ; C5000394*:gi|12737280|ref|XP_006682.2| keratin 18 [Homo sapiens]||6633; none;TM=M;; 2.89
431868; BE246400; Hs.285176; acetyl-Coenzyme A transporter; none;TM=Y;; 2.89
421558; AB011125; Hs.105749; KIAA0553 protein; none;TM=M;; 2.89
444100; AA383343; Hs.22116; CDC14 (cell division cycle 14, S. cerevisiae) homolog B; Y_phosphatase,DSPc;TM=M;; 2.89
447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupled, 2; 7tm_1,SH2;TM=Y;SS=M; 2.89
431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh,ldh_C,SH3,pkinase,UBA;TM=M;; 2.89
446601; AI312783; Hs.155772; Homo sapiens thymic stromal co-transporter mRNA, complete cds; sugar_tr;TM=Y;; 2.89
420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M;; 2.88
449459; BE546846; Hs.195048; ESTs; ank,ras,PH,ArfGap,HCO3_cotransp; 2.88
405099; ; ; Target Exon; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 2.88
445890; AF055019; Hs.21906; Homo sapiens clone 24670 mRNA sequence; pkinase,pkinase; 2.88
401445; ; ; NM_021161*:Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA.; Ion_trans;TM=Y;SS=M; 2.87
405480; ; ; Target Exon; none,none; 2.87
400189; ; ; Eos Control; LRR,PPTA;TM=M;; 2.87
450125; AA005418; Hs.158186; ESTs; CIDE-N,7tm_1,none; 2.87
432056; AB040973; Hs.272385; G protein-coupled receptor 72; 7tm_1;TM=Y;SS=M; 2.86
423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1,7tm_2;TM=Y;SS=M; 2.86
417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; xan_ur_permease,RA; 2.86
420035; F26725; Hs.187908; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; HATPase_c,MOZ_SAS,zf-C2H2; 2.86
425480; AB023198; Hs.158135; KIAA0981 protein; PIP5K;SS=M; 2.86
446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc finger protein, ESTs, STSs, GSSs and a putative CpG; none;TM=M;; 2.86
444595; AL121094; Hs.83572; hypothetical protein MGC14433; Y_phosphatase,SH2,Y_phosphatase,SH2; 2.85
411331; AW837178; ; gb:QV1-LT0037-070300-100-d11 LT0037 Homo sapiens cDNA, mRNA sequence; SH2,none; 2.85
410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 2.85
440617; AA894880; Hs.181181; ESTs; none,none; 2.85
454071; AI041793; Hs.42502; ESTs; 7tm_1,none; 2.85
411040; AF007393; Hs.177574; protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor); HLH;TM=M;; 2.85
402183; ; ; NM_004491*:Homo sapiens glucocorticoid receptor DNA binding factor 1 (GRLF1), mRNA.; none;SS=M; 2.85
428753; AW939252; Hs.192927; hypothetical protein FLJ20251; none;TM=M;; 2.84
417070; Z19077; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M;; 2.84
458456; AI122709; Hs.153609; ESTs; bZIP,Armadillo_seg,rrm,NTF2,none; 2.84
421226; AL096748; Hs.102708; DKFZP434A043 protein; Armadillo_seg,integrin_B,PSI,TIG;TM=M;SS=M; 2.84
436733; BE327477; Hs.166941; ESTs; 7tm_3,oxidored_q5_N,Presenilin,PWI; 2.84
427161; AI024595; Hs.97508; a disintegrin and metalloproteinase domain 6; ig;TM=Y;SS=M; 2.84
419462; AF071076; Hs.112255; nucleoporin 98kD; DEAD,helicase_C,Nucleoporin_FG,homeobox;SS=M; 2.83
413658; AA055369; Hs.75456; A kinase (PRKA) anchor protein 10; none,none; 2.83
400749; ; ; NM_003105*:Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 2.83
447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; TB2_DP1_HVA22;TM=Y;SS=M; 2.83
413243; AA769266; Hs.193657; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.83
423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]; ion_trans,IQ,none; 2.82
447993; AW139525; Hs.170362; ESTs; none,none; 2.82
423061; AI290473; Hs.44807; ESTs; integrin_B,Sema,PSI,TIG,none; 2.82
440619; AW408586; Hs.91052; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; abhydrolase_2,none; 2.82
423497; U92642; Hs.129701; G protein-coupled receptor 45; 7tm_1;TM=Y;SS=M; 2.81
446126; AW085909; Hs.10177; pleckstrin homology domain interacting protein; none,none; 2.81
452488; N74921; Hs.184389; ESTs; none;TM=M;; 2.80
449515; AI653378; Hs.302012; ESTs; ion_trans;TM=Y;SS=M; 2.79
443881; R64512; Hs.237146; hypothetical protein FLJ12752; none,none; 2.79
449636; AI656608; Hs.281328; ESTs, Weakly similar to T00378 KIAA0641 protein [H.sapiens]; pkinase,hormone3;TM=Y;SS=M; 2.78
424348; AB020523; Hs.266258; endonuclease G-like 1; Endonuclease;TM=M;SS=M; 2.78
418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M;; 2.78
442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; MIF,sugar_tr,none; 2.78

450010; AW293801; Hs.255052; ESTs; ARID,7tm_1; 2.78
452813; U54727; Hs.191445; ESTs; pkinase,Activin_recp,none; 2.78
418177; N44967; ; ESTs; pkinase,none; 2.78
408014; AA723782; Hs.41749; protein kinase, cGMP-dependent, type II; cNMP_binding,pkinase;SS=M; 2.77
448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 similar to HIAT1; sugar_tr;TM=Y;SS=M; 2.77
423994; X01057; Hs.1724; interleukin 2 receptor, alpha; sushi;TM=Y;SS=M; 2.77
427342; AL110150; Hs.176680; Homo sapiens mRNA; cDNA DKFZp586D0724 (from clone DKFZp586D0724); none;NA;NA; 2.76
447574; AF162666; Hs.18895; tousled-like kinase 1; pkinase;TM=M;; 2.76
442681; AI809182; Hs.130907; ESTs; transketolase,E1_dehydrog,transket_pyr,transketolase_C,pkinase; 2.75
433637; AW024214; Hs.102307; ESTs; Na_sulph_symp,aa_permeases;TM=Y;SS=M; 2.75
458997; AW937420; Hs.69662; ESTs; SH3,RhoGAP,FCH;TM=M;; 2.75
432284; AA532807; Hs.105822; ESTs; pkinase,none; 2.74
406139; ; ; Target Exon; ig,Tub;TM=Y;SS=M; 2.74
439518; W76326; ; gb:zd60d04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5' similar to contains Alu repetitive element;, mRNA sequence; Armadillo_seg,none; 2.74
428536; AI143139; Hs.2288; visinin-like 1; efhand;SS=M; 2.73
400211; ; ; NM_003899*:Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. VERSION NM_003897.1 GI; SH3,PH,RhoGEF,Terpene_synth;TM=M;; 2.73
402129; ; ; Target Exon; SH2,Peptidase_C9;TM=M;; 2.73
424238; AA337401; Hs.137635; ESTs; none;TM=M;SS=M; 2.73
433834; AA620742; Hs.130786; ESTs; SPX,EXS;TM=Y;; 2.73
409339; AB020686; Hs.54037; ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function); Sulfatase,Phosphodiest;TM=M;SS=M; 2.73
408163; AW779842; Hs.258217; ESTs; 7tm_1,zf-B_box,zf-C3HC4,7tm_1,zf-B_box,zf-C3HC4; 2.73
422358; AL133030; Hs.115429; Homo sapiens mRNA for KIAA1666 protein, partial cds; SH3;TM=M;; 2.73
426409; AA594207; ; gb:nn29e01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,Fibrillarin,none; 2.72
400645; ; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor,none; 2.72
443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylatekinase,none; 2.71
442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 2.71
409317; U20165; Hs.53250; bone morphogenetic protein receptor, type II (BMPR2); pkinase,Activin_recp;TM=M;SS=M; 2.71
403201; ; ; Target Exon; none;; 2.71
459357; AW848421; ; gb:IL3-CT0214-150200-075-B11 CT0214 Homo sapiens cDNA, mRNA sequence; ABC_tran,ABC_membrane,ion_trans; 2.70
439935; S75105; Hs.8358; glutamate receptor, ionotropic, kainate 2; ANF_receptor,lig_chan,none; 2.70
414924; C06267; Hs.44247; ESTs; none,none; 2.69
421008; BE259378; Hs.103147; hypothetical protein FLJ21347; DUF255;; 2.69
449951; AA004982; Hs.120904; ESTs; DED,Calsequestrin; 2.69
411226; AW833022; ; gb:RC3-TT0005-191099-012-d04 TT0005 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.68
417625; U59305; Hs.44708; Ser-Thr protein kinase related to the myotonic dystrophy protein kinase; pkinase,bZIP,G-gamma,K-box,pkinase_C;SS=M; 2.68
408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 2.68
412521; AW753481; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 2.68
413922; AI535895; Hs.221024; ESTs; ion_trans,RYDR_ITPR,MIR,UDPGT; 2.68
432188; AI362952; Hs.2928; solute carrier family 7 (cationic amino acid transporter, y system), member 1; aa_permeases;TM=Y;SS=M; 2.67
415516; F11411; ; gb:HSC2WF081 normalized infant brain cDNA Homo sapiens cDNA clone c-2wf08, mRNA sequence; ion_trans,none; 2.67
419749; X73608; Hs.93029; sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican); kazal,thyroglobulin_1;SS=M; 2.66
416095; AW014327; Hs.221951; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ig,zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3,none; 2.66
403609; ; ; C3001199:gi|7494834|pir||T15308 hypothetical protein B0286.2 - Caenorhabditis elegans||41; 7tm_1,7tm_2,GPS,WIF;TM=Y;SS=M; 2.66
458213; AL047521; Hs.12210; hypothetical protein FLJ13732 similar to tensin; pkinase,none; 2.66
426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.66
435410; AL135067; Hs.117182; ESTs; none,pkinase,RBD,DAG_PE-bind; 2.66
437838; AI307229; Hs.184304; ESTs; CARD,ICE_p20,ICE_p10,HIT,voltage_CLC,CBS,HCCA_isomerase; 2.66
430293; AI416988; Hs.238272; inositol 1,4,5-triphosphate receptor, type 2; ion_trans,RYDR_ITPR,MIR,none; 2.65
433090; AI720050; ; immortalization-upregulated protein; none;SS=M; 2.65
432103; T15803; Hs.272458; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); Metallophos;TM=M;; 2.65
435852; H72303; Hs.36011; ESTs; pkinase,none; 2.64
433327; AI674779; Hs.126744; ESTs; none,7tm_1; 2.64
438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 2.64
432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface receptor; none;TM=M;SS=M; 2.63
446963; AI862668; Hs.176333; ESTs; OMPdecase,Pribosyltran,pkinase,RhoGEF,PH; 2.63
444821; AA053564; Hs.12040; STE20-like kinase; pkinase;TM=M;; 2.63
436206; AK001451; ; CD2-associated protein; none,none; 2.63
434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic receptor; death,Kunitz_BPTI;TM=Y;SS=M; 2.63
439039; AI656707; Hs.48713; ESTs; pkinase,none; 2.63
449656; AA002008; Hs.188633; ESTs; PIP5K,none; 2.63
429341; X73874; Hs.2393; phosphorylase kinase, alpha 1 (muscle); none;TM=M;; 2.62
445174; AV652850; Hs.172004; titin; fn3,ig,SGXXSG,none; 2.62
424950; AA602917; Hs.156974; ESTs; none,CDP-OH_P_transf; 2.62
438141; AW946871; ; gb:RC2-ET0022-080500-012-d02 ET0022 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prot,none; 2.61
434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, complete cds; pkinase,TBC,Rhodanese;TM=M;; 2.61
409264; NM_014937; Hs.52463; KIAA0966 protein; Syja_N;TM=M;; 2.60
458438; AI141520; Hs.151464; ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]; pkinase,none; 2.60
400719; ; ; NM_004055*:Homo sapiens calpain 5 (CAPN5), mRNA. VERSION NM_004335.2 GI; C2,Peptidase_C2,Calpain_III;TM=M;; 2.60
427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 2.59
426086; T94907; Hs.188572; ESTs; PH,Ets,CH,spectrin,Ca_channel_B,none; 2.59
430105; X70297; Hs.2540; cholinergic receptor, nicotinic, alpha polypeptide 7; Neur_chan_LBD,Neur_chan_memb,pkinase;TM=Y;SS=M; 2.58
411495; AP000693; Hs.70359; KIAA0136 protein; HATPase_c,bZIP;TM=M;; 2.58
438167; R28363; Hs.24286; ESTs; none;TM=Y;SS=M; 2.58
418749; N75147; Hs.22488; ESTs; none,zf-C2H2,KRAB,pkinase; 2.58
454289; AL137554; Hs.49927; protein kinase NYD-SP15; dCMP_cyt_deam;TM=M;; 2.58
443605; H06865; Hs.134131; ESTs; efhand,ion_trans,none; 2.57
429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 2.57
403088; ; ; NM_003319*:Homo sapiens titin (TTN), mRNA. mRNA.; fn3,ig,SGXXSG;TM=M;; 2.57
409190; AU076536; Hs.50984; sarcoma amplified sequence; transmembrane4;TM=Y;SS=M; 2.57
426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fis, clone HRC04468; ig;TM=Y;SS=M; 2.56
403328; ; ; Target Exon; Glyco_hydro_35;TM=M;; 2.56

426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg,HEAT_PBS;; 2.56
428695; AI355647; Hs.189999; purinergic receptor (family A group 5); 7tm_1;TM=Y;SS=M; 2.54
419285; D31887; Hs.89868; KIAA0062 protein; Zip;TM=Y;SS=M; 2.54
415740; N80486; Hs.39911; Homo sapiens mRNA for FLJ00089 protein, partial cds; CBM_21;TM=M;; 2.53
403305; NM_006825; ; transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment; pkinase;TM=Y;SS=M; 2.53
443804; AL135352; Hs.255883; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Peptidase_M18,Peptidase_M18,Y_phosphatase; 2.53
450425; H06607; Hs.6099; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,none; 2.51
401702; ; ; NM_001171*:Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), mRNA.; ABC_tran,ABC_membrane;TM=Y;SS=M; 2.50
439463; W69304; ; gb:zd46f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5', mRNA sequence; fn3,Y_phosphatase,none; 2.50
425975; AB011082; Hs.165559; organic cationic transporter-like 4; sugar_tr;TM=Y;; 2.50
443259; AW090601; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1,none; 2.50
400777; ; ; NM_007325*:Homo sapiens glutamate receptor, ionotrophic, AMPA 3 (GRIA3), transcript variant flip, mRNA.; lig_chan,SBP_bac_3,ANF_receptor;TM=M;SS=Y; 2.49
426044; AA502490; Hs.170290; ESTs; none,none; 2.48
454564; AW807573; ; gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.48
415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; KH-domain,TUDOR;TM=M;SS=M; 2.47
426481; AW963941; ; gb:EST376014 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence; Y_phosphatase,Band_41,DSPc,none; 2.46
426005; AA377499; ; gb:EST90341 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence; tubulin,FKBP,COX6B,7tm_1,tubulin_C;SS=M; 2.46
424879; AA348013; Hs.273385; ESTs; arf,G-alpha,none; 2.46
415156; X84908; Hs.78060; phosphorylase kinase, beta; none;TM=M;; 2.46
416508; R39769; ; ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; SH3,PDZ,Guanylate_kin,ZU5,none; 2.46
408087; AW150645; ; gb:xg54f07.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone 3', mRNA sequence; XYPPX,ABC_membrane,ABC_tran; 2.46
433434; AA588429; ; gb:no22b03.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,DNA_mis_repair,HATPase_c; 2.45
446768; AV660305; Hs.110286; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 2.45
437158; AW090198; ; KIAA1150 protein; none;NA;NA; 2.45
430177; AW969233; Hs.302746; MSTP028 protein; K_tetra,none; 2.45
422270; AF114494; Hs.114062; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a; none;TM=Y;; 2.45
430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; Y_phosphatase,Adaptin_N,Y_phosphatase; 2.44
446569; AW248031; Hs.155839; hypothetical protein MGC12934; adh_zinc,PGK,Semialdhyde_dh;SS=M; 2.44
411902; AW875344; ; gb:RC1-PT0009-220300-013-f06 PT0009 Homo sapiens cDNA, mRNA sequence; none,pkinase,ank; 2.43
430057; AW450303; Hs.2534; bone morphogenetic protein receptor, type IA (BMPR1A) (ALK-3); Activin_recp,pkinase;TM=Y;SS=M; 2.43
446338; AI289121; Hs.206978; ESTs; none,SH3; 2.42
426221; AB007881; Hs.110613; KIAA0421 protein; none,Ribosomal_S8; 2.42
446796; AI652497; Hs.110103; RNA polymerase I transcription factor RRN3; none,none; 2.41
428360; H10291; Hs.30974; ESTs; pkinase,PBD,none; 2.40
428379; X06026; Hs.2259; CD3G antigen, gamma polypeptide (TiT3 complex); ITAM;TM=Y;SS=M; 2.40
432488; AA551010; Hs.216640; ESTs; Na_sulph_symp,none; 2.40
407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, yeast, homolog)-like; none,Ribosomal_S13,Galactosyl_T,Zip,adh_short,zf-C3HC4; 2.40
448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.40
428283; AI439096; Hs.323079; Homo sapiens mRNA; cDNA DKFZp564P116 (from clone DKFZp564P116); Y_phosphatase,fn3,Ig,none; 2.39
432460; H12912; Hs.274691; adenylate kinase 3; adenylatekinase,none; 2.38
429549; AI333013; Hs.250505; retinoic acid receptor, alpha; none,zf-C3HC4,BRCT,lig_chan; 2.38
429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; Phosphodiest,Somatomedin_B,Endonuclease,none; 2.36
417473; M55268; Hs.82201; casein kinase 2, alpha prime polypeptide; pkinase,ABC1;TM=M;; 2.35
453186; AK001708; Hs.32271; hypothetical protein FLJ10846; TK,DUF300;TM=Y;SS=M; 2.33
447276; AL049795; Hs.17987; hypothetical protein MGC1203; none;TM=M;; 2.33
445310; AI242490; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,pkinase; 2.31
432942; AF083955; Hs.279852; G protein-coupled receptor; 7tm_1,globin;TM=Y;SS=M; 2.30
434693; AW976001; Hs.337603; ESTs; none,none; 2.26
452034; F12234; Hs.75893; ankyrin 3, node of Ranvier (ankyrin G); ZU5,death,none; 2.25
423732; AF058056; Hs.132183; solute carrier family 16 (monocarboxylic acid transporters), member 7; sugar_tr;TM=Y;SS=M; 2.25
404956; ; ; C1003210*:gi|6912582|ref|NP_036524.1| pefilin [Homo sapiens] gi|6009487|dbj|BAA84922.1| (AB; none,PI3_PI4_kinase,PI3K_C2,PI3K_rbd,PX,PI3Ka,C2; 2.24
452183; NM_006594; Hs.28298; adaptor-related protein complex 4, beta 1 subunit; Adaptin_N,Y_phosphatase; 2.23
420529; D25259; Hs.319844; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase,DAG_PE-bind,RBD,ras,DC1,GFP;TM=M;; 2.21
408808; BE074219; Hs.17230; hypothetical protein FLJ22087; Armadillo_seg;TM=M;SS=M; 2.21
451932; AA360954; Hs.27268; Homo sapiens cDNA: FLJ21933 fis, clone HEP04337; SH3,PH,RhoGEF;TM=M;; 2.21
432008; AW296791; Hs.193170; hypothetical protein FLJ21687; LIM,Synaptophysin,ion_trans,KOW; 2.20
455840; BE145897; ; gb:MR0-HT0208-221299-204-b07 HT0208 Homo sapiens cDNA, mRNA sequence; PI3_PI4_kinase,PI3Ka,PI3_PI4_kinase,PI3Ka; 2.19
429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor type, R; Y_phosphatase;TM=Y;SS=M; 2.19
430975; AA490055; ; gb:ab05b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 3', mRNA sequence; adenylatekinase,Thymidylate_kin;TM=M;; 2.17
407174; T79938; Hs.77062; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5; ig,none; 2.16
450921; AA098790; Hs.146245; ESTs, Moderately similar to T17242 hypothetical protein DKFZp586B1417.1 [H.sapiens]; none;NA;NA; 2.15
427209; H06509; Hs.92423; KIAA1566 protein; pkinase;TM=M;; 2.14
401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,ion_trans,PAC,PAS,none; 2.12
426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylatekinase,none; 2.07
439520; W76548; Hs.336621; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ion_trans,none; 2.06
410439; R35943; Hs.63758; transferrin receptor 2; PA;TM=Y;; 2.05
448696; AI564769; Hs.173070; EST, Weakly similar to ZN42_HUMAN ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1) [H.sapiens]; none,zf-C2H2; 2.04
449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra,ion_trans,none; 2.04
453496; AA442103; Hs.33084; solute carrier family 2 (facilitated glucose/fructose transporter), member 5; sugar_tr;TM=Y;SS=M; 2.02
443952; AI149106; Hs.143530; ESTs; pkinase,none; 2.02
437589; AA761322; Hs.269662; ESTs; SH2,SH3,C2,PH,RasGAP,none; 2.02
422637; AA399024; Hs.118836; myoglobin; globin;TM=M;; 2.01
450253; AL133047; Hs.24715; Homo sapiens mRNA; cDNA DKFZp434D0215 (from clone DKFZp434D0215); partial cds; SH3;TM=M;; 1.97
401984; ; ; C17000146*:gi|2143629|pir||A57156 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I; pkinase;; 1.96
453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying protein 1; none;TM=Y;; 1.95
417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown protein; none;NA;NA; 1.94
411450; H49619; Hs.127301; ESTs; pkinase,none; 1.82
406303; ; ; C16000922:gi|7499103|pir||T20903 hypothetical protein F14F4.3b - Caenorhabditis elegans gi; ABC_tran,GTP_EFTU,PRK,ABC_membrane;TM=Y;; 1.80
425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor type, M; fn3,Ig,Y_phosphatase,MAM;TM=Y;SS=M; 1.74

425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (soluble); PEPCK;TM=M;; 1.65
425958; AW163271; Hs.301839; intracellular antigen detected by monoclonal antibody KI-1; intracellular hyaluronan-binding protein; Y_phosphatase,DSPc;TM=M;; 1.63
432563; NM_013261; Hs.198468; peroxisome proliferative activated receptor, gamma, coactivator 1; rrm;TM=M;; 1.51

TABLE 49B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
411089	5597_6	BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680
439285	22495_1	AF086101 AL133916 AW955684 AW950828 AI346341 AI867454 BM263376 BF432231 AI421279 AI655270 AW014882 BF439949 AA775552 N62351 AA626243 N59253 AI341407 AA456968 AA457077 AI358918 AA364013 N79113 N54784 BE175639 N76721 AV727392 Z45529 Z44343 F05908 F05403 F05398
438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
451320	12225_2	AK057826 AI631982 AA224195 AI701458 AA890570 AW966562 AW071907 AI671352 AI375892 T03517 AI124088 R88265 AI084316 BF223720 AI354686 T33652 AW205836 BE931115 AI720211 T03490 BF084055 AI372637 T15415 BG054890 AA630384 F26326 AI140719 AA443303 T33230 T33623 T33511 T33785 AW118072 W20198 AI657180 T15734 AI419606 N90552 AA224388 T15909 T03515 D55612 W27899
400205	2538_1	NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355 AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750 BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802 BF758454 BG960772 BF757769 BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628 AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF590668 AI017447 AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365 AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533751 BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858 AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818 AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896 AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890 AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427 BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471 BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236 AL579993 BG108733 BG483503 BG571032 BG492505
400210	133_1	BC014030 NM_004068 BC004996 AK057883 D63475 BM468205 BG386792 BG750447 BG575842 BG479084 BG741027 AU118129 BE901043 AU141281 BG825395 BG338276 BE396231 AU121493 AU131489 BF341132 BG335659 BI769251 AU142779 AU124483 BG480828 AU121353 BG702326 AU137866 BG759046 BI460601 BE887290 BG750415 BF127710 BG757819 BI160266 AU122086 BG824046 BG744180 BE884943 BM006610 BG702599 BI870749 BF307033 BI334771 BG480606 AU142599 AU141336 BM018563 BI335565 AU136308 BE391241 BG774488 BE278025 BG717959 BG706920 BE312567 AU138300 BE303034 BE303016 AU139252 BE336797 BG470940 BE336735 BF305197 AU134288 AU139907 BE261245 BE208718 BG761912 BF212890 AW732692 BM011258 AW247629 AU136696 BF530078 BF204146 AL048752 BG328927 BE388385 BE260122 AU138789 BE253465 BF733914 AW249415 AW239535 BE311791 BE256236 BF529742 BG770465 AW245777 AW245813 BE296677 BE266852 BE168115 BE396596 BE280057 BE168229 AI750820 AU134137 BF792191 AI272215 AI907348 AW238875 BF805152 BF568397 BE712727 BE081443 BE001805 BF724536 BF744705 AW247385 BE796369 AU133759 AV705142 BE794402 BM465821 BG281284 AW384831 BM450689 AU134125 BE311650 BF356318 BM462831 BG420555 BE749127 AU134590 BM019438 BC013796 BG761223 BG122058 BE872076 BG748496 BG821374 BE619159 BG423244 AU137110 AU127210 BE270081 AA496860 AA351380 AA356303 AU099781 AA355912 AA371411 AA325535 U36188 AL569574 AL577204 AL525543 AL567342 AL567334 AL567122 AL536527 AL567098 BG681585 BG824951 BI870652 BI225855 AW393878 BG750632 BI223803 BE877552 BE270473 BE389392 BE779021 BM017845 BI117816 BE396513 BM049006 AW393945 BE786941 BE267724 BE562981 BE314236 BF744102 BM019781 BF806063 BF828673 BF829181 BI008788 BF829180 BF829175 BF433802 BE909928 BF839784 AW578564 BF943095 AW328030 AA448596 AW882688 AA909845 BF924341 AW361460 AA425174 BE940557 BF761585 BF931276 BF934886 W68597 BF933977 BI035906 BE836064 BF837576 BI018368 AA205908 H54612 R88902 BE812330 BE932300 BF924562 AW805376 BE769859 R87381 AA371901 BE838855 AA326381 W56191 AA341231 AA464093 AL575977 AL518650 AL547393 BG338327 AL517563 AL536921 BG207096 BG207589 BG199290 BG220159 BG744842 BG104730 AA555035 AA618009 AA861062 AA610582 AW245418 AI040983 AA521380 AW245455 AU147292 AU155236 BE620286 AW250767 BF888236 BE620819 AU154343 AU150827 AU148334

		AW069495 AA701091 AU155225 AW250019 AA666235 AU147764 AA449739 BF907598 AW043731 AU144390 AI924565 BE300631 AW874021 BE208088 BF732773 BF594057 AI159873 AU143930 N24100 AI052499 AI989370 AI366151 AI139248 AU144776 AA838250 AI095433 AI269227 BF811358 AU151352 AA477554 AI131290 AI049797 AU157349 AA620559 AA581533 AI338299 AA402755 AI050079 AU157614 AI280691 AA706590 BE206615 AA861056 AU153214 AU155712 AW069554 AI081124 AU155846 AI081123 AA719876 AI754976 AI027763 AA723095 BI518782 AW050706 F37521 R79062 AA565530 H39826 AA404670 AU156884 AI139682 AA513633 AI283202 AA651856 AI623515 AA427413 AW248474 BF841432 BM453246 AI302390 AA808269 AI249357 AA132775 AA716732 AA479932 AI198296 AI208674 AI088433 F36977 AA496899 AW615762 AA602541 AA341161 D58785 T15399 AI286077 W69152 F28418 AI272156 AA338034 AA568455 BE206121 AI080033 AI699680 AA861255 AI953465 AI613240 AL581773 AL531577 BF526361 AA657809 AW152670 BE621523 AW078705 AW673719 AA102613 AA195604 R72209 AA402208 AA404305 N24999 AI963535 D54741 BI461415 BM475959 BI260926 BI116213 BE280120 BE940258 BE280044 AI905744 BG001474 BE937718 BF799283 BI091621 BG421006 BG289235 BF736825 BI253429 BG170064 R72512 T92815 BF931257 BM455183 BG033362 BG574220 N31395 BF739185 AA371995 BE879011 BI198754 BF378989 T12266 BM019421 BI194570 BF378992 AW996595 BI858649 W94605 W61345 AA122384 AA171923 T92736 AA761504 AI819039 AI439358 AL517777 AL565919 AA622001 AA642695 AA704144 AA081465 AA070621 AA375562 AA700011 AA925863 W37310 AL566236 BF677809 BG750021 AW361433 BE828605 BE268449 BF805977 BG292452 BF981071 BF217108 BF928698 R33993 AW882841 AI857453 AW078733 AI433035 AI018103 R90927 AA804720 AA551734 R33835 H19741 R78754 BF930494 BG109583 AA631926 BE834008 BG996533
	433470	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI151312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
	430563	62_38	BC015334 AA805670 AW014586 N66615 BG029745 AA481269 H91728
	454042	30254_1	AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570
	426136	1222789_1	AW957244 AA370585 AW957239
	436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI151312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
	435542	132718_1	AW975503 BE763276 H74234 AA687376
	418869	12789_14	AA229762 AA230035
	400261	23110_1	BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472 AI357070 AI865365 AW014799 AI767973 AW518041 AA909398 AW768506
	422940	58443_1	BC012771 BG397153 BF366196 AA337277 AA319285 AW843252

410032	1490765_1	BE065985 BE066083 BE066008 BE066093 BE065944
400263	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW025128 N23684 AW006041 AI337521 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
413227	25501_86	BE072622 M79082
426966	349_1	NM_025237 AF326739 AW771508 AI498457 AI493134 AI383985 AI498691 BF431247 AI580267 D79813 AF331844 AA393939 AI783624 AA969408 AI768408 AA393768
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183
452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
439096	1241997_1	AW978432 AA830185 N67023 R80000
425505	1228213_1	AL036458 AA358606 AW962990
400208	16640_1	X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 AI913055 AW083235 AI078474 AI925022 AW504628 AW129725 BE466589 AW002786 AW591760 AI968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 AI248207 AI762509 AI812070 AI249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 BI014177 AL519126 BE675314 AW806520 BI870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 BI013066
422667	224778_1	AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848 AA398070 AI383375 AW611490
407305	2466680_1	AA715338 AA715284 AA715344
443068	18695_17	AV752763 AI032142 N30308 N22181 H95390 AW675632
433075	78_6	X98248 NM_002959 AU127082 AU143346 BE327147 AI168442 AA426361 BF056336 AA418378 AI470560 AI365213 BI032745 BI032986 AA969895 AA233278 AW291971 AA418326 AI198417 AI337018 BI032747 AA888000 AU099083 AU129681 AL036861 AA418275 BF887436 BF767448 AA232975 BI094065 BI859449 AL079651 BF877391 AW902319 BF878798 BG281450 AA418268 BG770672 BE890328 BI520437 BE387505 AW375004 BI020046 BI033747 BF800905 BF869732 N99710 BF905459 BE715637 BE746496 BF918537 BF751392 BF751390 BF369123 BG949840 AA984366 H85743 AW593418 AI990196 T92267 AA018359 H38111 BM050097 BF692315 AW805907 AI547305 AA631091 BF845219 BG949806 T92310 BE277220
400252	2656_2	U44839 NM_004651 BC000350 BI458316 AU117940 BG759024 BG749694 BE799505 BG831537 AI816335 AA325352 AL547005 AW157038 AI859331 AI816186 AU150786 AL043549 AW162880 AU159233 AI143169 T03478 BE727648 AA764725 BE206603 AI369814 AI984369 AW157545 BE221486 H99016 AU159025 AI074496 AI494516 BE245950 AA704385 AA280862 AI479595 AI369776 BE671398 T05538 AA682249 BI677303 BE645335 AI359434 H92868 D52599 D53609 D54715 T06015 BE222174 AI954706 D53218 D53787 R69889 W86896 AI497670 R70771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H56512 D55956 BI044097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600 AI858764 D52367 W22034 BG818979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267 W21941 AA328817
400209	16640_1	X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 AI913055 AW083235 AI078474 AI925022 AW504628 AW129725 BE466589 AW002786 AW591760 AI968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 AI248207 AI762509 AI812070 AI249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 BI014177 AL519126 BE675314 AW806520 BI870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 BI013066
444825	19904_1	AV659361 BE075267 BF743302 AL549208 AI950002 AI224961 AI471552 AI356537 AA768943 AA677028 AI358509 AI147596 AI208057 AI042009 AA156840 AA156603 AA151281 AA151341 N73171 AL540476 AI950893 BG960775 AL573355
414991	1785136_1	D78831 C17898 D78863
432236	1001131_1	AW747857 BI062758 AW629481 AA837630 AA557850 AA531132 AW973966 AW747856
417527	2431831_1	AA203524 W88451
425645	1283068_1	BE539344 AA361027
455608	1478902_1	BF328781 BE011406 BE011437 BE011402 BE011395 BE011428 BE011421 BE011407
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407393	6807_1	NM_018485 AB038237
400178	840_4	U69668 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AI870824 BE973573 BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687 BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859 AW167268 AI990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916 AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 AI650450 AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782 AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532 BE934857 BF925057 AW438446 R86246 AW179270 BE087782 BI832144
410927	3618_2	AW956025 AW956024 BE550261 BF747649 BF802668 AA369961 AV747207 AW973072 BE467756 N51927 AA531539 AW241296 AI797097 BI492823 AW021896 F10837 BE715542 BE715487 AW087443 AA533638 R51354 AW131541 R51852 N53741 R39257 T77635 BF955795 BF331656 F13236 AW810749
449343	14470_1	AK055378 BE896063 AV722833 BI032095 BF952019 BG547204 AI151418 W03542 W60401 AI346936 AA862855 W60310 N72501 BF963436 C04881 H90060 AA001203 AI863984 AI932612 AI499771 AI187944 AA501896 AA714924 H00689 AA918680 AA573996 AA521308 AW182868 BF996707 AA908959 AI628880 AW173363 AW665845 AA130178 AI818267 AI653663 AI828924 AA746655 AI951984 AI635625 AI093113 AI377976 AI624029 AI418242 R76291 W92652 AI207798 AV706224 AA742467 AA641806 W61229 AA130170 AA160170 H85007 W72474 W61163 H97873 AL047509 R76567 AA812071 H81599 AA021275 H85004 H85894 BG537537 BF830518 W76228 W46673 Z43839 R78710 C01747 H00789 BI036345 W92828 BE150445 AW380821 AW173095 H85630 H81598 H86032 R84855 R13223 AA774992
432639	1237887_1	AW973785 H60163 AA557608
417479	2356588_1	AI057052 AI241633 T89416
426477	1296538_1	AA379611 AA379464 AA379463
418342	295203_2	BG025680 AW890852 BE002723 BE763824

400275	18707_1	NM_006513 BC009390 X91257 BC000716 BM450041 BI771139 AV710955 AU120415 AU141179 AU121081 BE409287 AU141397 AU122238 BI256788 BE386217 AU143368 AU133780 AU139704 BG531086 BE268235 BE545230 AU143414 AV761720 AU129842 AU143343 BE270064 BG473378 BE298813 BI772360 BE617354 AU140124 BE277005 BG746716 BE814960 AW161287 AV762084 BG898985 AW674875 AA313975 AV749916 AA374328 BM011248 AU098465 AW238888 BG940091 BG284599 AW410037 AA378483 D49914 AL573323 AL549819 AL572282 AL572871 AL568117 AL571945 AL547790 AL581217 AL514659 AL573926 AL540816 AW410038 BI262249 BG284713 AI659394 AI093582 AW965846 AA652206 AI686014 AA654357 AU146982 AW273447 AW157715 AW574750 BG683509 AW887824 AI818522 AA703770 BE542873 AA515504 AU154982 AA831254 AA828521 AI088602 AA854654 AA190869 BF062816 AA464944 BG261335 AI003584 BG402820 AA932098 W68695 AW182900 W37334 AI073864 C17924 C18528 AI299318 BF154399 BG319570 BF764242 BF764209 AI620320 T06029 BF447193 F29285 AL548949 BI333775 BE743602 BE618230 BE268139 BF036434 BE562718 BG774381 AA659833 AA297649 AA010945 BG105512 BE269205 T32623 BG015679 AL518518 AL517118 AL538396 AI049861 AL581976 AV752041 W26586 BE181609 AI963015 BG057603 AI720256 AA844560 AA055570 BE619606 C17428 AI042174 N93945 N69743 BF795208 AW057940 BI091399 AW975179 AA909936 H28712 W65445 AL515439 W37117 H66514 T85737 W37369
414087	1632850_1	W19712 BE247277
423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138
412283	1163164_1	AW936035 AW935951 AW935789 AW935881 AW936018 AW935892 BE069084
409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
413285	12794_9	BE078405 BE078404 BE168534
426578	358276_1	AV742719 R23027 R63874 AA381749
438005	694209_2	BG542693 D63271 T94955 AA774994
454701	352355_1	BF697879 BG984482 AW854930 AW854941 AW814115 AW814431 AW814190 BF325887 BF325890 BF985536
411140	1071177_1	AW819463 AW819514 AW819617 AW819618 AW819609
407013	2073_7	U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376
432925	225876_1	AA878324 AI619686 AI014377
417670	2139687_1	T85948 R07785 T86972
400189	2140_1	Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536 AW589886 AI244419 AA749261 AA535435 AW205689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051 AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG828155 BF093014
411331	1076355_1	AW837178 T77002 F13038
418177	6503_2	AK056654 AJ420421 AI127111 AA705921 AA749298 AA776967 AI343758 AW070583 AA766587 AA804876 AA460658 AA394137 W72279 AW071467 AI343843 AA393817 AW769379 AA861873 AA715043 AW512448 AI452856 AI819873 T17354 AW779778 BF477620 AI783605 AI624523 AA261906 AA514931 BI964124 AW576481 AI864544 AA490863 AA860972 BI963076 AI632879 AA291985 AA255873 BI966876 BI963833 Z38970 BI495302 BI495301 AI784395 AU185472 AA652150 AA652026 D20449 BI088167 BI250636 BE869946 AI935271 BI792882 AI762915 AI809275 AI813351 BF447139 AI052069 AI057127 AA398950 AA291984 AA292934 AA262543 BF760287 R64455 R72980 H90786 BE698016 AW959314 BI031449 AL574617 AA776284 AA393770 BM455617 BI602104 BI793150 N36710 H59529 BI005937 BI600748 BF085914 BF085907 BF835429 BF835210 BF085926 AA226136 BF836829 BF836606 BM007373 AI369807 BF085930 W25119 BI252884 BI001270 BE549079 BF238403 R56934
439518	23842_1	AF086341 W76326 W72300
400211	3532_1	NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW186378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
426409	320121_1	AW964027 AA377709
459357	1086411_1	AW848421 T71427
411226	1073516_1	T62567 AW833022 AW833054
415516	1875286_1	H20760 R15237 Z43915 BF372479 F11411
433090	7504_2	AB038318 BC008888 BE905346 BE301941 AA705936 AW014954 BE378742 AI720050 BE395327 BG951204
436206	31207_1	AK001451 AU151098 AW515640 AW439618 AI671555 AW304963 AA565885 AI829434 AW590882 AI889234 AW117522 AA847824 AI636224 AA883540 AA169387 AW771571 AI130803 BF438773 AA088710 AI972691 AI972638 AI762358 AI473907 AI925905 AA502277 BG943806 BG218468 AA194853 AU128875 AA306025 BG986896
438141	1173217_1	AA778849 AW946871 AW946782 AW946955
439463	23351_1	AF086283 W69200 W69304
454564	1051820_1	AW807573 AW807572
426481	1229053_1	AW963941 AA379825 AW963944 AA379564
426005	MH790_19	NM_054014 X52220 BC005147 BI551326 AI393601 AW592611 AA608921 AA731598 W96331 AW590007 AI076813 AI022644 AA158365 AI699321 AI146747 AW296894 H85337 AA017692 AA354519 AA018512 D20081 R02704 AA825671 AA017651 AL135600 R02585 AA018849 BG749616 BF689840 R85326 AA577955 AA702354 AI076645 AI057359 H53178 W86484 H53074 BG988909 AW962456 AA367326 AA377499
416508	1974161_1	R39769 T53143 H60012
408087	633688_1	AW150645 AW811024 AW811148 AW811068
433434	194862_1	BF812525 AW504832 AI972567 AA588429 AI299694
437158	59575_1	AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847
411902	1141058_1	AW875344 AW875287 AW875285 AW875286 BF361295 AW875402 AW875400
455840	1518844_1	BE145816 BE145897 BF349721 BE145885
430975	56593_2	AK057266 BI767614 BI828586 AW069362 BI829572 AI826091 BI819382 AL040402

TABLE 49C

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Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
401027	7230983	Minus	70407-70554,71060-71160
400991	8096825	Plus	159197-159320
405137	9166422	Minus	30487-31058
404083	9944029	Minus	16650-17082
404440	7528051	Plus	80430-81581
400792	7382433	Plus	134339-134593
404289	2769644	Plus	15049-15286,30267-30457
401083	3242744	Plus	33192-33360
402211	7689783	Minus	67414-68229
402705	8782736	Plus	89961-90114,90773-90895,91131-91261
402233	7690102	Plus	90281-91477
405370	2078469	Minus	38980-39111
400846	9188605	Plus	39310-39474
405484	5922025	Plus	199214-199579,199672-199920,200252-20049
401345	9926424	Plus	148042-148392
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
406364	9256114	Minus	50715-50833
405490	7705240	Plus	20583-20850
400755	8119083	Minus	120084-120889
404276	9885189	Plus	127624-127856
402915	7406502	Minus	140-276
405616	5649378	Minus	2782-3308
400847	9188605	Plus	44643-44835
402328	4464283	Minus	13758-13922,14558-14752
405369	2078469	Minus	34183-34357,35686-35751
400845	9188605	Plus	34428-34612
403716	7239669	Plus	86899-87122
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
404140	9843520	Plus	37761-38147
405516	9454624	Plus	112707-112876,113676-113854
405110	8096888	Minus	118940-119100
403608	8308256	Minus	121321-121476
401241	4827300	Minus	30503-30844,31056-31248
405102	8076881	Minus	120922-121296
404185	4572584	Minus	129171-129327
405545	1054740	Plus	118677-118807,119091-119296,121626-12182
405411	3451356	Minus	17503-17778,18021-18290
405602	4753260	Plus	44647-44778
403391	9438337	Plus	42410-42544,83317-83540,86840-86922,8797
403869	7280046	Minus	34379-34583
404942	7382153	Plus	92095-92252
403142	9444521	Plus	89286-90131
400844	9188605	Plus	24746-24872,25035-25204
402704	8782736	Plus	37368-37493
402833	8918545	Plus	26987-27778
401851	7770425	Minus	146443-146664,147794-147971,148351-14848
401242	4827300	Minus	32616-32863
401943	4914397	Plus	65925-66371
402807	6456148	Minus	101542-101660,103476-103656
402603	9909396	Minus	141663-141852
405328	3253114	Plus	21399-21583
402974	9663349	Plus	124035-124321
400987	8086488	Minus	22052-22185
403335	8568884	Plus	112307-112524,114074-114703
401113	9966541	Minus	19419-19959
401185	9625304	Minus	177393-177691
404537	8247909	Minus	188775-189573
405266	4156171	Minus	63337-63552
402615	9926801	Plus	131390-132157
400566	9884730	Plus	64486-64714
403212	7630897	Minus	156037-156210
403290	8083176	Plus	19288-20076
401342	9908882	Plus	3096-3242
400471	9931670	Minus	105629-105760
405588	5002511	Plus	46180-46366
400539	7574902	Plus	8559-8721
403743	7652003	Minus	136463-136646
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
405099	8074292	Minus	114365-114514,128635-128831
401445	8218584	Minus	93700-93886
405480	2766593	Plus	33325-33659
402183	7658390	Minus	100618-104298
400749	7331445	Minus	9162-9293
406139	9166768	Minus	72397-72602

402129	7704953	Minus	166156-166365
400645	8117693	Minus	58471-58716
403201	9958297	Minus	109782-109934
403609	8308266	Minus	125974-126320
400719	8118911	Minus	44579-44656,45294-45487,46449-46641
403088	8954241	Plus	169894-170193,170504-170806
403328	8469086	Minus	120428-120703
403305	8099945	Plus	114632-114805
401702	1871197	Minus	68182-68325
400777	8131563	Plus	70745-71121
404956	7387343	Plus	55883-56203
401917	9502466	Plus	25054-25229
401984	4454511	Plus	103825-104024
406303	8575868	Plus	173622-173786

Table 50A lists about 414 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 85th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 51A lists about 518 genes up-regulated in seminomatous testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" seminomatous testicular cancer level was set to the 85th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 52A lists about 673 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal testicular adult tissues was greater than or equal to 6. The "average" testicular cancer level was set to the 75th percentile amongst testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 53A lists about 735 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal adult tissues was greater than or equal to 3. The "average" testicular cancer level was set to the 95th percentile amongst testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 54A lists about 476 testi-specific genes downregulated in testicular cancer (non-seminomatous and seminomatous). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio (R1) of normal testi to normal adult tissues was greater than or equal to 3. R1 was calculated as the mean number of interquartile range values over the median normal adult body tissue expression among normal testicular samples. The ratio (R2) of "average" normal testi to "average" testicular cancer among these genes was greater than or equal to 2. The "average" normal testi level was set to the 50th percentile amongst normal testis. The "average" normal testicular cancer level was set to the 95th percentile amongst testicular cancer samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 55A lists about 586 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 95th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 56A lists about 812 genes up-regulated in seminomatous testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" seminomatous testicular cancer level was set to the 50th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 50A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues

Pkey	ExAccn	UniGene	Unigene Title	R1
432666	AW204069		ESTs, Weakly similar to unnamed protein	74.60
432730	AI066520	Hs.131358	ESTs	50.55
450581	AF081513	Hs.25195	TGF-beta 4	47.85
418696	AW959433	Hs.326290	hypothetical protein FLJ12561	44.05
423458	AI204212		ESTs	36.60
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	30.60
448981	AI968719	Hs.195387	ESTs	26.40
407710	AW022727	Hs.23616	ESTs	24.00
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.35
451106	BE382701	Hs.25960	N-MYC oncogene	18.85
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	18.40
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	18.25

	424578	AK001973	Hs.150890	hypothetical protein	17.86
	418756	AA252254	Hs.226949	ESTs	17.20
	404996			Target Exon	16.15
	447534	AW953935	Hs.288655	ESTs	15.80
5	456847	AI360456	Hs.37775	ESTs	15.00
	446979	AI654443	Hs.197683	ESTs	14.80
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	14.75
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	14.70
	449322	AI638616	Hs.196566	ESTs	14.35
10	416007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	12.95
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	12.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	12.55
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.43
15	406547			Target Exon	12.35
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	12.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	11.65
	408908	BE296227	Hs.250822	serine/threonine kinase 15	11.55
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	11.05
20	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (	10.08
	426866	U02330	Hs.172816	neuregulin 1	10.05
	446791	AI632278	Hs.195922	ESTs	10.05
	433159	AB035898	Hs.150587	kinesin-like protein 2	9.85
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.95
25	427521	AW973352		ESTs	8.92
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	8.90
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.52
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
	408465	AW196940	Hs.253277	ESTs	8.47
30	444971	AI651116	Hs.148659	ESTs	8.35
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	8.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.95
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75
35	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.65
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	7.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	7.36
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	7.25
	432239	X81334	Hs.2935	matrix metalloproteinase 13 (collagenase	7.25
40	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	7.22
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.13
	435918	AF263538	Hs.86232	growth differentiation factor 3	7.13
	412537	AL031778		nuclear transcription factor Y, alpha	7.08
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	7.05
45	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.88
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	437052	AA861697	Hs.120591	ESTs	6.75
	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.72
50	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.71
	457465	AW301344	Hs.122908	DNA replication factor	6.62
	442632	AW206560	Hs.253569	ESTs	6.54
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	6.30
	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	6.30
55	448586	AI970276	Hs.156905	KIAA1676	6.12
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	6.09
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	5.95
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	5.85
	443068	AI188710		ESTs	5.85
60	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	441287	AW293132	Hs.131373	ESTs	5.80
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	5.76
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
	436902	AW247145	Hs.192729	ESTs	5.70
65	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.56
	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Su	5.55
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.51
70	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransferase 3 be	5.51
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.45
	435663	AI023707	Hs.134273	ESTs	5.40
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.40
75	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.21
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	5.15
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.12
	427961	AW293165	Hs.143134	ESTs	5.05
80	424315	AW614850	Hs.193384	putatative 28 kDa protein	5.05
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	5.00
	418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	5.00
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95

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	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.94
	443537	D13305	Hs.203	cholecystokinin B receptor	4.92
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	4.90
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
5	423642	AW452650	Hs.157148	hypothetical protein MGC13204	4.80
	449592	AI655494	Hs.195718	ESTs	4.75
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	4.73
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.68
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
10	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.60
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	4.48
	402145			Target Exon	4.48
15	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	4.47
	453289	AI188161	Hs.144627	ESTs	4.45
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	4.40
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	4.32
	426427	M86699	Hs.169840	TTK protein kinase	4.30
20	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.20
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.18
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (	4.15
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.10
	438188	AA779975	Hs.128859	ESTs	4.10
25	435514	AW592804		ESTs	4.10
	442333	AI650877	Hs.129302	ESTs	4.05
	413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	448038	AW015073	Hs.232026	ESTs, Weakly similar to RO52_HUMAN 52 KD	4.00
30	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.95
	419423	D26488	Hs.90315	KIAA0007 protein	3.95
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	3.95
	441553	AA281219	Hs.121296	ESTs	3.95
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.91
35	409757	NM_001898	Hs.123114	cystatin SN	3.89
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.88
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	3.85
	403780			C4001759:gi|133250|sp|P19474|RO52_HUMAN	3.84
	421917	AB028943	Hs.109445	KIAA1020 protein	3.84
40	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.84
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	3.82
	410193	AJ132592	Hs.59757	zinc finger protein 281	3.80
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.80
	415829	AW450198	Hs.163742	ESTs	3.78
45	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.77
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.70
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.68
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.66
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	3.65
50	420900	AL045633	Hs.44269	ESTs	3.65
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.65
	426496	D31765	Hs.170114	KIAA0061 protein	3.60
	452461	N78223	Hs.108106	transcription factor	3.60
	418379	AA218940	Hs.137516	fidgetin-like 1	3.50
55	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.45
	419384	AA490866	Hs.39429	ESTs	3.44
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (defline not ava	3.43
	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	3.41
60	422094	AF129535	Hs.272027	F-box only protein 5	3.40
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.40
	423198	M81933	Hs.1634	cell division cycle 25A	3.39
	424153	AA451737	Hs.141496	MAGE-like 2	3.38
	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.37
65	443715	AI583187	Hs.9700	cyclin E1	3.34
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.34
	449571	AW016812	Hs.200266	ESTs	3.34
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31
	452807	AA028933	Hs.162434	ESTs	3.31
70	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	3.30
	421650	AA781795	Hs.122587	ESTs	3.30
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	3.28
	438494	AA908678	Hs.130183	ESTs	3.23
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.22
75	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	3.18
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.18
	442618	R56222	Hs.26514	ESTs	3.17
80	415799	AA653718	Hs.225841	DKFZP434D193 protein	3.17
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.15
	450431	AW136797	Hs.266041	ESTs	3.13
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.12

	430835	AI240006	Hs.192326	ESTs	3.12
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.10
	417791	AW965339	Hs.111471	ESTs	3.10
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	3.05
5	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.04
	411975	AI916058	Hs.144583	ESTs	3.01
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.99
	440207	AI371978	Hs.128326	ESTs	2.98
10	435726	BE535787	Hs.113170	ESTs	2.97
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.97
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	2.95
	435373	AW665538	Hs.117689	ESTs	2.93
	452571	W31518	Hs.34665	ESTs	2.93
15	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	2.91
	414972	BE263782	Hs.77695	KIAA0008 gene product	2.90
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.90
	420092	AA814043	Hs.88045	ESTs	2.89
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.89
20	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.87
	422746	NM_004484	Hs.119651	glypican 3	2.87
	446258	AI283476	Hs.263478	ESTs	2.86
	444371	BE540274	Hs.239	forkhead box M1	2.86
	409517	X90780		troponin I, cardiac	2.85
25	414034	U89277	Hs.305985	early development regulator 1 (homolog o	2.84
	443169	AI038687	Hs.133338	ESTs	2.84
	447519	U46258	Hs.339665	ESTs	2.84
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.84
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.83
30	416201	AA467752	Hs.195161	ESTs	2.83
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.83
	457191	AI376228		Friend leukemia virus integration 1	2.82
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.81
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.80
35	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	2.75
	427719	AI393122	Hs.134726	ESTs	2.75
	451684	AF216751	Hs.26813	CDA14	2.75
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	2.74
	442032	AW016786		ESTs	2.73
40	437123	AL049285	Hs.302053	Homo sapiens mRNA; cDNA DKFZp564M193 (fr	2.72
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	2.72
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	2.71
	438180	AA808189	Hs.272151	ESTs	2.70
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.70
45	423765	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.69
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	2.69
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	2.68
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.67
	445413	AA151342	Hs.12677	CGI-147 protein	2.66
50	448769	N66037	Hs.38173	ESTs	2.66
	411022	AW936378		gb:QV4-DT0021-301299-071-f05 DT0021 Homo	2.65
	423600	AI633559	Hs.310359	ESTs	2.65
	447175	AI365208	Hs.293606	ESTs	2.65
	414151	AW976468	Hs.257245	ESTs	2.65
55	448877	AI583696	Hs.253313	ESTs	2.62
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.61
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	2.61
	449665	AI655391	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.61
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.60
60	429228	AI553633		ESTs	2.60
	410929	H47233	Hs.30643	ESTs	2.59
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.58
	446142	AI754693	Hs.145968	ESTs	2.56
	445093	AI207197		ESTs	2.56
65	413686	AI469213	Hs.71404	ESTs	2.55
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	2.55
	420218	AW958037		ribosomal protein L4	2.55
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	2.55
	414312	AA155694	Hs.191060	ESTs	2.55
70	421535	AB002359	Hs.105478	phosphoribosylformylglycinamidine syntha	2.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.52
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.51
	435096	AA664977		gb:nu73b07.s1 NCI_CGAP_Alv1 Homo sapiens	2.50
	422468	AA355210		gb:EST63589 Jurkat T-cells V Homo sapien	2.50
75	449576	AW014631	Hs.225068	ESTs	2.50
	415684	D59356		sorbitol dehydrogenase	2.50
	452226	AA024898	Hs.157103	ESTs	2.50
	421451	AA291377	Hs.50831	ESTs	2.50
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.50
80	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.49
	453941	U39817	Hs.36820	Bloom syndrome	2.49
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.49
	449655	AI021987	Hs.59970	ESTs	2.49

	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.49
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	2.48
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.48
	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	2.47
5	452404	AW450675	Hs.212709	ESTs	2.46
	444823	BE262989	Hs.12045	putative protein	2.46
	427675	AW138190	Hs.180248	zinc finger protein 124 (HZF-16)	2.45
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like 2 (bright	2.45
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.45
10	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.45
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.45
	447350	AI375572		v-erb-a avian erythroblastic leukemia vi	2.45
	428728	NM_016625	Hs.191381	hypothetical protein	2.43
	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.43
15	410276	AI554545		angiopoietin-2	2.42
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.42
	419029	AA233397	Hs.326290	hypothetical protein FLJ12581	2.42
	437908	AI082424		ESTs	2.41
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.41
20	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	2.40
	425212	AW962253	Hs.171618	ESTs	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.38
	425601	AW629485	Hs.140720	GSK-3 binding protein FRAT2	2.38
	449676	AW380579	Hs.209657	ESTs	2.38
25	429467	NM_004477	Hs.203772	FSHD region gene 1	2.37
	453227	AW135862	Hs.243991	ESTs	2.37
	417833	AW003251	Hs.86264	hypothetical protein FLJ14549	2.36
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.36
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.35
30	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	2.35
	410060	NM_001448	Hs.58367	glypican 4	2.35
	449138	AW294215	Hs.195631	ESTs	2.35
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.35
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	2.35
35	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.34
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.34
	407818	AL021938	Hs.40154	jumonji (mouse) homolog	2.34
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	2.33
	401704			NM_021195*:Homo sapiens claudin 6 (CLDN6	2.33
40	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	2.32
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.32
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.31
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.30
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.30
45	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	2.30
	448755	AW503807	Hs.21907	histone acetyltransferase	2.30
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	2.29
	441031	AI110664	Hs.7645	fibrinogen, B beta polypeptide	2.29
50	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.28
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	2.27
	425910	AA630797	Hs.184760	CCAAT-box-binding transcription factor	2.26
	401220			branched chain aminotransferase 1, cytos	2.26
	453985	N44545	Hs.251865	ESTs	2.25
55	414890	BE281095	Hs.77573	uridine phosphorylase	2.25
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.25
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	2.25
	424765	AA426211		hypothetical protein FLJ14033 similar to	2.25
	419278	AU076799	Hs.1247	apolipoprotein A-IV	2.24
60	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	2.24
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	2.23
	417273	AK002209	Hs.81831	Homo sapiens cDNA FLJ11347 fis, clone PL	2.23
	449722	BE280074	Hs.23960	cyclin B1	2.22
	443184	AI638728	Hs.131973	ESTs	2.22
65	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	2.21
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	2.21
	435045	BE297155	Hs.143698	ESTs	2.21
	414883	AA926960		CDC28 protein kinase 1	2.21
	446323	AI288274	Hs.345792	ESTs	2.20
70	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.20
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	2.20
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	2.20
	418973	AA233056	Hs.191518	ESTs	2.20
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.20
75	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.20
	443748	AW206447		gb:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su	2.20
	415989	AI267700		ESTs	2.20
	400195			NM_007057*:Homo sapiens ZW10 interactor	2.20
	428878	AA436884	Hs.48926	ESTs	2.20
80	431805	NM_014053	Hs.270594	FLVCR protein	2.19
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.19
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	2.18
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.18

	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	2.18
	413992	W26276	Hs.104557	RNA, U2 small nuclear	2.18
	412722	AI343300	Hs.15091	ESTs	2.18
	409089	NM_014781	Hs.50421	KIAA0203 gene product	2.17
5	430809	AI791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	2.17
	406542			C19000728*:gi|12585552|sp|Q9Y2Q1|Z257_HU	2.17
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfami	2.17
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetl	2.17
	425580	L11144	Hs.1907	galanin	2.16
10	439398	AA284267	Hs.221504	ESTs	2.16
	452833	BE559681	Hs.30736	KIAA0124 protein	2.15
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	2.15
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	2.15
	449410	AA001356	Hs.18159	ESTs	2.15
15	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.15
	427953	AA417944	Hs.44331	ESTs	2.15
	422281	M36803	Hs.346935	hemopexin	2.15
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.14
	444960	AI611317	Hs.341531	ESTs	2.14
20	415890	H08225	Hs.268712	ESTs	2.14
	402099			ENSP00000217725*:Laminin alpha-1 chain p	2.14
	427779	AA906997	Hs.180780	TERA protein	2.14
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	2.14
	422170	AI791949	Hs.112432	anti-Mullerian hormone	2.14
25	414161	AA136106	Hs.184852	KIAA1553 protein	2.14
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.13
	449810	AB008681	Hs.23994	activin A receptor, type IIB	2.11
	450663	H43540	Hs.25292	ribonuclease HI, large subunit	2.11
	419525	T79257	Hs.1259	asialoglycoprotein receptor 2	2.11
30	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.10
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.10
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.10
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	2.09
	418552	AF198254	Hs.86088	IGF-II mRNA-binding protein 1	2.09
35	408291	AB023191	Hs.44131	KIAA0974 protein	2.09
	425474	Z48054	Hs.158084	peroxisome receptor 1	2.09
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.09
	447831	AI433293	Hs.164115	ESTs	2.08
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.08
40	429166	AB033096	Hs.197668	KIAA1270 protein	2.08
	432446	AA542845	Hs.294088	GAJ protein	2.08
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.07
	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.07
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.07
45	449569	AI656634	Hs.195389	ESTs	2.07
	429999	AI761902	Hs.99597	ESTs	2.06
	420552	AK000492	Hs.98806	hypothetical protein	2.06
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	2.05
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.05
50	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.05
	450375	AA009647		a disintegrin and metalloproteinase doma	2.05
	409066	AA062980	Hs.66960	ESTs	2.05
	425700	AF076292	Hs.159251	forkhead box H1	2.05
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	2.05
55	409093	BE243834	Hs.50441	CGI-04 protein	2.05
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.04
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	2.04
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.04
	429840	AA459699	Hs.99496	ESTs	2.03
60	409717	AW452871	Hs.56043	CGI-115 protein	2.02
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.02
	448275	BE514434	Hs.20830	kinesin-like 2	2.02
	432731	R31178	Hs.287820	fibronectin 1	2.02
	405157			NM_003213*:Homo sapiens TEA domain famil	2.02
65	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	2.01
	423739	AA398155	Hs.97600	ESTs	2.01
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	2.00
	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	2.00
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.00
70	407259	L02256		gb:Human Fab fragment binding syncytial	2.00

TABLE 50B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539 BG215094 BG198867 BG196332 BG208220 BG212418

	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603 AI352469 BE061601 BI062752 AW818206 BF887722
	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
5	427486	684159_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
	412537	14066_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI664577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA362555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
10	443068	18695_17	AV752763 AI032142 N30308 N22181 H95390 AW675632
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
	418477	4172_1	BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092 AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
	418378	1227421_1	AA218925 AW962081 AA354237
15	422689	874209_1	AW954733 AA315006 AW856665
	435514	132288_1	AA683356 AW592804 AI150287
	439780	49082_1	AL109688 R23665 R26578
	434609	14739_1	AF147390 R76593 R76594
	454679	174325_1	AW813110 BF771370 BF771371 AW813113 AW003381
20	434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
	409517	4537_1	NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070
25			C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339
	406687	0_0	M31126
	457191	1389182_1	AI216469 AI354789 AA446136 H24336 AA446443 AI376228 R48940
	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
30			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866 AW840571
	413646	1525656_1	BE155042 BE155040 BE154987 BE155012
	442032	15407_1	BF223060 BF222818 AI950472 AW016786 AI207136 AI969730 BF222890 AI633857 AI968711 AA974235 AI352637
	411022	1066666_1	AW936378 AW936544 AW813513
35	429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
	445093	175963_1	AI207197 BF773544 AW196462
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
40	435096	125215_1	H30075 AA664977 AW975278
	422468	216674_1	AW962701 AA310998 AW962699
	415684	18695_18	BF666746 D59356 BG678312 N56640 AA166861
	447350	2267324_1	AI375572 AI480404 BF430912 T06882
	410276	641443_1	AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552
45	437908	13268_11	AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676
	418866	245947_1	T55754 AA229658 AA229857
	424765	6857_1	AK021881 AU145974 AU145787 C16964 AA428211 AU119698 AA993264 BF999192 AW903017 AA346559 AU119446 AW581679 AA991677 AW898165 AW386878 AW890957 Z18340
	414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360
50			AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
	443748	669881_1	BM467830 AI084433 AW206447 AI400976 AI248530 R16553
55	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
	400195	16894_2	BM477554 BM423967 BC020979 AF067656 NM_007057 BI869291 BG468263 BG760599 BI261788 AA855060 BE257094 BF212452 BE888249 BI259219 AW409765 BE089556 AL564377 BI258884 AW440401 AL578460 AL578434 AL556136 BG036804 AL531381 AW371757 BG610641
60			BF102552 BE294929 BF792282 BG121657 BG502285 BG777493 AL564510 AW770358 AA573448 AA564001 AA969560 AW078946 AW750065 AL573860 AA143778 H99221 AA969210 AW103401 AW750073
	450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758

65 TABLE 50C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

70 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
406547	7711513	Minus	172780-174358
75 402145	8018280	Plus	113086-114800
403780	8076989	Plus	93160-93409
403432	9719611	Minus	68204-68392
401704	3097841	Plus	24712-25374
403433	9719611	Minus	72225-72437
80 401220	9929324	Minus	48079-48279
406542	7711499	Plus	117335-118473
402099	8117697	Plus	121553-121742,123265-123423
406137	9166422	Minus	30487-31058

405157 9966228 Plus 156363-156502,157573-157746

TABLE 51A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of seminomatous testicular cancer compared to normal adult tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	56.62
432666	AW204069		ESTs, Weakly similar to unnamed protein	49.00
432730	AI066520	Hs.131358	ESTs	37.64
426534	U58096	Hs.2051	testis specific protein, Y-linked	37.60
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	32.70
420367	AA259090	Hs.257028	ESTs	29.98
420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	26.50
437052	AAB61697	Hs.120591	ESTs	26.42
407710	AW022727	Hs.23616	ESTs	23.85
420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	23.12
424578	AK001973	Hs.150890	hypothetical protein	22.27
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	22.06
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	20.46
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	18.44
434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	15.92
430252	AI638774	Hs.105328	testes development-related NYD-SP20	15.44
423458	AI204212		ESTs	15.28
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	15.26
427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	14.84
427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	12.98
426427	M86699	Hs.169840	TTK protein kinase	12.44
420401	AK001907	Hs.97464	hypothetical protein	12.40
406937	U14622		gb:Human transketolase-like protein gene	11.60
430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	11.55
425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	11.52
418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	10.94
434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	10.78
436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Su	10.54
437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	10.40
433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	10.32
421241	X91817	Hs.102866	transketolase-like 1	10.14
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	10.02
418134	AA397769	Hs.86617	ESTs	9.76
433159	AB035898	Hs.150587	kinesin-like protein 2	9.56
433975	AA971953	Hs.122055	ESTs	9.36
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	9.30
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	9.22
431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	9.16
436899	AA764852		ESTs	8.76
426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.76
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	8.64
408908	BE296227	Hs.250822	serine/threonine kinase 15	8.50
413627	BE182082	Hs.246973	Intron of Bicaudal D homolog 1	8.42
425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	8.30
415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.14
408728	AL137379	Hs.47125	hypothetical protein FLJ13912	8.14
406547			Target Exon	8.02
424153	AA451737	Hs.141496	MAGE-like 2	7.90
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.64
437421	AA917062		ESTs	7.53
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.50
419423	D26488	Hs.90315	KIAA0007 protein	7.38
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.38
431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.32
430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (	7.29
436608	AA628980	Hs.192371	down syndrome critical region protein DS	7.25
435206	AI432364	Hs.160594	ESTs	7.20
414972	BE263782	Hs.77695	KIAA0008 gene product	7.12
407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	7.10
426518	Z43039	Hs.170198	KIAA0009 gene product	7.10
436513	AJ278110	Hs.125507	DEAD-box protein	7.04
427521	AW973352		ESTs	6.96
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.92
422232	D43945	Hs.113274	transcription factor EC	6.90
420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	6.83
431041	AA490967	Hs.197955	KIAA0704 protein	6.76
427335	AA448542	Hs.251677	G antigen 7B	6.58
422797	AB033064	Hs.236463	KIAA1238 protein	6.55
418379	AA218940	Hs.137516	fidgetin-like 1	6.46

	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	6.45
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.44
	422665	AJ011812	Hs.119018	transcription factor NRF	6.38
	433701	AW445023	Hs.15155	ESTs	6.34
5	436909	AA907120		ESTs	6.28
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	6.27
	429228	AI553633		ESTs	6.26
	419384	AA490866	Hs.39429	ESTs	6.23
	435514	AW592804		ESTs	6.08
10	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	5.90
	430835	AI240006	Hs.192326	ESTs	5.89
	438188	AA779975	Hs.128859	ESTs	5.88
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	5.80
	408758	NM_003686	Hs.47504	exonuclease 1	5.78
15	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	5.70
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.67
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	5.64
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	5.58
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.58
20	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	5.55
	438494	AA908678	Hs.130183	ESTs	5.52
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	5.52
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.48
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	5.45
25	413623	AA825721	Hs.246973	intron of Bicaudal D homolog 1	5.36
	402145			Target Exon	5.30
	414136	AA812434		SMC2 (structural maintenance of chromoso	5.28
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	5.22
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	5.16
30	408460	AA054726	Hs.285574	ESTs	5.14
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.12
	420900	AL045633	Hs.44269	ESTs	5.08
	426496	D31765	Hs.170114	KIAA0061 protein	5.01
	407122	H20276	Hs.31742	ESTs	5.00
35	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.95
	402199			Target Exon	4.90
	409103	AF251237	Hs.112208	XAGE-1 protein	4.90
	416859	H43437	Hs.80305	hypothetical protein MGC14258	4.84
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	4.82
40	410929	H47233	Hs.30643	ESTs	4.73
	417886	AA214584		ESTs	4.73
	426223	AW977812	Hs.130391	ESTs	4.72
	409421	AA199883	Hs.67624	ESTs	4.72
	428249	AA130914	Hs.183291	zinc finger protein 268	4.71
45	429999	AI761902	Hs.99597	ESTs	4.68
	431721	AB032996	Hs.268044	KIAA1170 protein	4.68
	408321	AW405882	Hs.44205	cortistatin	4.67
	419197	N48921	Hs.27441	KIAA1615 protein	4.66
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	4.64
50	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	4.64
	427119	AW880562	Hs.272525	ESTs	4.64
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.64
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.64
	409066	AA062980	Hs.66960	ESTs	4.62
55	416201	AA467752	Hs.195161	ESTs	4.53
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.52
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.50
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	4.46
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.46
60	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.34
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	4.32
	418971	AA360392	Hs.87113	ESTs	4.30
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	4.29
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.21
65	415717	AA167270	Hs.130435	ESTs	4.18
	423198	M81933	Hs.1634	cell division cycle 25A	4.12
	433849	BE465884	Hs.280728	ESTs	4.12
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.11
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.07
70	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.07
	414725	AA769791		ring finger protein 21, interferon-respo	4.05
	408291	AB023191	Hs.44131	KIAA0974 protein	4.05
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.04
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.04
75	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.03
	421917	AB028943	Hs.109445	KIAA1020 protein	4.02
	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	4.02
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.01
	436360	AI962796	Hs.156100	ESTs	4.00
80	438624	AA889055	Hs.123468	ESTs	3.99
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	3.92
	411945	AL033527	Hs.92137	L-myc-2 protein(MYCL2)	3.90
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.90

	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.90
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.88
	438456	AA913381	Hs.20594	ESTs	3.88
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.87
5	412537	AL031778		nuclear transcription factor Y, alpha	3.86
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.85
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	3.83
	422094	AF129535	Hs.272027	F-box only protein 5	3.82
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.80
10	416350	AF188625	Hs.189507	phospholipase A2, group IID	3.78
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.76
	401435			C14000397*:gi|7499898|pir||T33295 hypoth	3.76
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	3.74
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.70
15	409089	NM_014781	Hs.50421	KIAA0203 gene product	3.70
	426067	AW664691	Hs.97053	ESTs	3.67
	415684	D59356		sorbitol dehydrogenase	3.66
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.62
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	3.62
20	427761	AA412205	Hs.140996	ESTs	3.61
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	3.60
	418216	AA662240	Hs.283099	AF15q14 protein	3.59
	436180	AA808189	Hs.272151	ESTs	3.58
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	3.56
25	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.55
	426878	AA436884	Hs.48926	ESTs	3.54
	438885	AI886558	Hs.184987	ESTs	3.53
	416445	AL043004	Hs.79337	KIAA0135 protein	3.52
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.51
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.49
	427298	AA400495		ESTs	3.48
	420218	AW958037		ribosomal protein L4	3.40
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	3.40
	410420	AA224053	Hs.172405	cell division cycle 27	3.40
35	432809	AA565509	Hs.131703	ESTs	3.36
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.34
	421373	AA808229	Hs.46677	ESTs	3.34
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.31
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	3.30
40	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.30
	418049	AA211457		Homo sapiens, Similar to nuclear localiz	3.26
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.22
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	3.21
	434288	AW189075	Hs.116265	fibrillin3	3.20
45	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.19
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.17
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.17
	420161	AI683069	Hs.120817	ESTs	3.17
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	3.16
50	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.14
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	3.14
	423419	R55336	Hs.23539	ESTs	3.13
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.12
	408092	NM_007057	Hs.42650	ZW10 interactor	3.12
55	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.12
	436378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.12
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.12
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.11
	420552	AK000492	Hs.98806	hypothetical protein	3.11
60	402408			NM_030920*:Homo sapiens hypothetical pro	3.10
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.10
	415829	AW450198	Hs.163742	ESTs	3.09
	423739	AA398155	Hs.97600	ESTs	3.07
	418459	R85436	Hs.268814	ESTs	3.07
65	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.07
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	3.06
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.06
	420524	AB010575	Hs.98547	amiloride-sensitive cation channel 3, te	3.06
	433023	AW864793		thrombospondin 1	3.04
70	421633	AF121860	Hs.106260	sorting nexin 10	3.04
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.04
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	3.03
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.03
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (	3.03
75	425312	AA354940	Hs.145958	ESTs	3.02
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.01
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.01
	432446	AA542845	Hs.294088	GAJ protein	3.01
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.00
80	436902	AW247145	Hs.192729	ESTs	3.00
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.00
	430056	X97548	Hs.228059	KRAB-associated protein 1	2.98
	427617	D42063	Hs.199179	RAN binding protein 2	2.98

	406367			NM_022357:Homo sapiens putative metallop	2.97
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	2.97
	435918	AF263538	Hs.86232	growth differentiation factor 3	2.97
	436511	AA721252	Hs.291502	ESTs	2.96
5	402680			Target Exon	2.96
	414161	AA136106	Hs.184852	KIAA1553 protein	2.95
	427239	BE270447		ubiquitin carrier protein	2.95
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.94
	417576	AA339449	Hs.82265	phosphoribosylglycinamide formyltransfer	2.94
10	402299			Target Exon	2.92
	420697	AA827705	Hs.26605	ESTs	2.90
	427719	AI393122	Hs.134726	ESTs	2.90
	419131	AA406293	Hs.109526	ESTs	2.89
	410048	W76467	Hs.343874	proline oxidase homolog	2.89
15	427314	AB033024	Hs.175475	KIAA1198 protein	2.89
	424315	AW614850	Hs.193384	putatative 28 kDa protein	2.88
	430335	D80007	Hs.239499	KIAA0185 protein	2.87
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.87
	413686	AI469213	Hs.71404	ESTs	2.87
20	429183	AB014604	Hs.197955	KIAA0704 protein	2.86
	430292	AK000634	Hs.238270	hypothetical protein FLJ20627	2.86
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	2.86
	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	2.86
	435159	AA668879	Hs.116649	ESTs	2.84
25	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	2.84
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.84
	434070	AF116652	Hs.270087	hypothetical protein PRO0813	2.83
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	2.83
	433247	AB040948	Hs.142856	KIAA1515 protein	2.82
30	415884	H22966	Hs.13471	ESTs	2.82
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	2.82
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.81
	401091			decay accelerating factor for complement	2.81
	425601	AW629485	Hs.140720	GSK-3 binding protein FRAT2	2.79
35	428597	AK000147	Hs.295909	hypothetical protein FLJ10700	2.79
	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	2.79
	438243	AI581311		ESTs	2.78
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.78
	410704	BE076754		gb:OM1-BT0601-180200-121-b10 BT0601 Homo	2.77
40	429063	AW363845	Hs.322903	ESTs, Weakly similar to A46010 X-linked	2.76
	427147	AA398587	Hs.97414	ESTs	2.76
	430552	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	2.76
	437660	W31708	Hs.55304	ESTs	2.74
	425237	U07695	Hs.155227	EphB4	2.72
45	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	2.72
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	2.70
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	2.70
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	2.70
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	2.68
50	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.68
	401464			histone deacetylase 5	2.68
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	2.68
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	2.68
	419029	AA233397	Hs.326290	hypothetical protein FLJ12581	2.67
55	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	2.66
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamidine syntha	2.66
	423453	AW450737	Hs.128791	CGI-09 protein	2.66
	412673	AL042957	Hs.31845	ESTs	2.65
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.65
60	434159	AW135214	Hs.191828	ESTs	2.65
	427260	AA663648		gb:ae70b06.s1 Stratagene schizo brain S1	2.64
	439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.64
	414706	AW340125	Hs.76989	KIAA0097 gene product	2.64
	433979	AA620999		gb:ag03a08.s1 Soares_testis_NHT Homo sap	2.64
65	403969			ENSP00000034663:Zinc finger protein 131	2.64
	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, cosmid R2837	2.64
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	2.63
	411127	AA668995	Hs.218329	hypothetical protein	2.62
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	2.62
70	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	2.61
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.60
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	2.59
	437033	AW248364	Hs.5409	RNA polymerase I subunit	2.58
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.58
75	415585	R59946	Hs.184852	KIAA1553 protein	2.57
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.57
	426470	AA528794	Hs.128644	ESTs	2.57
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	2.56
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	2.56
80	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.56
	401837			NM_025109:Homo sapiens hypothetical prot	2.56
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	2.56
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.55

	418648	AW979223	Hs.292478	ESTs	2.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.54
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.54
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	2.54
5	428728	NM_016625	Hs.191381	hypothetical protein	2.53
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	2.52
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	2.52
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.52
	422406	AF025441	Hs.116206	Opa-interacting protein 5	2.52
10	433228	F28212	Hs.14953	KIAA1491 protein	2.51
	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	2.51
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.50
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.50
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.48
15	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	2.48
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.47
	435726	BE535787	Hs.113170	ESTs	2.47
	404068			Target Exon	2.46
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	2.46
20	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.46
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.46
	429652	AA766810	Hs.259290	ESTs	2.45
	416204	AW972270	Hs.195161	ESTs	2.45
	414713	BE465243	Hs.12664	ESTs	2.44
25	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.44
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.44
	435244	N77221	Hs.187824	ESTs	2.44
	402679			NM_000478:Homo sapiens alkaline phosphat	2.43
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.42
30	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.41
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	2.41
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.41
	423232	BE244625	Hs.125742	leucine-rich neuronal protein	2.40
	427578	AI591305	Hs.169084	ESTs, Highly similar to TUL3_HUMAN TUBBY	2.40
35	409934	R91601	Hs.190466	hypothetical protein FLJ22584	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	2.39
	438869	AF075009		gb:Homo sapiens full length insert cDNA	2.38
	434981	AW182577	Hs.293077	ESTs	2.38
40	417911	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (	2.38
	409210	AA251812	Hs.51120	cathelicidin antimicrobial peptide	2.37
	424425	AB031480	Hs.146824	SPR1 protein	2.37
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	2.37
	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	2.37
45	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.37
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	2.36
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	2.36
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	2.36
	410968	AA199907	Hs.67397	homeo box A1	2.36
50	421305	BE397354	Hs.324830	diptheria toxin resistance protein requi	2.36
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	2.36
	412389	AW947655		gb:RC0-MT0003-140300-031-b07 MT0003 Homo	2.35
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.35
	403780			C4001759:gi|133250|sp|P19474|RO52_HUMAN	2.34
55	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	2.34
	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	2.34
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	2.34
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.34
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	2.33
60	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.33
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.32
	418821	AA436002	Hs.183161	ESTs	2.32
	437437	AA226869		hypothetical protein DKFZp762L0311	2.32
	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.31
65	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	2.30
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	2.30
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	2.30
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	2.29
	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	2.29
70	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	2.29
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.28
	412721	AW183165	Hs.95600	ESTs	2.28
	404071			C12000514*:gi|7302471|gb|AAF57556.1| (AE	2.27
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.26
75	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.26
	424935	AI655010	Hs.120363	hypothetical protein MGC15634	2.26
	415791	H09366	Hs.78853	uracil-DNA glycosylase	2.26
	431667	AA812573	Hs.246787	ESTs	2.26
	424169	AA336399	Hs.153797	ESTs	2.25
80	436540	BE397032	Hs.14468	hypothetical protein MGC14226	2.25
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.24
	403242			Target Exon	2.24
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.24

	421002	AF116030	Hs.100932	transcription factor 17	2.24
	438833	BE612940	Hs.88252	ESTs	2.24
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	2.23
	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	2.23
5	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.23
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	2.23
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.23
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.23
	418826	AK000375	Hs.88820	HDCMC28P protein	2.23
10	428612	AA770001		ESTs	2.22
	433220	AI076192	Hs.131933	ESTs	2.22
	422225	BE245652	Hs.116281	zinc finger protein 266	2.22
	437549	AA759149	Hs.126757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	2.22
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.22
15	408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.22
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.21
	420062	AW411096	Hs.94785	TGF(beta)-induced transcription factor 2	2.21
	432820	AI554057	Hs.152477	ESTs	2.21
	430255	AK000703	Hs.323622	Homo sapiens mRNA for KIAA1551 protein,	2.21
20	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.20
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	2.20
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	2.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	2.20
	433698	H24201	Hs.247423	adducin 2 (beta)	2.19
25	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	2.19
	435541	AA687361	Hs.221318	ESTs	2.19
	412019	AA485890	Hs.69330	Homo sapiens cDNA FLJ13835 fis, clone TH	2.19
	418753	BE217818	Hs.87016	hypothetical protein FLJ22938	2.19
	435461	AI075846	Hs.133996	ESTs	2.19
30	402260			NM_001436*:Homo sapiens fibrillarin (FBL	2.18
	421098	AI697901	Hs.192425	ESTs	2.18
	400587			C10000649*:gi|7296574|gb|AAF51857.1| (AE	2.18
	407832	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.18
	427159	U80735	Hs.173854	PAX transcription activation domain inte	2.17
35	405770			NM_002362:Homo sapiens melanoma antigen,	2.17
	412722	AI343300	Hs.15091	ESTs	2.16
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.16
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.16
	417420	T85150	Hs.268814	ESTs	2.16
40	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	2.16
	412851	AI826502	Hs.97269	ESTs	2.16
	414702	L22005	Hs.76932	cell division cycle 34	2.16
	409670	AI368109		KIAA1856 protein	2.16
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.15
45	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.15
	434750	BE019254	Hs.4112	t-complex 1	2.15
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	2.15
	418574	N28754		M-phase phosphoprotein 9	2.15
	409019	AW385412		myosin regulatory light chain 2, smooth	2.15
50	416608	R11499	Hs.189716	ESTs	2.14
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.14
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	2.13
	422805	AA436989	Hs.121017	H2A histone family, member A	2.13
	410284	U50939	Hs.61826	amyloid beta precursor protein-binding p	2.13
55	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.12
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	2.12
	433252	AB040957	Hs.151343	KIAA1524 protein	2.12
	416819	U77735	Hs.80205	pim-2 oncogene	2.12
	437218	AL117497	Hs.58185	ESTs, Weakly similar to T42727 prolifera	2.12
60	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	2.12
	433947	AA927996	Hs.112876	ESTs, Weakly similar to AF129535 1 F-box	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.11
	435703	AW630133	Hs.83313	GK003 protein	2.11
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.11
65	422192	AA305159	Hs.113019	fis485	2.11
	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	2.10
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.10
	414151	AW976468	Hs.257245	ESTs	2.10
	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.10
70	424196	AL133660	Hs.142926	Homo sapiens beta cysteine string protei	2.10
	408831	AF090114	Hs.48433	endocrine regulator	2.10
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	2.09
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	2.09
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	2.09
75	403532			NM_024638:Homo sapiens hypothetical prot	2.09
	432141	BE410964	Hs.272736	nuclear receptor binding protein	2.08
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.08
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.08
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	2.08
80	418755	Y14443	Hs.88219	zinc finger protein 200	2.08
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.07
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.07
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	2.07

	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.07
	417230	U40998	Hs.81728	unc119 (C.elegans) homolog	2.07
	425966	NM_001761	Hs.1973	cyclin F	2.07
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.06
5	407162	N63855	Hs.142634	zinc finger protein	2.06
	422382	D79988	Hs.115778	KIAA0166 gene product	2.06
	402677			NM_000478:Homo sapiens alkaline phosphat	2.06
	433017	Y15067	Hs.279914	zinc finger protein 232	2.05
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	2.05
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.05
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.05
	402678			Target Exon	2.05
	408146	R45621	Hs.81057	hypothetical protein MGC2718	2.05
	420027	AF009746	Hs.94395	ATP-binding cassette, sub-family D (ALD)	2.04
15	427447	T65414	Hs.6647	Homo sapiens cDNA FLJ13088 fis, clone NT	2.04
	433219	AB040916	Hs.24106	KIAA1483 protein	2.04
	431126	AF085243	Hs.283619	zinc finger protein 236	2.04
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	2.04
	419669	AJ007041	Hs.92236	KIAA0304 gene product	2.04
20	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.03
	426242	AL096727	Hs.168249	Homo sapiens mRNA; cDNA DKFZp434B104 (fr	2.02
	432185	AA221032	Hs.272838	hypothetical protein FLJ10494	2.02
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	2.02
	408636	BE294925	Hs.46680	CGI-12 protein	2.02
25	420005	AW271106	Hs.133294	ESTs	2.02
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.02
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.02
	425358	AL079658	Hs.338207	FK506 binding protein 12-rapamycin assoc	2.01
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.01
30	438450	AI050866	Hs.65853	nodal, mouse, homolog	2.00
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.00
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial (DNA dire	2.00
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.00
	414251	AL042306	Hs.97689	VASA protein	2.00
35					

TABLE 51B
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539 BG215094 BG198867 BG196332 BG208220 BG212418
418477	4172_1	BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092 AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
436899	1000797_1	AA764852 AA736937
437421	978554_1	AA917062 AA757369 AW592218
430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603 AI352469 BE061601 BI062752 AW818206 BF887722
427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
436909	596835_1	AW102570 AA907150 AA907120 AA737188 AI248890 AW977353
429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
435514	132288_1	AA683356 AW592804 AI150287
422689	874209_1	AW954733 AA315006 AW856665
421974	864120_1	AA301270 AA301379 AA301366
414136	30243_1	AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920 AI566634 AA211796 BG615512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AU154486 AW605017 AW450072 AA446459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
418235	886897_1	BE072634 BE072653 AA830615 AA214736 AA331718
414725	19377_1	NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936 AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338826 AI650258 AI628362 AA227117 AI207149 AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112 BI054316
434609	14739_1	AF147390 R76593 R76594
408065	101881_1	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
412537	14066_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
415684	18695_18	BF666746 D59356 BG678312 N56640 AA166861
433641	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951 N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833 AA207155 BI004756 AA206262 AI365204 H77608 AW590511
424281	892055_1	AA338252 AA338213

	427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
	418049	12052_4	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234 AV731417 R42406 H04996 T98498 R12489 R12577 R42405
	433023	3970_8	BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871
	418866	245947_1	T65754 AA229658 AA229857
	427239	20459_2	AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074866 BE857822
	437834	294580_1	BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573
	438243	2532601_1	AI581311 AA781682 AA781678
	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523 BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866 AW840571
	430968	1237115_1	AW972830 AA489620 AA527647 AA570362
	427260	11272_50	AA401424 AA400100 AA663848
	433979	2076469_1	N50454 AA620999 T16375
	426919	347372_1	BI917595 AI203314 AL041228 AV727959 D61361 D62004 BI753157 AA961066 AI990307 BF439651 AI453076 AI376075 AI014836 AI018308 AW183530 AA393346 AA935601 AA628633 AI150282 AI028574 AI217182 AA431478 AW087473 AW900295 H50055 AL041229 BI917726
	438869	52134_1	AF075009 R63109 R63068
	412389	1174403_1	AW947655 AW984020
	400205	2538_1	NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355 AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750 BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N64710 AW993470 BF086802 BF758454 BG960772 BF757769 BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888662 BG536628 AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF590668 AI017447 AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365 AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761 BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858 AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818 AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896 AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890 AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427 BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471 BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236 AL579993 BG108733 BG483503 BG571032 BG492505
	425331	1227464_1	AA427363 AW962128 AA355353
	437437	6087_1	BC009352 BC014630 AU131857 AL527140 AU131768 BI769362 BI753220 AU129886 AU128771 AA314135 AU126819 AI333799 AA479336 AA258503 AL597351 AL359619 BG697218 BI254283 AI743846 AA236444 AA397533 AA247450 AI051464 AI224533 AU153442 AU151001 AU152621 AU151829 AU153069 AW269958 AU154195 AI862754 AI589780 AW273839 AI338155 AI126632 BE046048 AA976930 AI289304 AI625961 AI222288 AI280054 AA973329 AI524262 AI242371 AA296517 AI567865 AI590681 AJ346616 AW247913 AI422051 AI475352 AI689531 AW469308 AW198034 AA936939 AU151059 AU148134 AA486419 AU151953 AI830968 BI493265 BI493264 AU149861 BE268763 AV763495 AW962827 BM480300 AA226869 AL529368 BM451957 AU132714 BI871319 AA380739 BI911351 BF795906 BE548853 AW579751
	430183	17316_1	AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038
	430504	5477_6	BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575 AW300064 AW262133 H21568 AI363015 AI884914 H86948
	428612	1383189_1	AA770001 AA431112 AA432126
	409670	8882_8	AI625045 AW504152 AI469086 AA905873 AW504662 AW136114 AI927270 BE041754 AI648386 AA662655 AA400052 AI143501 AI744934 AI400147 AI381657 AA676551 AA974367 AW117437 AI570383 AI242456 AI274581 AA678138 R49939 AI393926 AA345854 AW605850 AI869780 AW391171 R77044
	418574	12009_2	AW955043 AI990326 AA776406 AI016250 AW451882 AA843678 BF916900 AW945895 AI979339 N23129 W70051 AA322672 N23137
	409019	32320_4	BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA489668 AW968806 AW085196 AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285
	430935	15297_3	BC017923 AA789302 AW466994 BF513878 AI819642 AI184913 AW469044 AI220572 AW072916 AI280239 AI473611 AW841126 D60937 AA489195 N59350 AA693435 BG531204 AA484243 AW514092
	424677	2518_37	U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708

TABLE 51C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406547	7711513	Minus	172780-174358
402145	8018280	Plus	113086-114800
402199	8576116	Minus	84187-84744
401435	8217934	Minus	54508-55233
402408	9796239	Minus	110326-110491
406367	9256126	Minus	58313-58489
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
402299	6693370	Plus	23367-25175
401091	9958240	Plus	94760-94898

401464	6682291	Minus	170688-170834
403969	8569909	Plus	31237-31375,32405-32506
401637	7630990	Minus	120993-121095,121660-121729
404068	3168621	Minus	18123-18766
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
402679	8113438	Plus	132079-132216
403780	8076989	Plus	93160-93409
404071	7210053	Minus	167354-167859,168810-168920,169000-16910
403242	7637817	Minus	11297-12511
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
400587	9887626	Plus	25435-25588,25668-25747
405770	2735037	Plus	61057-62075
403532	8076842	Minus	81750-81901
406137	9166422	Minus	30487-31058
402677	8113438	Plus	22135-22309,23063-23238
402678	8113438	Plus	37395-37514,37866-37981

TABLE 52A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of testicular cancer (non-seminomatous and Seminomatous) compared to normal adult testicular tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
414438	AI879277	Hs.76136	thioredoxin	51.77
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	49.93
416680	AW245540	Hs.79516	brain abundant, membrane attached signal	49.20
412948	BE243313	Hs.334851	LIM and SH3 protein 1	44.46
438091	AW373062		nuclear receptor subfamily 1, group I, m	40.70
406658	AI920965	Hs.77961	major histocompatibility complex, class	39.64
418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	38.70
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	38.25
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	37.50
430542	AI557486	Hs.119122	ribosomal protein L13a	37.22
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	35.98
432730	AI066520	Hs.131358	ESTs	35.25
444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	31.69
446525	AW967069	Hs.211556	hypothetical protein MGC5487	31.33
417088	M54915	Hs.81170	pim-1 oncogene	31.20
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	29.93
433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	29.35
426295	AW367283		zinc finger protein 6 (CMPX1)	29.32
406856	AW515336	Hs.29797	ribosomal protein L10	28.93
417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	27.99
440207	AI371978	Hs.128326	ESTs	27.75
422578	AF239666	Hs.1545	caudal type homeo box transcription fact	26.95
432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.90
420367	AA259090	Hs.257028	ESTs	26.50
429978	AA249027		ribosomal protein S6	26.43
440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	26.36
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	26.23
412636	NM_004415		desmoplakin (DPI, DPII)	26.15
435538	AB011540	Hs.4930	low density lipoprotein receptor-related	25.25
446899	NM_005397	Hs.16426	podocalyxin-like	25.25
442562	BE379584		dolichyl-diphosphooligosaccharide-protei	25.15
406656	M16714	Hs.89643	major histocompatibility complex, class	25.13
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	24.78
423961	D13666	Hs.136348	periostin(OSF-2os)	24.48
425543	R23313	Hs.334895	ribosomal protein L10a	24.38
420676	AI434780	Hs.4248	vav 2 oncogene	24.18
406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	23.96
440869	NM_014297	Hs.7486	protein expressed in thyroid	23.80
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	23.56
414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	23.22
446627	AI973016	Hs.15725	hypothetical protein SBBI48	22.93
449571	AW016812	Hs.200266	ESTs	22.83
413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	22.81
410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	22.68
414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	22.45
422714	AB018335	Hs.119387	KIAA0792 gene product	22.45
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	22.30
444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.69
406648	AA563730	Hs.277477	major histocompatibility complex, class	21.58
448588	AI970276	Hs.156905	KIAA1676	21.23
433423	BE407127	Hs.8997	heat shock 70kD protein 1A	21.19
429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.70
432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	20.60
407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	20.57

	420754	W79431	Hs.346911	ribosomal protein L22	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	20.15
	424800	AL035588	Hs.153203	MyoD family inhibitor	20.10
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	20.01
5	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	19.89
	410143	AA188169		KIAA1191 protein	19.41
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	19.08
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.03
	425535	AB007937	Hs.156287	KIAA0468 gene product	18.78
10	411573	AB029000	Hs.70823	KIAA1077 protein	18.63
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.53
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	18.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	18.50
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	18.50
15	429183	AB014604	Hs.197955	KIAA0704 protein	18.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	18.44
	450377	AB033091		KIAA1265 protein	18.40
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.15
	440528	BE313555	Hs.7252	KIAA1224 protein	18.05
20	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	17.98
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	17.80
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	17.75
	428782	X12830	Hs.193400	interleukin 6 receptor	17.48
	415221	W07418	Hs.78225	annexin A1	17.47
25	429614	AI371172	Hs.211539	hypothetical protein MGC4248	17.40
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	17.30
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	17.14
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	17.13
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	17.10
30	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	17.03
	425996	W67330		hypothetical protein AL110115	16.98
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	16.98
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	16.98
	427521	AW973352		ESTs	16.93
35	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.93
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	16.53
	449338	H73444	Hs.394	adrenomedullin	16.36
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	16.23
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	16.21
40	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	16.15
	427691	AW194426	Hs.20726	ESTs	16.13
	406786	AW161678	Hs.111334	ferritin, light polypeptide	16.11
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.10
	451106	BE382701	Hs.25960	N-MYC oncogene	16.09
45	408380	AF123050	Hs.44532	diubiquitin	16.00
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	15.93
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	15.69
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	15.64
50	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	15.55
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	15.55
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	15.53
	410185	BE294068	Hs.737	immediate early protein	15.49
	422105	AI929700	Hs.111680	endosulfine alpha	15.23
55	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	15.23
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	15.05
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	15.02
	426552	BE297660	Hs.170328	moesin	14.96
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.88
60	436860	H12751	Hs.5327	PRO1914 protein	14.85
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	14.84
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	14.78
	412623	R28898	Hs.74170	metallothionein 1E (functional)	14.70
	408989	AW361666	Hs.49500	KIAA0746 protein	14.53
65	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	14.48
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	14.31
	410325	AB023154	Hs.62264	KIAA0937 protein	14.23
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	14.20
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	14.19
70	418151	AA864238.	Hs.83583	actin related protein 2/3 complex, subun	14.18
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.13
	447211	AL161961	Hs.17767	KIAA1554 protein	14.08
	417426	NM_002291	Hs.82124	laminin, beta 1	14.08
	414420	AA043424	Hs.76095	immediate early response 3	14.04
75	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.02
	454413	AI653672	Hs.40092	PNAS-123	13.93
	452651	AI218918	Hs.30209	KIAA0854 protein	13.86
	450581	AF081513	Hs.25195	TGF-beta 4	13.85
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.78
80	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.63
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.59
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.57
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	13.53

	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	13.43
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	13.41
	447534	AW953935	Hs.288655	ESTs	13.33
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.31
5	428065	AI634046	Hs.157313	ESTs	13.30
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	13.28
	436398	H87136	Hs.5174	ribosomal protein S17	13.18
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	12.93
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	12.90
10	445817	NM_003642	Hs.13340	histone acetyltransferase 1	12.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	12.90
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	12.89
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.83
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	12.79
15	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	12.78
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	12.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	12.73
	430630	AW269920	Hs.2621	cystatin A (stefin A)	12.68
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	12.65
20	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	12.50
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	12.48
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	12.43
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.43
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	12.41
25	412247	AF022375	Hs.73793	vascular endothelial growth factor	12.41
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	12.40
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	12.38
	432409	AA806538	Hs.130732	KIAA1575 protein	12.33
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.33
30	419384	AA490866	Hs.39429	ESTs	12.33
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.32
	432805	X94630	Hs.3107	CD97 antigen	12.32
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	12.25
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	12.13
35	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	12.12
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	12.03
	402145			Target Exon	12.01
	407179	AA206465		thymosin, beta 4, X chromosome	12.00
	433208	AW002834	Hs.24095	ESTs	11.95
40	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.90
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	11.83
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	11.75
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	11.75
	427761	AA412205	Hs.140996	ESTs	11.68
45	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	11.58
	436075	BE090176	Hs.179902	transporter-like protein	11.50
	440774	AI420611	Hs.153934	ESTs	11.35
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	11.25
	419223	X60111	Hs.1244	CD9 antigen (p24)	11.08
50	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	11.08
	444656	AI277924	Hs.145199	ESTs	10.98
	420943	AI718702	Hs.279930	major histocompatibility complex, class	10.96
	450294	H42587	Hs.238730	hypothetical protein MGC10823	10.92
	413686	AI469213	Hs.71404	ESTs	10.83
55	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	10.78
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	10.75
	407252	AA659037	Hs.163780	ESTs	10.75
	445929	AI089660	Hs.323401	dpy-30-like protein	10.70
	451864	N20370	Hs.69547	ESTs	10.69
60	429307	AU076592	Hs.198951	jun B proto-oncogene	10.64
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	10.63
	447519	U46258	Hs.339665	ESTs	10.63
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	10.59
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	10.55
65	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	10.54
	437103	AW139408	Hs.152940	ESTs	10.50
	449961	AW265634	Hs.133100	ESTs	10.50
	441244	BE612935	Hs.184052	PP1201 protein	10.49
	450139	AK001838		serum/glucocorticoid regulated kinase	10.48
70	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	10.48
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rhotekin, clone	10.47
	446682	AW205632	Hs.211198	ESTs	10.43
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.43
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	10.40
75	424950	AA602917	Hs.156974	ESTs	10.40
	434442	AA737415		ESTs	10.33
	438089	W05391		nuclear receptor subfamily 1, group I, m	10.33
	432559	AW452948	Hs.257631	ESTs	10.30
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	10.30
80	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	10.28
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	10.27
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	10.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	10.23

	445245	AB032973	Hs.12461	LCHN protein	10.18
	446488	AB037782	Hs.15119	KIAA1361 protein	10.15
	410611	AW954134	Hs.20924	KIAA1628 protein	10.15
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	10.14
5	416926	H03109	Hs.263395	HT018 protein	10.07
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	10.05
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	10.04
	411975	AI916058	Hs.144583	ESTs	10.03
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	10.00
10	408784	AW971350	Hs.63386	ESTs	9.95
	444795	AI193356	Hs.160316	ESTs	9.93
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.90
	400440	X83957	Hs.83870	nebulin	9.90
	414829	AA321568	Hs.77436	pleckstrin	9.88
15	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.88
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	9.85
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	9.83
	446795	AI797713	Hs.156471	ESTs	9.78
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	9.67
20	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	9.65
	419904	AA974411	Hs.18672	ESTs	9.63
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	9.63
	414405	AI362533		KIAA0306 protein	9.58
	418840	AI821614	Hs.185831	ESTs	9.53
25	453716	AA037675	Hs.152675	ESTs	9.50
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	9.50
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.45
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.45
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	9.43
30	434423	NM_006769	Hs.3844	LIM domain only 4	9.43
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	9.43
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	9.42
	410397	AF217517	Hs.63042	DKFZp564J157 protein	9.37
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	9.37
35	434524	AA635931	Hs.249716	ESTs	9.36
	422960	AW890487		cadherin 13, H-cadherin (heart)	9.35
	414774	X02419	Hs.77274	plasminogen activator, urokinase	9.32
	411960	R77776	Hs.18103	ESTs	9.30
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	9.28
40	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.28
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.27
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	9.27
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	9.25
	427968	AI857607	Hs.181301	cathepsin S	9.23
45	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	9.23
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	9.23
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.18
	417315	AI080042	Hs.180450	ribosomal protein S24	9.18
	421098	AI697901	Hs.192425	ESTs	9.18
50	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.18
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	9.17
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	9.17
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.15
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	9.14
55	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.13
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	9.12
	420099	D80011	Hs.95140	KIAA0189 gene product	9.10
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	9.08
	441436	AW137772	Hs.185980	ESTs	9.08
60	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	9.08
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	9.08
	430556	AW967807	Hs.13797	ESTs	9.07
	450147	AW373713	Hs.146324	CGI-145 protein	9.06
	442806	AW294522	Hs.149991	ESTs	9.05
65	431187	AW971146	Hs.293187	ESTs	9.05
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	9.03
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	9.03
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	9.02
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	9.00
70	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.99
	432314	AA533447	Hs.312989	ESTs	8.98
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.95
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	8.94
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	8.93
75	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.90
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	8.90
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.89
	417228	AL134324	Hs.7312	ESTs	8.88
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	8.88
80	422616	BE300330	Hs.118725	selenophosphate synthetase 2	8.88
	438980	AW502384		gb:UI-HF-BR0p-aka-f-12-0-UI.r1 NIH_MGC_5	8.85
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	8.85
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	8.85

	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	8.83
	445612	N94126	Hs.12969	hypothetical protein	8.80
	427254	AL121523	Hs.97774	ESTs	8.80
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.80
5	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	8.79
	430162	AW450843	Hs.346348	ESTs	8.75
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.73
	446659	AI335361	Hs.226376	ESTs	8.73
	447198	D61523	Hs.283435	ESTs	8.73
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	8.70
	401091			decay accelerating factor for complement	8.68
	442832	AW206560	Hs.253569	ESTs	8.68
	442495	AI184717		ESTs	8.63
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	8.63
15	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	8.61
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	8.59
	425580	L11144	Hs.1907	galanin	8.55
	449656	AA002008	Hs.188633	ESTs	8.55
	412093	BE242691	Hs.14947	ESTs	8.54
20	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.54
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.53
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	8.51
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.45
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	8.45
25	425284	AF155568		NS1-associated protein 1	8.45
	441623	AA315805		desmoglein 2	8.43
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	8.42
	441021	AW578716	Hs.7644	H1 histone family, member 2	8.40
	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	8.40
30	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	8.35
	433655	AL036559	Hs.3463	ribosomal protein S23	8.33
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.32
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	8.31
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.30
35	414662	AL036058	Hs.76807	major histocompatibility complex, class	8.30
	414601	AV660804	Hs.301417	AHNAK nucleoprotein (desmoyokin)	8.29
	406699	L06505	Hs.182979	ribosomal protein L12	8.28
	443884	N20617	Hs.194397	leptin receptor	8.28
	442621	BE391929	Hs.8752	transmembrane protein 4	8.26
40	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	8.24
	435968	AW161481	Hs.111577	integral membrane protein 3	8.23
	440327	R12581	Hs.191146	ESTs	8.23
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.22
	435684	NM_001290	Hs.4980	LIM domain binding 2	8.16
45	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	8.15
	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	8.14
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	8.13
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	8.10
	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	8.09
50	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	8.08
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	8.07
	423523	AW299828	Hs.193580	ESTs	8.03
	426759	AI590401	Hs.21213	ESTs	8.03
	426780	BE242284	Hs.172199	adenylate cyclase 7	8.03
55	426215	AW963419	Hs.155223	stanniocalcin 2	8.03
	435748	AA699756	Hs.117335	ESTs	8.00
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	8.00
	447500	AI381900	Hs.159212	ESTs	8.00
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	8.00
60	428728	NM_016625	Hs.191381	hypothetical protein	8.00
	434511	R28982	Hs.18106	ESTs	7.99
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	7.98
	424875	AI187945	Hs.199310	ESTs	7.95
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	7.95
65	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7.93
	425277	NM_001241	Hs.155478	cyclin T2	7.91
	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	7.90
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	7.90
70	429999	AI761902	Hs.99597	ESTs	7.90
	445493	AI915771		metallothionein 1E (functional)	7.89
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.88
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	7.88
	453485	BE620712	Hs.33026	hypothetical protein PP2447	7.87
75	434159	AW135214	Hs.191828	ESTs	7.85
	432666	AW204069		ESTs, Weakly similar to unnamed protein	7.83
	430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GCB1 Homo sapiens	7.83
	425913	AA365799		SEC22, vesicle trafficking protein (S. c	7.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	7.80
80	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	7.79
	435905	AW997484	Hs.5003	KIAA0456 protein	7.78
	406663	U24683		immunoglobulin heavy constant mu	7.78
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.78

	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	7.75
	438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	7.75
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.73
	422900	AA641201	Hs.222051	ESTs	7.73
5	432598	AI341227	Hs.157106	ESTs	7.72
	449322	AI638616	Hs.196566	ESTs	7.71
	416987	D86957	Hs.80712	KIAA0202 protein	7.67
	410800	BE280421	Hs.94499	ESTs	7.67
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	7.67
10	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.65
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.65
	401466			vesicle-associated membrane protein 4	7.65
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	7.64
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.63
15	457250	AA811987	Hs.125779	ESTs	7.63
	412949	AI471639	Hs.71913	ESTs	7.63
	406819	AA908472		gb:og82a10.s1 NCI_CGAP_Ov8 Homo sapiens	7.62
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.62
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	7.61
20	435937	AA830893	Hs.119769	ESTs	7.60
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.60
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.60
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	7.56
	418134	AA397769	Hs.86617	ESTs	7.55
25	451812	X81889	Hs.152151	plakophilin 4	7.55
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.54
	429063	Y09397	Hs.227817	BCL2-related protein A1	7.54
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	7.52
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.52
30	407784	AW139585	Hs.12708	ESTs	7.52
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	7.50
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	7.50
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	7.48
	446013	AI360167	Hs.152774	ESTs	7.48
35	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.48
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.45
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.45
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	7.44
	447082	T85314	Hs.54629	thioredoxin-like	7.43
40	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	7.43
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.43
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	7.43
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypotheti	7.43
	436394	AA531187	Hs.126705	ESTs	7.39
45	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	7.39
	446258	AI283476	Hs.263478	ESTs	7.38
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	7.37
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.36
	435541	AA687361	Hs.221318	ESTs	7.35
50	453932	AW006303	Hs.329296	ESTs, Weakly similar to (defline not ava	7.35
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.35
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.35
	418336	BE179882		glutathione peroxidase 3 (plasma)	7.35
	448877	AI583696	Hs.253313	ESTs	7.35
55	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.35
	444838	AV651680	Hs.208558	ESTs	7.33
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	7.31
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.30
	441878	AI801869	Hs.127982	ESTs	7.29
60	406542			C19000728*:gi|12585552|sp|Q9Y2Q1|Z257_HU	7.28
	408418	AW963897	Hs.44743	KIAA1435 protein	7.28
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	7.26
	442492	AA526489	Hs.234518	ribosomal protein L23	7.25
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	7.25
65	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	7.25
	426501	AW043782	Hs.293616	ESTs	7.25
	411251	R19774	Hs.22835	HHGP protein	7.25
	444670	H58373	Hs.332938	hypothetical protein MGC5370	7.25
	418117	AI922013	Hs.83496	linker for activation of T cells	7.24
70	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	7.24
	434817	AA082118	Hs.102737	goliath protein	7.23
	419970	AW612022		ESTs	7.23
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	7.23
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	7.23
75	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	7.21
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	7.21
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	7.20
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.20
	441224	AU076964	Hs.7753	calumenin	7.18
80	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.18
	447687	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	7.15
	447341	AF106941	Hs.18142	arrestin, beta 2	7.15
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	7.14

	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	7.14
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.13
	421633	AF121860	Hs.106260	sorting nexin 10	7.10
	410668	BE379794	Hs.159651	hypothetical protein	7.09
5	435812	AA700439	Hs.188490	ESTs	7.08
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	7.08
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	7.08
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	7.06
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	7.06
10	416401	N80139	Hs.268916	ESTs	7.05
	415799	AA653718	Hs.225841	DKFZP434D193 protein	7.05
	415995	NM_004573		phospholipase C, beta 2	7.05
	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.05
	417535	AA203569	Hs.191482	ESTs	7.04
15	449567	AI990790	Hs.188614	ESTs	7.03
	429355	AW973253	Hs.292689	ESTs	7.03
	442460	NM_014135	Hs.8345	PRO0641 protein	7.03
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	7.03
	430280	AA361258	Hs.237868	interleukin 7 receptor	7.03
20	426124	AI268389	Hs.250697	phosphatidylinositol glycan, class F	7.02
	442685	AB033017	Hs.8594	KIAA1191 protein	7.01
	433735	AA608955	Hs.109653	ESTs	7.00
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.98
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.96
25	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.95
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.95
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.93
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	6.93
	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.93
30	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	6.93
	451838	AW005866	Hs.193969	ESTs	6.91
	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Su	6.90
	443749	R38828	Hs.143463	ESTs	6.90
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.90
35	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	6.90
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.90
	435655	AW105663	Hs.6947	HSPC069 protein	6.90
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	6.85
	418259	AA215404		ESTs	6.85
40	407244	M10014		fibrinogen, gamma polypeptide	6.85
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	6.83
	441321	H17182	Hs.7771	B-cell associated protein	6.80
	433162	AI025842		ESTs	6.80
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.80
45	434372	AA631373		gb:np86c01.s1 NCI_CGAP_Thy1 Homo sapiens	6.80
	456629	AW891965		histone deacetylase 3	6.78
	430283	BE391688		RAB7, member RAS oncogene family	6.77
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	6.76
	406858	AI865720	Hs.29797	ribosomal protein L10	6.75
50	429582	AI569068	Hs.22247	ESTs	6.75
	401113			solute carrier family 22 (organic cation	6.75
	449576	AW014631	Hs.225068	ESTs	6.75
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	6.72
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.72
55	430451	AA836472	Hs.297939	cathepsin B	6.72
	410503	AW975746	Hs.188662	KIAA1702 protein	6.70
	415682	AI347128	Hs.191870	ESTs	6.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	6.70
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.70
60	457073	AA233210	Hs.179943	ribosomal protein L11	6.69
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	6.68
	436137	AI056769	Hs.133512	ESTs	6.68
	425787	AA363867	Hs.155029	ESTs	6.67
	437802	AI475995	Hs.122910	ESTs	6.65
65	432636	AA340864	Hs.278562	claudin 7	6.65
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	6.65
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	6.65
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	6.63
	441355	AI822034	Hs.137097	ESTs	6.63
70	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.63
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.63
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	6.62
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	6.60
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	6.60
75	449057	AB037784	Hs.22941	KIAA1363 protein	6.60
	446979	AI654443	Hs.197683	ESTs	6.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	6.60
	424868	AI568170	Hs.96886	ESTs	6.59
	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	6.58
80	451603	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	6.58
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.58
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	6.57
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.56

	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	6.56
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.55
	418459	R85436	Hs.268814	ESTs	6.55
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.55
5	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	6.55
	446173	BE565849	Hs.14158	copine III	6.53
	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	6.53
	423825	NM_004402	Hs.133089	DNA fragmentation factor, 40 kD, beta po	6.53
	443441	AW291196	Hs.92195	ESTs	6.51
10	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	6.50
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smo	6.50
	450219	AI826999	Hs.224624	ESTs	6.50
	408896	AI610447	Hs.48778	niban protein	6.50
	442618	R56222	Hs.26514	ESTs	6.49
15	422773	AB028962	Hs.301552	KIAA1039 protein	6.48
	413663	BE247585	Hs.75462	BTG family, member 2	6.48
	418905	BE539674		actinin, alpha 4	6.48
	405086			NM_006662*:Homo sapiens Snf2-related CBP	6.45
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	6.45
20	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.45
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	6.45
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	6.43
	426496	D31765	Hs.170114	KIAA0061 protein	6.43
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	6.42
25	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	6.41
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.40
	435918	AF263538	Hs.86232	growth differentiation factor 3	6.38
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.38
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.38
30	436716	AI433540		gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien	6.38
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	6.38
	413326	H88621	Hs.19762	ESTs, Weakly similar to KIAA1140 protein	6.38
	441970	AW959918	Hs.73737	ESTs	6.38
	430835	AI240006	Hs.192326	ESTs	6.38
35	414890	BE281095	Hs.77573	uridine phosphorylase	6.37
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.37
	414768	AW376989	Hs.259855	elongation factor-2 kinase	6.36
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	6.36
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	6.35
40	432586	AA568548		ESTs	6.35
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	6.35
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	6.35
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.35
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.35
45	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	6.35
	437296	AA350994	Hs.20281	KIAA1700	6.35
	427747	AW411425	Hs.180655	serine/threonine kinase 12	6.33
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	6.33
	410387	AI277367	Hs.47094	ESTs	6.33
50	413677	AW503116	Hs.301819	zinc finger protein 146	6.31
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	6.31
	443634	H73972	Hs.134460	ESTs	6.30
	409453	AI885516	Hs.95612	ESTs	6.29
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	6.29
55	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.29
	410532	T53088	Hs.155376	hemoglobin, beta	6.28
	428453	AB011110	Hs.184367	GTPase activating protein-like	6.27
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	6.26
	458965	AA010319	Hs.60389	ESTs	6.25
60	419926	AW900992	Hs.93796	DKFZP586D2223 protein	6.25
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	6.25
	412528	AI123478	Hs.32112	ESTs	6.25
	410079	U94362	Hs.58589	glycogenin 2	6.25
	427477	AW973119	Hs.178391	ribosomal protein L44	6.24
65	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.24
	435961	BE293127	Hs.283722	GTT1 protein	6.23
	424090	X99699	Hs.139262	XIAP associated factor-1	6.23
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.23
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	6.23
70	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.23
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	6.22
	428773	BE256238	Hs.193163	bridging integrator 1	6.20
	436372	AW972301	Hs.310286	ESTs	6.19
	440719	AA150869	Hs.26267	ATP-dependant interferon response protei	6.18
75	406685	M18728		gb:Human nonspecific crossreacting antig	6.18
	421305	BE397354	Hs.324830	diptheria toxin resistance protein requi	6.17
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	6.16
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	6.15
	406806	AW088535		ribosomal protein, large, P0	6.15
80	420151	AA255931	Hs.186704	ESTs	6.14
	413441	AI929374	Hs.75367	Src-like-adapter	6.13
	449317	AW293413	Hs.132906	19A24 protein	6.13
	421568	W85858	Hs.99804	ESTs	6.13

	435919	AI052189	Hs.114104	ESTs	6.13
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	6.13
	448946	AI652855	Hs.23363	hypothetical protein FLJ10963	6.13
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.13
	406857	AA613726	Hs.29797	ribosomal protein L10	6.11
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	6.11
	425095	AW014160	Hs.182585	KIAA1276 protein	6.10
	435756	AI418466	Hs.33665	ESTs	6.10
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	6.10
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	6.10
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	6.10
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	6.08
	447832	AI433357		ESTs	6.08
	434421	AI915927	Hs.34771	ESTs	6.08
	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	6.08
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	6.08
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	6.07
	433339	AF019226	Hs.8036	glioblastoma overexpressed	6.06
	435511	AA683336	Hs.189046	ESTs	6.06
	423458	AI204212		ESTs	6.06
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.06
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.06
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	6.06
	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	6.05
	432925	AA878324	Hs.264750	ESTs	6.05
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	6.05
	449810	AB008681	Hs.23994	activin A receptor, type IIB	6.04
	406797	AI432224		ribosomal protein L6	6.04
	450157	AW961576	Hs.60178	ESTs	6.03
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.03
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-lin	6.03
	453331	AI240665		ESTs	6.03
	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	6.02
	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	6.01
	409945	AW015935	Hs.122642	ESTs	6.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	6.00
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	6.00
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	6.00

TABLE 52B
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
426295	510_1	BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI263836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA668626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627
429978	35194_2	BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963196 C06195 AI678018
412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999689 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723

			AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487
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	413787	7612_1	BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 AI082748 AI470204 BI711078 BF350700 BI496963 AI087141 AA720584 AA862331 AA605146 BM313650 AI089749 AI359738 N69107 AW995424 AI086917 AI083995 AW340217 N99662 AI829449 AI089839 AI608761 AI342365 AI199076 AA908944 AI248943 AU160053 AI191245 AI218477 AI077943 AA864930 AI310394 AA872478 AI279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 AI469689 BE464590 AW664539 H67097 AL534332 C21397 AI085941 AW028427 BG939820 AI697089 AI039008 AI125315 AI655561 AW150042 L20422 X57345 BI458375 AU142852 BI666601 BE888276 AU119302 BI603754 BG705953 BI598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AV683116 AV708195 AA127798 AI124697 D54224 F08031 AA340253 BF923383 BM467808 BI546644 BG777200 BG705941 BG468577 AU127209 AW403970 BI597630 BI458091 AV689560 BI669267 BG506219 BI837163 BI667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 BI869271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 BI493502 AW273118 AI473820 AA608688 AI359337 AV712091 AA084101 BF592036 H13301 AI864305 AA505883 AI423963 AW084401 AI917740 R69858 AA033631 N79962 BE885276 AI635674 AA096126 AA700018 AV707753 AI082545 AU145681 AA629032 AI421367 AA740589 AA150830 AI248541 AA988608 AA150478 W65437 BM310234 AA262704 T28031 AI811116 BM272753 H21979 T15405 AA938406 F04963 AI186296 AW152629 AA905196 BG223058 AI831016 AI766457 AI811102 AA776573 AI922133 AA775958 AI261476 AA219489 AI688035 AI872093 BE537084 AW189078 D82630 AI123121 AL583492 BE350791 R69901 W65436 BE155392 BI089081 BE155394 AL120538 AW166100 AI359620 AI174338 N20527 W47413 AA155615 AI272249 H25293 BE614558 H69864 AW383484 H78021 H11617 R56892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W46459 AI866231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AL537424 BE814866 BF823254 R82553 AI809817 AI559406
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	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651629 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
	444060	6315_1	AK055070 AK055612 AK000174 BG619806 BG108086 AI741949 AI004176 BF891936 BF378565 AW197163 BE856860 BE245124 AW674411 AA490531 AW674981 AA740788 AW274758 BF512523 AI521278 AA548759 AI802431 AW051682 AI628247 AI799606 AW088103 AA236549 AI191529 AW273168 AI168451 AW073812 AW090611 AW003593 AI215845 AI799616 AW474940 AA954927 BM193740 AW662704 AW090127 AA969444 AI080438 AA552500 AW237538 AA481060 AI246378 AA565227 AA398921 AA207051 AA721378 BF438608 AI086295 AI886630 AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766664 AI453279 AA435673 AI619515 AA879080 AA234592 AA890223 AA766824 BI259822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05809 N41323 T87376 R68544 H88711 BI087136
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	413497	1518002_1	BE177661 H06215 BE144709 BE144829
	434280	1474904_1	BE005398 AA628622 AA994155
	450139	34017_1	AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 AU135386 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI886459 AU155873 H04255 AW243986 AA557749 AI286227 R68691 R33453 AW388097
	430068	1177709_-2	AA947566
	434442	111738_1	AA662701 AA633929 AA737415
	438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701
	451129	1495511_1	BE072881 AI762181 BE072946
	414405	112689_1	AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545
	422960	11862_2	BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260
	410730	114639_1	BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823
	422689	874209_1	AW954733 AA315006 AW856665

438980	917280_1	AW502384 AA828822 AI982587
442495	928718_1	AI184717 AW518883 AF121173
425284	3834_5	BM476120 BE672181 AI697653 AA938187 AI280879 AW340123 AI912727 AI081775 AI089556 AI191349 AI871604 AI631607 AI890800 AI701917 AW771624 AA663041 AI991576 AI160622 AA771763 BE089784 BE089788 AI222942 AW418516 AA329211 AI095736 BE550294 AA738345 BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634
441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BG496559 BF248373 BG494800
445493	423456_1	AV711317 AI809938 AI808768 AI240593 AI915771
432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
430915	197844_1	BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
425913	4123_2	AV703649 AW959818 AI582119 AI523459 AI674473 AW663543 AA825476 AI935231 BF742805 AA426156 AI253626 AA846477 AI024230 BF221780 AI493027 AW006841 AA814699 H99650 AI088977 AA442691 AI783526 BF207915 AI752847 AA782635 AI978980 AA788634 BG119454 BF678528 AI627829 BG993975 AV701283
438962	195763_1	AI207343 BF813684 BF928775 AA828585
406870	0_0	AA075144
406819	0_0	AA908472
447197	2176805_1	R36075 R36167 AI366546
418336	58817_1	AW969583 BI772505 BE179578 AI493714 AI937718 AA663709 BI868925 AW138743 AI911314 BE645538 BG911947 AI380325 AI265803 W56175 AI658779 AI675997 AW665991 AI459263 AI420121 Z38874 AA570115 AW301008 AA216257 BF062662 BI772789 H05989 BF085523 BI001277
424677	2518_37	U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708
419970	13569_1	AK055270 BE348291 AI190289 AW612022 AI269506 AI266578 AI269675 AW271406 BE879851 BF574163 BI497126 AW903775 BI917368 AW150900 BF244813 H79201
433891	647290_1	AW182329 AA613792 T05304 AW858385
415995	2117_1	M95678 NM_004573 AL530754 AI439623 AW374413 BF898880 AW630959 BF875526 AW402206 BF818690 BF893068 AW504110 AW408049 BG002913 AL530753 AI524064 AW769231 AA464970 AA293723 AI095051 AI953375 AI982938 BM146050 AW575804 AA962489 AI655426 BM146046 T28538 BE241936 T89023 BI910963 AI416986 AI767111 AI422290 AW468260 BE676853 AI656771 AI961755 F04675 AA682826 AA737606 BM194382 AA912021 AW183098 BE676682 AI962227 AI591366 AA621765 AA293724 R51642 F10194 BI909727 BF892632 AW950600 AW950138 BG258587 BF892649 AI800647 BF892710 AA353176 BF894726 AA465038 BI040869 BI837749 BE244320 H18054 T74300 AW797026 AA926790 F32814 AW751282 AI933994 AA578823 T78372 BF899896 BF882808 BF974969
451653	MH115364_1	BG119563 AW975776 BG498478 BE245304 AW450934 BF508792 AA599489 AA599477 AI805268 AA055489 AI128758 AA761425 AA731858 AI302271 BE219432 AA687294 AA018972 AW629429 Z45675 AW961626 T30940 R34554 T84712 BG986694
436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
433162	2167905_1	AI742311 AI025842 AA578843
434372	858779_1	BG622121 AA631424 AA988296 AA631373
456629	207_22	AW891965 AW604749 BE080872 R15559 BE177623 AW883520 AW945343 AI246167 T07082 AW805679 W96278 AA135796 W32615 AW995418 AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239 BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AI378548 AW890438 AA077172 AI288683 AA229639 AA091945 AW945454 AA063629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399 AW885686 BE244086 BE005035 AW861913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW861939 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI248811 BE179917 BE002200 AW607506 AW392889 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW601420 AI695314 BE083790 AW858568 AW945550 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW885979 AW794240 AW945566 AI688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW664582 AW877775 AW838449 BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099 BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 AI904717 AW610318 AW996909 AW610296 AW901923 AW880003 AI762171 AW062582 AW368713 AW062593 AW176663 AW842064 AW842089 AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577 AI909628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835656 AW606765 AW606770 AW835578 AW606758 AW606778 AI907484 BE172821 AW606768 AW999517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA090510 AW844117 BE173367 AW999878 AI124870 BE163472 AW841823 AW379762 AW893297 AI290295 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629 BE089008 BE178350 BE178214 BE063291 AW820236 AW999653 BE089486 BE173126 BE171775 BE185787 AA558280 AI174840 AW999112 BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998972 AA767189 AW044272 H50689 AA768399 AA767764 AI087888 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945 AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI681913 AI759983 N69591 N69276 BE467722 AW392780 BE172467 H92861 AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H87220 AW374781
430283	1418_1	BC013728 BI084032 BF090365 BE410706 N36391 W80436 BF813124 R90857 R62778 H00591 H02329 AA355285 AK000826 BC008721 BG744004 BG479141 BG823656 BG479061 AU121103 AU138175 BG702567 BI599840 BG422775 BG700944 BE280747 AU138529 BE269929 BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AU139772 BG714385 BF568538 BE304393 BF971755 BE267965 BE272012 AU135396 AU124535 BI551682 BG700612 AI815488 BG475195 BE388273 BE391517 BM148991 BF929247 AV653435 AW250299 AW249189 BF093150 BF093173 AW205325 BF057101 BF000551 AI341108 AL162009 AK026136 BE907957 W73238 BI711467 BG926027 AI816428 AA837518 AI754405 BG179142 AA481485 AW023435 BE855747 AI885101 N52163 AI016096 AI090204 BE677045 AI523320 AI126855 N26501 AA043680 AA976459 AI039590 AI937917 AI361000 W94866 AI375797 AI079801 AI168236 AA599882 AA084368 AI342635 AI190294 N26093 AI085234 AI298169 BF939715 AI223164 H98704 BE218925 N29394 AI918735 N41520 AI147784 AI918796 AA854317 N22193 AA199850 AI149728 AA121263 AI051074 AA565116 AI097349 N22209 AA552917 N33151 D52422 BF477483 AA476599 AA525787 AI279198 D53353 AA738063 AA558406 BI496334 AA999948 AA425847 BI496335 AA909624 BF197591 AW023259 AI652819 T31424 AA088213 T31115 AI206650 AA976796 AI948989 AW248762 AA449265 AA290687 AI682521 AA310227 Z38743 AA935369 AW119141 BF941087 AI470657 AI349451 AW079338 D45665 N21640 T30071 AI446705 R60220 BE833481 R49680 R70049 R41223 R32402 R69984 R70111 BM476906 BE293615 BE382443 BF155692 BE720638 BE931983 BE720594 BF085890 AA336953 BF081638 AA359915 AA384116 AA360142 BI667664 BG823235 BE315559 BE301958 BE891114 BG826267 BE253680 BG979094 AV722757 N67529 BG997927 BI915769 BG680692 R62777 BE251116 H56358 AW369586 BG677759 BI044604 R75787 BE770960 H69529 R69983 AA259238 R97827 AA310379 W01103 AI873384 AL554578 BF038102 H87182 H87517 H01574 T52573 N28881 AA301397 T92375 R68401 AW800466 AI268172 BE876949 D54019 AI909769 AW798415 BI222383 AI393171 C15260 N26959 H17129 T53095 T52494 R68602 AI364765 BF687869 AI817035 AW105354 BE293820 H14206 BI093066 C14053 AL534349 BE255883 BE254088 AA428399 AW579360 AW579381 N53144 D60748 D54020 BG292106 H96705 D52423 T36174

			D54161 R73016 D55021 BI857200 H83444 BI016954 D54163 R15563 BI818664 BE152207 BI048502 BF885667 BE613212 BE165773 BF149332 AW607045 BE305200
	430968	1237115_1	AW972830 AA489820 AA527647 AA570362
	444207	9172_3	BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI470335 AI247243 BG533994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658 AW393133 AW073080 AI707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 AI565004 AW819026 BE843092 AV686437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AI962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497
	418905	517_1	BM469076 AA533027 AI127512 AI368802 AA533141 AA700560 AW576028 AI610851 AI435361 BM129172 AW474544 BM128899 AI814292 AW502039 AA531243 BF941858 AW502037 AA702337 AI419854 AA662755 AA934364 AI300510 AI291136 AA505263 AI144527 AI076919 AI633534 AI242473 AA938561 BG055372 AA512894 AI671356 AA962403 BF808010 AA663911 AA847056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 AI305842 AW800873 AA302492 AA478427 AI817291 AW801104 AW801028 AA865744 BF155979 AI374743 AA478431 AI159846 AI369757 AI800672 BF435788 AA255451 AI937707 AW006198 AI280363 BF062434 AW801115 AI919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 AI302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 BI087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 AI142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605
	436716	2472838_1	AI433540 AA804981 AA728984
	413703	376077_1	BG015794 BE158357 BE158353 BE158358 BE158360 BE158352 BE158351 BE158355
	432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
	440129	2607882_1	AI732997 AA977633 AA865818
	406685	0_0	M18728
	406806	0_0	AW088535 AI889321 AA954221 AI337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA857965 AI625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 AI149335 AA936925 AA581684 AA954198 AW238461 AI281504 AI265812 AA583267 AW236162 AA876535 AW304286 AW474334 AI559415 AI589241 AI660952 AA641137 AI431696 AI688844 AA552513 AA564954 AW090553 AI205612 AI245753 AA954883 AA947909 AI866014
	431155	1235742_1	AW971213 AA493925 AA493567 AA876839 AA934462
	447832	1036795_1	AI628543 AI433357 AW772732
	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
	423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539 BG215094 BG198867 BG196332 BG208220 BG212418
	455263	26143_1	BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 BI596425 AA115605 AI589156 BF439839 BG188832 AI359615 BG190473 AI024233 BF439574 AW118065 AI672797 AA610042 BG212008 AI204382 R70913 AA033534 AA781036 AI627278 AA307285 AA034218 BG482749 AW162429 BI602460 AA721969 AA476516 AA476416 AA903019 BF110864 AA307286 AA115471 AW964555 AA423826 AA115129 AI419107
	406797	0_0	AI432224 AW276890 AI499346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640
	453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
	430504	5477_6	BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575 AW300064 AW262133 H21568 AI363015 AI884914 H86948

TABLE 52C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402145	8018280	Plus	113086-114800
401091	9958240	Plus	94760-94898
401466	6682292	Plus	28748-29023
406542	7711499	Plus	117335-118473
401113	9966541	Minus	19419-19959
405086	8072509	Plus	73664-73841,74081-74217,74610-74779,7492

TABLE 53A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
432666	AW204069		ESTs, Weakly similar to unnamed protein	78.20
452838	U65011	Hs.30743	preferentially expressed antigen in mela	75.45
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	58.80
432730	AI066520	Hs.131358	ESTs	51.80
450581	AF081513	Hs.25195	TGF-beta 4	48.40

	426534	U58096	Hs.2051	testis specific protein, Y-linked	44.05
	423458	AI204212		ESTs	36.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	34.65
	420367	AA259090	Hs.257028	ESTs	32.60
5	451106	BE382701	Hs.25960	N-MYC oncogene	30.10
	437052	AA861697	Hs.120591	ESTs	29.35
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	29.05
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	28.45
	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	28.25
10	407710	AW022727	Hs.23616	ESTs	26.86
	448981	AI968719	Hs.195387	ESTs	26.40
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	25.55
	420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	25.10
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	23.70
15	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.95
	454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	21.73
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	20.15
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	19.65
	424578	AK001973	Hs.150890	hypothetical protein	19.16
20	427335	AA448542	Hs.251677	G antigen 7B	19.05
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	18.95
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	18.86
	449322	AI638616	Hs.196566	ESTs	18.30
	430691	C14187	Hs.157208	aristaless-related homeobox protein ARX	18.00
25	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (	17.96
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	17.41
	418756	AA252254	Hs.226949	ESTs	17.20
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	16.20
	447534	AW953935	Hs.288655	ESTs	16.04
30	407122	H20276	Hs.31742	ESTs	15.95
	446979	AI654443	Hs.197683	ESTs	15.90
	406547			Target Exon	15.70
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.65
	456847	AI360456	Hs.37776	ESTs	15.50
35	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	15.00
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	14.95
	408908	BE296227	Hs.250822	serine/threonine kinase 15	14.65
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
	422828	AL133396		prion protein 2 (dublet)	14.08
40	433330	AW207084	Hs.132816	hypothetical protein MGC14801	14.05
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	14.05
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	13.90
	418134	AA397769	Hs.86617	ESTs	13.85
	454438	AA224053	Hs.172405	cell division cycle 27	13.70
45	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	13.40
	426427	M86699	Hs.169840	TTK protein kinase	13.35
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.20
	419384	AA490866	Hs.39429	ESTs	13.10
	418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	12.85
50	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	12.80
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.78
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	12.72
	443068	AI188710		ESTs	12.65
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	12.60
55	420401	AK001907	Hs.97464	hypothetical protein	12.50
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	12.50
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	12.45
	406937	U14622		gb:Human transketolase-like protein gene	12.25
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	12.10
60	404996			Target Exon	11.86
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	11.85
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	11.60
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	11.55
	421241	X91817	Hs.102866	transketolase-like 1	11.50
65	414972	BE263782	Hs.77695	KIAA0008 gene product	11.45
	426866	U02330	Hs.172816	neuregulin 1	11.37
	433159	AB035898	Hs.150587	kinesin-like protein 2	11.35
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	11.24
	440207	AI371978	Hs.128326	ESTs	11.12
70	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	11.10
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	11.05
	449576	AW014631	Hs.225068	ESTs	10.95
	414251	AL042306	Hs.97689	VASA protein	10.95
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	10.90
75	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Su	10.85
	427521	AW973352		ESTs	10.81
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	10.80
	442832	AW206560	Hs.253569	ESTs	10.62
	436899	AA764852		ESTs	10.60
80	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	10.55
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	10.45
	435206	AI432364	Hs.160594	ESTs	10.15
	433975	AA971953	Hs.122055	ESTs	10.10

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	446791	AI632278	Hs.195922	ESTs	10.05
	422232	D43945	Hs.113274	transcription factor EC	10.00
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	9.71
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	9.50
5	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.44
	438188	AA779975	Hs.128859	ESTs	9.30
	418973	AA233056	Hs.191518	ESTs	9.25
	413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	9.25
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.15
10	436608	AA628980	Hs.192371	down syndrome critical region protein DS	9.11
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	9.08
	426518	Z43039	Hs.170198	KIAA0009 gene product	9.05
	440968	N36327		gb:yx82b06.r1 Soares melanocyte 2NbHM Ho	9.05
	440952	AI291804	Hs.118101	ESTs	9.05
15	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	9.05
	442618	R56222	Hs.26514	ESTs	8.96
	419423	D26488	Hs.90315	KIAA0007 protein	8.95
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	8.80
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	8.76
20	444971	AI651116	Hs.148659	ESTs	8.75
	436513	AJ278110	Hs.125507	DEAD-box protein	8.60
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.59
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.58
	428847	AI954833	Hs.98881	ESTs	8.57
25	408465	AW196940	Hs.253277	ESTs	8.54
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	8.53
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	8.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.50
	450480	X82125	Hs.25040	zinc finger protein 239	8.50
30	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	8.42
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	430835	AI240006	Hs.192326	ESTs	8.33
	416859	H43437	Hs.80305	hypothetical protein MGC14258	8.30
35	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	8.26
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	8.25
	449260	AA741180	Hs.29879	ESTs	8.25
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	8.18
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	8.17
40	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	8.14
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.14
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.03
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	7.98
	410420	AA224053	Hs.172405	cell division cycle 27	7.90
45	453878	AW964440	Hs.19025	DC32	7.75
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	7.66
	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	7.65
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	7.65
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	7.65
50	451950	AW292317	Hs.213307	ESTs	7.60
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.59
	435514	AW592804		ESTs	7.55
	431041	AA490967	Hs.197955	KIAA0704 protein	7.55
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.51
55	418830	BE513731	Hs.88959	hypothetical protein MGC4816	7.38
	409421	AA199883	Hs.67624	ESTs	7.35
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	7.35
	458570	AW971698	Hs.12627	TJ6 protein	7.30
	441287	AW293132	Hs.131373	ESTs	7.30
60	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	7.25
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	441425	AA933590	Hs.28937	homeobox protein from AL590526	7.25
	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	7.21
	414136	AA812434		SMC2 (structural maintenance of chromoso	7.20
65	409089	NM_014781	Hs.50421	KIAA0203 gene product	7.19
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.18
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	7.15
	452226	AA024898	Hs.157103	ESTs	7.15
	435918	AF263538	Hs.86232	growth differentiation factor 3	7.14
70	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.10
	436360	AI962796	Hs.156100	ESTs	7.10
	442950	AI500417	Hs.46764	ESTs	7.00
	415684	D59356		sorbitol dehydrogenase	7.00
	448336	R53848	Hs.44976	ESTs	7.00
75	453183	AW086185	Hs.223856	ESTs	7.00
	444434	NM_004849	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like	6.95
	422665	AJ011812	Hs.119018	transcription factor NRF	6.95
	437421	AA917062		ESTs	6.95
	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.94
80	408045	AW138959	Hs.245123	ESTs	6.90
	448588	AI970276	Hs.156905	KIAA1676	6.89
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.85
	439780	AL109688		gb:Homo sapiens mRNA full length insert	6.85

	449911	AI262106	Hs.12653	ESTs	6.85
	417791	AW965339	Hs.111471	ESTs	6.80
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
	453160	AI263307		H2B histone family, member L	6.75
5	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.73
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.70
	418379	AA218940	Hs.137516	fidgetin-like 1	6.70
	407366	AF026942	Hs.17518	gb:Homo sapiens clg33 mRNA, partial sequ	6.70
10	414618	AI204600	Hs.96978	hypothetical protein MGC10764	6.69
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	6.66
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	6.65
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	6.65
	433247	AB040948	Hs.142856	KIAA1515 protein	6.65
15	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	6.65
	417886	AA214584		ESTs	6.64
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	6.62
	412537	AL031778		nuclear transcription factor Y, alpha	6.61
	426614	AA411925	Hs.301960	ESTs	6.57
20	457465	AW301344	Hs.122908	DNA replication factor	6.52
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	6.50
	440801	AA906366		ESTs	6.50
	453116	AI276680	Hs.146086	ESTs	6.50
	436909	AA907120		ESTs	6.50
25	402199			Target Exon	6.50
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	6.46
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	6.41
	438494	AA908678	Hs.130183	ESTs	6.41
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	6.40
30	408758	NM_003686	Hs.47504	exonuclease 1	6.40
	442671	AI005668	Hs.130673	EST	6.40
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.38
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.35
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	6.33
35	441878	AI801869	Hs.127982	ESTs	6.31
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	6.31
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	6.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	6.30
	421650	AA781795	Hs.122587	ESTs	6.30
40	453932	AW006303	Hs.329296	ESTs, Weakly similar to (defline not ava	6.28
	408291	AB023191	Hs.44131	KIAA0974 protein	6.26
	438180	AA808189	Hs.272151	ESTs	6.25
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	6.25
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	6.20
45	423642	AW452650	Hs.157148	hypothetical protein MGC13204	6.20
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.18
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	6.12
	426223	AW977812	Hs.130391	ESTs	6.10
	445038	AI635444	Hs.143917	dJ467N11.1 protein	6.10
50	419197	N48921	Hs.27441	KIAA1615 protein	6.09
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	6.05
	436902	AW247145	Hs.192729	ESTs	6.05
	429228	AI553633		ESTs	5.99
	457065	AI476318	Hs.192480	ESTs	5.90
55	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	5.90
	449132	BE045641	Hs.197573	ESTs	5.90
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.89
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.85
	457289	AW573204	Hs.137078	ESTs	5.85
60	433849	BE465884	Hs.280728	ESTs	5.85
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.80
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.77
65	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.77
	408460	AA054726	Hs.285574	ESTs	5.75
	442461	AW062564	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	5.75
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
	428249	AA130914	Hs.183291	zinc finger protein 268	5.74
70	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (	5.72
	402145			Target Exon	5.71
	447178	AW594641	Hs.192417	ESTs	5.70
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.65
	442980	AA857025	Hs.8678	kinesin-like 1	5.65
75	419131	AA406293	Hs.109526	ESTs	5.60
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	5.60
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	5.58
80	442333	AI650877	Hs.129302	ESTs	5.58
	453941	U39817	Hs.36820	Bloom syndrome	5.57
	415799	AA653718	Hs.225841	DKFZP434D193 protein	5.57
	413623	AA825721	Hs.246973	intron of Bicaudal D homolog 1	5.55

	427147	AA398587	Hs.97414	ESTs	5.55
	451050	AW937420		ESTs	5.55
	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.54
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	5.54
5	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debriscqu	5.53
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransferase 3 be	5.51
	449592	AI655494	Hs.195718	ESTs	5.50
	445517	AF208855	Hs.12830	hypothetical protein	5.50
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	5.48
10	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.47
	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	5.46
	409103	AF251237	Hs.112208	XAGE-1 protein	5.45
	420900	AL045633	Hs.44269	ESTs	5.45
15	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.45
	440738	AI004650	Hs.225674	WD repeat domain 9	5.45
	412723	AA648459	Hs.335951	hypothetical protein AF301222	5.45
	441122	H56777	Hs.121084	eppin-3	5.42
	414151	AW976468	Hs.257245	ESTs	5.40
20	435663	AI023707	Hs.134273	ESTs	5.40
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	5.39
	433701	AW445023	Hs.15155	ESTs	5.39
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.35
	440842	AA907288	Hs.130173	ESTs	5.35
25	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.34
	401837			NM_025109:Homo sapiens hypothetical prot	5.32
	423739	AA398155	Hs.97600	ESTs	5.31
	424315	AW614850	Hs.193384	putatative 28 kDa protein	5.31
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.30
30	415717	AA167270	Hs.130435	ESTs	5.30
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	5.26
	427119	AW880562	Hs.272525	ESTs	5.25
	432117	AL036195	Hs.2909	protamine 1	5.24
	446837	AW273055	Hs.156598	ESTs	5.23
35	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	5.21
	422797	AB033064	Hs.236463	KIAA1238 protein	5.19
	446258	AI283476	Hs.263478	ESTs	5.18
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	5.17
	445413	AA151342	Hs.12677	CGI-147 protein	5.17
40	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	5.16
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.15
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	5.15
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	5.15
	448038	AW015073	Hs.232026	ESTs, Weakly similar to RO52_HUMAN 52 KD	5.15
45	430272	X04898	Hs.237658	apolipoprotein A-II	5.14
	422094	AF129535	Hs.272027	F-box only protein 5	5.13
	420424	AB033036	Hs.97594	KIAA1210 protein	5.13
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.10
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	5.10
50	453448	AL036710	Hs.209527	ESTs	5.10
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	5.06
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	5.05
	427961	AW293165	Hs.143134	ESTs	5.05
	441553	AA281219	Hs.121296	ESTs	5.05
55	429999	AI761902	Hs.99597	ESTs	5.04
	426496	D31765	Hs.170114	KIAA0061 protein	5.02
	410929	H47233	Hs.30643	ESTs	5.01
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	5.01
	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	5.00
60	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.00
	407568	AA740964	Hs.62699	ESTs	5.00
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	5.00
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	5.00
65	416350	AF188625	Hs.189507	phospholipase A2, group IID	4.99
	452197	AW023595	Hs.232048	ESTs	4.98
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.97
	403780			C4001759;gi|133250|sp|P19474|RO52_HUMAN	4.97
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.96
70	418894	W73921	Hs.50743	ESTs	4.95
	426623	AA382826	Hs.132793	ESTs	4.95
	443537	D13305	Hs.203	cholecystokinin B receptor	4.94
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.94
	453716	AA037675	Hs.152675	ESTs	4.90
75	402299			Target Exon	4.90
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	4.89
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.87
	409066	AA062980	Hs.66960	ESTs	4.85
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.85
80	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	450375	AA009647		a disintegrin and metalloproteinase doma	4.85
	416201	AA467752	Hs.195161	ESTs	4.85
	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	4.84

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	423198	M81933	Hs.1634	cell division cycle 25A	4.82
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.81
	418971	AA360392	Hs.87113	ESTs	4.80
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.80
5	409517	X90780		troponin I, cardiac	4.80
	424322	AL157491	Hs.145211	Homo sapiens mRNA; cDNA DKFZp434K1111 (f	4.80
	443169	AI038687	Hs.133338	ESTs	4.80
	438624	AA889055	Hs.123468	ESTs	4.79
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	4.76
10	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.76
	443715	AI583187	Hs.9700	cyclin E1	4.76
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	4.75
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	4.71
	444431	AW513324	Hs.42280	Homo sapiens, clone MGC:9010, mRNA, comp	4.71
15	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	4.71
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	4.70
	447175	AI365208	Hs.293606	ESTs	4.70
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.69
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	4.68
20	416445	AL043004	Hs.79337	KIAA0135 protein	4.66
	429652	AA766810	Hs.259290	ESTs	4.65
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	4.65
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	4.64
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.62
25	427298	AA400495		ESTs	4.62
	412863	AA121673	Hs.59757	zinc finger protein 281	4.62
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.60
	446751	AA766998	Hs.79126	Human DNA sequence from clone RP11-16L21	4.60
30	432656	NM_000246	Hs.3076	MHC class II transactivator	4.60
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	4.60
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	4.60
	421830	AA789269	Hs.122509	ESTs, Weakly similar to dJ1018D12.3 [H.s	4.59
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	4.58
35	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	4.58
	431721	AB032996	Hs.268044	KIAA1170 protein	4.55
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.55
	453529	AA036729	Hs.335639	ESTs	4.55
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.55
40	444386	BE065183		gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.55
	428976	AL037824	Hs.194695	ras homolog gene family, member I	4.55
	449510	AI653154	Hs.328147	ESTs	4.55
	414725	AA769791		ring finger protein 21, interferon-respo	4.54
	424153	AA451737	Hs.141496	MAGE-like 2	4.53
45	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA (choleste	4.52
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	458443	AV647010	Hs.27	glycine dehydrogenase (decarboxylating;	4.48
	453289	AI188161	Hs.144627	ESTs	4.48
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	4.45
50	440196	N72847	Hs.125221	ESTs	4.45
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.45
	428855	AI435901	Hs.89563	nuclear cap binding protein subunit 1, 8	4.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	4.45
	442240	AI791883	Hs.292719	ESTs	4.45
55	421917	AB028943	Hs.109445	KIAA1020 protein	4.45
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	4.44
	449676	AW380579	Hs.209657	ESTs	4.43
	433183	AF231338	Hs.222024	transcription factor BMAL2	4.40
	439314	AA382413	Hs.178144	ESTs	4.40
60	425312	AA354940	Hs.145958	ESTs	4.39
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.39
	430444	AW296421	Hs.121035	ESTs	4.35
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.35
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.34
65	418216	AA662240	Hs.283099	AF15q14 protein	4.32
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	4.32
	454073	AW206286	Hs.116727	ESTs	4.30
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	4.30
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.30
70	448877	AI583696	Hs.253313	ESTs	4.28
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.27
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	4.25
	430292	AK000634	Hs.238270	hypothetical protein FLJ20627	4.25
	427778	AA412323	Hs.105323	ESTs	4.25
75	418768	T39310		gb:ya04a09.r2 Stratagene lung (937210) H	4.25
	409268	AA625304		ESTs	4.25
	442010	AI032680	Hs.132213	ESTs	4.24
	452807	AA028933	Hs.162434	ESTs	4.23
	401435			C14000397*:gi|7499898|pir||T33295 hypoth	4.23
80	447519	U46258	Hs.339665	ESTs	4.21
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.21
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	4.20
	453909	AW004045	Hs.203365	ESTs	4.20

	431126	AF085243	Hs.283619	zinc finger protein 236	4.20
	429628	H09604	Hs.13268	ESTs	4.20
	415989	AI267700		ESTs	4.20
	421373	AA808229	Hs.46677	ESTs	4.20
5	433979	AA620999		gb:ag03a08.s1 Soares_testis_NHT Homo sap	4.20
	408321	AW405882	Hs.44205	cortistatin	4.19
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.17
	430335	D80007	Hs.239499	KIAA0185 protein	4.17
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	4.16
10	438885	AI886558	Hs.184987	ESTs	4.15
	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	4.15
	432446	AA542845	Hs.294088	GAJ protein	4.13
	445076	AI206888	Hs.154131	ESTs	4.11
	420218	AW958037		ribosomal protein L4	4.10
15	453628	AW243307	Hs.83937	hypothetical protein	4.10
	418459	R85436	Hs.268814	ESTs	4.10
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.08
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	4.06
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.06
20	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	4.05
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	4.05
	449687	W68520		intermediate filament protein syncoilin	4.05
	452109	AI525873	Hs.61164	hypothetical protein FLJ14909	4.05
	401464			histone deacetylase 5	4.05
25	444670	H58373	Hs.332938	hypothetical protein MGC5370	4.05
	415884	H22966	Hs.13471	ESTs	4.05
	442066	BE502147	Hs.128418	ESTs	4.04
	402098			ENSP00000217725*:Laminin alpha-1 chain p	4.02
	404287			FGENESH predicted novel CUB-domain conta	4.01
30	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	4.01
	449704	AK000733	Hs.23900	GTPase activating protein	4.00
	445685	AW779829		gb:hn88a05.x1 NCI_CGAP_Kid11 Homo sapien	4.00
	444379	N99035	Hs.30352	ESTs	4.00
	435373	AW665538	Hs.117689	ESTs	4.00
35	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	4.00
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	4.00
	418648	AW979223	Hs.292478	ESTs	4.00
	446074	AA079799	Hs.343103	hypothetical protein FLJ11896	4.00
	447353	AI375701	Hs.25884	ESTs	4.00
40	410100	AA081636	Hs.271916	ESTs, Weakly similar to S41044 chromosom	4.00
	428856	AA436735	Hs.183171	hypothetical protein FLJ22002	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	406367			NM_022357:Homo sapiens putative metallop	3.99
	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	3.99
45	453985	N44545	Hs.251865	ESTs	3.98
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	3.97
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	3.97
	414713	BE465243	Hs.12664	ESTs	3.96
	426067	AW664691	Hs.97053	ESTs	3.96
50	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.96
	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	3.95
	451865	H43737	Hs.33186	ESTs, Weakly similar to unknown protein	3.95
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	3.95
	445730	AI624342	Hs.179082	ESTs	3.95
55	451993	AA765776	Hs.122983	ESTs	3.95
	428819	AL135623	Hs.193914	KIAA0575 gene product	3.92
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	3.91
	420812	AA715303	Hs.107369	ESTs	3.90
	423806	AA331247	Hs.86617	ESTs	3.90
60	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	3.90
	449211	AI922972	Hs.196073	ESTs	3.90
	409757	NM_001898	Hs.123114	cystatin SN	3.90
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	3.89
	432512	NM_003284	Hs.3017	transition protein 1 (during histone to	3.89
65	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	3.88
	449099	AI629041	Hs.46908	ESTs	3.88
	408092	NM_007057	Hs.42650	ZW10 interactor	3.85
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	3.85
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.84
70	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.83
	433023	AW864793		thrombospondin 1	3.82
	452571	W31518	Hs.34665	ESTs	3.81
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	3.80
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.80
75	420697	AA827705	Hs.26605	ESTs	3.80
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	3.80
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.80
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	3.80
	449529	AI990559	Hs.232033	ESTs	3.80
80	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.78
	444656	AI277924	Hs.145199	ESTs	3.77
	448674	W31178	Hs.154140	ovary-specific acidic protein	3.77
	415829	AW450198	Hs.163742	ESTs	3.76

	436188	AK001049	Hs.48712	hypothetical protein FLJ20736	3.75
	402178			C19001998*:gi|6453813|ref|NP_008926.2| b	3.75
	418179	X51630	Hs.1145	Wilms tumor 1	3.75
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.75
5	429063	AW363845	Hs.322903	ESTs, Weakly similar to A46010 X-linked	3.75
	437440	AA846804		ESTs	3.75
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associate	3.74
	438456	AA913381	Hs.20594	ESTs	3.73
	418821	AA436002	Hs.183161	ESTs	3.73
10	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.73
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.71
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	3.70
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	3.70
	414206	AW276887	Hs.46609	ESTs	3.70
15	427761	AA412205	Hs.140996	ESTs	3.69
	428728	NM_016625	Hs.191381	hypothetical protein	3.68
	452631	AI188658	Hs.87496	ESTs	3.68
	427719	AI393122	Hs.134726	ESTs	3.68
	431869	AA521136	Hs.190176	ESTs	3.67
20	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.67
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.66
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.66
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.65
	456030	AA136106	Hs.184852	KIAA1553 protein	3.65
25	402408			NM_030920*:Homo sapiens hypothetical pro	3.65
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	3.65
	416608	R11499	Hs.189716	ESTs	3.65
	417553	L09190		trichohyalin	3.65
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.65
30	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.64
	452461	N78223	Hs.108106	transcription factor	3.60
	437660	W31708	Hs.55304	ESTs	3.60
	420552	AK000492	Hs.98806	hypothetical protein	3.60
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.59
35	420161	AI683069	Hs.120817	ESTs	3.59
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	3.59
	449571	AW016812	Hs.200266	ESTs	3.56
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	3.55
	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein	3.55
40	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.55
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.55
	437700	AA766060	Hs.301209	myeloid/lymphoid or mixed-lineage leukem	3.55
	438176	AW138970	Hs.122113	ESTs	3.55
	453062	AW207538	Hs.61603	KIAA1677	3.55
45	447064	AB002350	Hs.17262	KIAA0352 gene product	3.55
	430056	X97548	Hs.228059	KRAB-associated protein 1	3.54
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.54
	434288	AW189075	Hs.116265	fibrillin3	3.54
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	3.52
50	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.52
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	3.52
	412123	BE251328	Hs.73291	hypothetical protein FLJ10681	3.51
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.50
	449467	AW205006	Hs.197042	ESTs	3.50
55	405935			Target Exon	3.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	3.50
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.50
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.49
	429183	AB014604	Hs.197955	KIAA0704 protein	3.49
60	428878	AA436884	Hs.48926	ESTs	3.49
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.49
	435068	H16262	Hs.31415	ESTs	3.48
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.48
65	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.48
	406542			C19000728*:gi|12585552|sp|Q9Y2Q1|Z257_HU	3.47
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.46
	402099			ENSP00000217725*:Laminin alpha-1 chain p	3.45
	418826	AK000375	Hs.88820	HDCMC28P protein	3.45
70	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.45
	427617	D42063	Hs.199179	RAN binding protein 2	3.45
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.45
	400268			NM_003292:Homo sapiens translocated prom	3.45
	443596	AW026048	Hs.134124	ESTs	3.45
75	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.45
	416031	T30290	Hs.107515	ESTs, Weakly similar to T00329 hypothet	3.45
	435244	N77221	Hs.187824	ESTs	3.45
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.45
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.45
80	420686	AI950339	Hs.40782	ESTs	3.44
	429467	NM_004477	Hs.203772	FSHD region gene 1	3.43
	448769	N66037	Hs.38173	ESTs	3.43
	423453	AW450737	Hs.128791	CGI-09 protein	3.41

	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.41
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.41
	404068			Target Exon	3.40
	401644			Target Exon	3.40
5	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	3.40
	452907	BE256966	Hs.31652	ESTs, Moderately similar to I54374 gene	3.40
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.39
	452404	AW450675	Hs.212709	ESTs	3.39
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	3.39
10	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	3.39
	440606	AI828751		ESTs, Weakly similar to I38022 hypotheti	3.38
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.37
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.37
	446214	AK001322	Hs.14347	hypothetical protein FLJ10460	3.36
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.36
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.36
	421633	AF121860	Hs.106260	sorting nexin 10	3.36
	438192	AI659065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.36
	436511	AA721252	Hs.291502	ESTs	3.35
20	402680			Target Exon	3.35
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.35
	449477	AI652602	Hs.197043	ESTs	3.35
	413686	AI469213	Hs.71404	ESTs	3.35
	401091			decay accelerating factor for complement	3.35
25	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.35
	433220	AI076192	Hs.131933	ESTs	3.34
	453200	AA033832	Hs.212433	ESTs	3.33
	427239	BE270447		ubiquitin carrier protein	3.33
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	3.33
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamidine syntha	3.31
	441243	AI767056	Hs.193002	ESTs	3.30
	440716	AW105245	Hs.146509	ESTs	3.30
	400587			C10000649*:gi|7296574|gb|AAF51857.1| (AE	3.30
	401148			Target Exon	3.30
35	411752	AW236047	Hs.126497	ESTs	3.30
	433252	AB040957	Hs.151343	KIAA1524 protein	3.30
	434008	AA740878	Hs.112982	ESTs	3.30
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.30
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.30
40	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.29
	452761	BE244742	Hs.30532	CGI-77 protein	3.29
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.29
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.28
	432809	AA565509	Hs.131703	ESTs	3.27
45	449426	T92251	Hs.198882	ESTs	3.27
	425174	D87450	Hs.154978	KIAA0261 protein	3.25
	435159	AA668879	Hs.116649	ESTs	3.25
	446597	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	3.25
	411554	W22895	Hs.112360	prominin (mouse)-like 1	3.25
50	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	3.25
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.25
	445093	AI207197		ESTs	3.25
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.24
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.24
55	453293	AA382267	Hs.10653	ESTs	3.24
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.23
	430552	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	3.22
	411975	AI916058	Hs.144583	ESTs	3.22
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.22
60	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.21
	436515	AJ278111	Hs.195292	putative tumor antigen	3.21
	456505	AA504595		ESTs	3.21
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	3.21
	452794	AI192444	Hs.25892	ESTs, Weakly similar to I37356 epithelia	3.20
65	427314	AB033024	Hs.175475	KIAA1198 protein	3.20
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.20
	452028	AK001859	Hs.27595	hypothetical protein FLJ21142	3.20
	421002	AF116030	Hs.100932	transcription factor 17	3.20
	422225	BE245652	Hs.118281	zinc finger protein 266	3.20
70	437549	AA759149	Hs.128757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	3.20
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	442765	BE567353	Hs.99480	ESTs	3.20
	410048	W76467	Hs.343874	proline oxidase homolog	3.20
75	412008	NM_001841	Hs.73037	cannabinoid receptor 2 (macrophage)	3.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	3.20
	453895	AA039843	Hs.61948	Homo sapiens, clone MGC:16466, mRNA, com	3.20
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.19
	428612	AA770001		ESTs	3.19
80	422805	AA436989	Hs.121017	H2A histone family, member A	3.19
	444371	BE540274	Hs.239	forkhead box M1	3.18
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.17
	451684	AF216751	Hs.26813	CDA14	3.17

	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	3.17
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.16
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.16
	444823	BE262989	Hs.12045	putative protein	3.15
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.15
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.15
	447801	H88923	Hs.270247	Homo sapiens cDNA FLJ11977 fis, clone HE	3.15
	424188	AW954552	Hs.142634	zinc finger protein	3.15
	436941	AA860383	Hs.292791	ESTs	3.15
	400592			Target Exon	3.15
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.15
	450405	AI694913	Hs.279637	ESTs	3.15
	414161	AA136106	Hs.184852	KIAA1553 protein	3.15
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	3.14
	438538	AA832203	Hs.291955	ESTs	3.14
	441013	AI125252	Hs.126419	ESTs	3.14
	450431	AW136797	Hs.266041	ESTs	3.14
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	3.13
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.13
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.12
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	3.12
	412673	AL042957	Hs.31845	ESTs	3.11
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.11
	423419	R55336	Hs.23539	ESTs	3.11
	428925	AW242474	Hs.98960	ESTs	3.11
	426108	AA622037	Hs.166468	programmed cell death 5	3.10
	439398	AA284267	Hs.221504	ESTs	3.10
	449138	AW294215	Hs.195631	ESTs	3.10
	441795	N58115	Hs.21137	AD024 protein	3.10
	456053	S57498	Hs.76252	endothelin receptor type A	3.10
	403610			C3001199:gi|7494834|pir||T15308 hypothet	3.10
	421281	AI299139	Hs.17517	ESTs	3.10
	429274	AI379772	Hs.99206	ESTs	3.10
	438243	AI581311		ESTs	3.10
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.09
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.08
	416443	N69469	Hs.194225	ESTs	3.08
	421230	AW958439	Hs.105633	ESTs	3.07
	427906	AA864330	Hs.166520	ESTs	3.07
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.06
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.06
	445679	AI343868	Hs.301059	hypothetical protein FLJ12488	3.06
	434456	AW452621	Hs.116832	ESTs	3.05
	433228	F28212	Hs.14953	KIAA1491 protein	3.05
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.05
	415227	AW821113	Hs.72402	ESTs	3.05
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	3.05
	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.05
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.04
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.04
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.04
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	3.04
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	3.04
	435726	BE535787	Hs.113170	ESTs	3.03
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	3.03
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.02
	427953	AA417944	Hs.44331	ESTs	3.01
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.01
	421305	BE397354	Hs.324830	diptheria toxin resistance protein requi	3.00
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.00
	434776	AA648988		gb:ns41f11.s1 NCI_CGAP_GCB1 Homo sapiens	3.00
	414132	AI801235	Hs.48480	ESTs	3.00
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
	433493	AA594915	Hs.155087	ESTs	3.00
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	3.00
	453416	NM_003037	Hs.32970	signaling lymphocytic activation molecul	3.00

TABLE 53B
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539 BG215094 BG198867 BG196332 BG208220 BG212418
430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603 AI352469 BE061601 BI062752 AW818206 BF887722
422828	227063_1	BE671981 BE503379 AI655440 AI337054 AI288920 AI242370 AI825182 AA758081 BF855141 BF091068
418477	4172_1	BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092 AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
443068	18695_17	AV752763 AI032142 N30308 N22181 H95390 AW675632
436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673

427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
436899	1000797_1	AA764852 AA736937
422689	874209_1	AW954733 AA315006 AW856665
440968	518029_1	AI964001 AI634418 AW236545 AI824860 BF223710 AW139686 AI672051 AI655566 AW025712 N36327 BF222876 N34083 AA911045 N40303 AW835451
427486	684159_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
421974	864120_1	AA301270 AA301379 AA301366
435514	132288_1	AA683356 AW592804 AI150287
434609	14739_1	AF147390 R76593 R76594
414136	30243_1	AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920 AI566634 AA211796 BG615512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AU154486 AW605017 AW450072 AA446459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812
415684	18695_18	BF666746 D59356 BG678312 N56640 AA166861
437421	978554_1	AA917062 AA757369 AW592218
439780	49082_1	AL109688 R23665 R26578
453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
412537	14066_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
440801	2635916_1	AA906366 AA938956 AI910938
436909	596835_1	AW102570 AA907150 AA907120 AA737188 AI248890 AW977353
429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
451050	11847_4	BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839
418235	886897_1	BE072634 BE072653 AA830615 AA214736 AA331718
418378	1227421_1	AA218925 AW962081 AA354237
450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758
409517	4537_1	NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070 C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339
442562	39593_1	AK056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 AI653056 AW973709 AI653173 BG054997 AI266043 BI054879 AI656750 AI492830 AW021142 AI472184 AW170056 AI082443 AI167921 D59940 BI492088 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832
451105	1145037_1	BI015205 AI761324 AW880937 AW880941
424281	892055_1	AA338252 AA338213
430183	17316_1	AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038
427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
444386	1490237_1	BE065183 AI144398 BE065367 BF377924
414725	19377_1	NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936 AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338826 AI650258 AI628362 AA227117 AI207149 AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112 BI054316
433641	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951 N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833 AA207155 BI004756 AA206262 AI365204 H77608 AW590511
418768	2293204_1	T39328 T39310 T39303 T39284
409268	109625_1	BE893356 AA625304 AI765607 AI624898 R76060 AA069651 BG998885 R35783 BF086499 AA428755 AI245055
415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
433979	2076469_1	N50454 AA620999 T16375
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
418866	245947_1	T65754 AA229658 AA229857
449687	25369_2	AK056550 AK056356 AI926212 AI742073 AW300558 BG058755 AA058343 AI554842 AW207438 BF509981 BF444954 AW026234 AI620104 AA973460 AI370934 N63066 AA493129 AW590688 AI682952 AI167202 AA631394 AI421915 AI222883 BF477519 AI208777 AA765849 AI675076 AI370922 AI339579 AA486224 AA453524 AW771805 AI492842 H54679 AA961022 AW023555 H06192 AA910222 AI660021 AI032525 AI375480 AI361860 AI032919 AA833599 BG057928 AA553913 AW235737 AA002124 AA913636 F04607 AI867699 AA648100 BE091446 AA486378 BE002022 H84627 BI059837 BF917659 BF917100 BF917043 BF917104 BF916878 BG290981 AW954251 AA757126 H11545 AA353384 N48448 AA379845 AA004943 AA379928 AA002123 BM470118 AL598847 AL598830 BG899239 R57470 BF939179 AI650642 AI758851 BF352505 W68422 W35297 H11435 AA937499 AI783996 R12500 AI819557 N39093 Z41619 H22849 AA004942 R09436 R02403 T90942 T85823
445685	381678_1	BG029663 AI248120 BI850480 AW779829 N22494
413646	1525656_1	BE155042 BE155040 BE154987 BE155012
437834	294580_1	BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573
454679	174325_1	AW813110 BF771370 BF771371 AW813113 AW003381
440840	29686_1	BI862319 AA204955 BF240507 BG212143 AW205739 BI760647 BM129481 BI760482 AW300025 AI288591 AW236114 AI302852 AI038548 AI797207 AA534496 BG188194 AA921877 BG191846 BG182959 BE620243 BF217428 BC009514 BM463015 AL529077 BM051874 BG773269 BM314351 BM314660 AW629666 AA316207 AI623431 AA504153 AA314700 BG195449 BG614101
433023	3970_8	BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871
437440	2497201_1	AA846804 AA757581 AI050950 AI092024 AA838807

	417553	258857_1	AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878 AI769345 R71250 AI363766 R22777 R17009 R27985 R28243
	408065	101881_1	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
	418049	12052_4	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234 AV731417 R42406 H04996 T98498 R12489 R12577 R42405
	430968	1237115_1	AW972830 AA489820 AA527647 AA570362
	400268	840_4	U69666 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AI870824 BE973573 BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687 BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859 AW167268 AI990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916 AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 AI650450 AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782 AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532 BE934857 BF925057 AW438446 R86246 AW179270 BE087782 BI832144
	440606	10075_1	BC017350 BC021031 AI220219 AI828751 AW134498 BE139642 AA894554 AI278594 AV747315 BE561749 BI085890 T80117 H69682 N70904 AV741999 H70098
	427239	20459_2	AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074866 BE857822
	445093	175963_1	AI207197 BF773544 AW196462
	456505	15472_2	BC017965 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312
	428612	1383189_1	AA770001 AA431112 AA432126
	437642	77594_1	AL079309 AA281819
	440129	2607882_1	AI732997 AA977633 AA865818
	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523 BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866 AW840571
	438243	2532601_1	AI581311 AA781682 AA781678
	438869	52134_1	AF075009 R63109 R63068
	434776	118129_1	AW974599 AA648988 R98760

TABLE 53C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406547	7711513	Minus	172780-174358
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402199	8576116	Minus	84187-84744
402145	8018280	Plus	113086-114800
401837	7630990	Minus	120993-121095,121660-121729
403780	8076989	Plus	93160-93409
402299	6693370	Plus	23367-25175
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
402098	8117697	Minus	44186-44330
404287	2326514	Plus	53134-53281
406367	9256126	Minus	58313-58489
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
402178	8575912	Plus	391138-391711
403433	9719611	Minus	72225-72437
402408	9796239	Minus	110326-110491
405935	6758795	Minus	163112-163652
406542	7711499	Plus	117335-118473
402099	8117697	Plus	121553-121742,123265-123423
404068	3168621	Minus	18123-18766
401644	8576138	Plus	82655-83959
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
401091	9958240	Plus	94760-94898
400587	9887626	Plus	25435-25588,25668-25747
401148	2547238	Minus	22521-23053
403432	9719611	Minus	68204-68392
400592	9887642	Minus	24642-24815
403610	8308266	Plus	157705-157860

TABLE 54A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of normal testi to normal adult tissues

R2: Ratio of "average" normal testi to "average" testicular cancer

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2

401979			C17000767:gi|11990770|emb|CAC19651.1| (A	10.08	43.3
421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	10.35	36.8
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.74	32.0
441728	AI797395	Hs.169797	Homo sapiens BOULE (BOULE) mRNA, complet	10.54	24.5
452215	AK002043	Hs.28472	hypothetical protein FLJ11181	4.86	22.0
415211	R64730.	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.93	19.8
418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.94	18.5
449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.94	17.5
420437	AA992768	Hs.97633	A kinase (PRKA) anchor protein 4	16.75	15.6
436632	AA724299	Hs.304020	ESTs, Weakly similar to CRTC_HUMAN CALRE	6.51	14.9
418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	4.96	14.6
406409			Target Exon	3.98	14.3
427060	AW378993	Hs.90286	ESTs	3.56	14.2
427310	AI613480	Hs.47152	tektin 3	4.50	14.0
427166	AA431576	Hs.99154	ESTs	4.28	13.9
427178	AA398866	Hs.97542	Homo sapiens testis-development related	10.19	13.7
410694	AL137538	Hs.65500	Homo sapiens mRNA; cDNA DKFZp434N2019 (f	5.76	13.4
424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.24	13.3
427441	AA412605	Hs.343879	SPANX family, member C	10.45	12.6
438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORNI	18.57	12.3
422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	5.18	12.3
427293	AA705799	Hs.183714	ESTs	10.79	12.1
444963	AI916973	Hs.213603	ESTs	3.18	12.1
428608	AI699329	Hs.99168	ESTs, Weakly similar to AF132972 1 CGI-3	15.40	11.8
453178	AA496086	Hs.61648	ESTs	4.13	11.8
428618	AA885360		Target CAT	7.53	11.5
401741			Target Exon	10.41	11.5
422086	AW182930	Hs.250182	ESTs	4.39	10.7
426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	7.04	10.6
442373	AI377758	Hs.164799	testes development-related NYD-SP17	8.23	10.3
427455	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax interacti	3.03	10.1
437248	AW449340	Hs.93090	ESTs	9.06	10.1
426606	AA444152	Hs.99344	hypothetical protein PRTD-NY3	3.68	10.0
427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	9.70	9.8
422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	11.85	9.7
451610	AW118604	Hs.207126	ESTs	5.63	9.7
410630	BE044562	Hs.266847	ESTs, Weakly similar to KIAA1214 protein	4.38	9.5
426677	AW949856	Hs.97165	ESTs	6.58	9.3
437558	AI126471	Hs.124112	ESTs, Moderately similar to HSJ2_HUMAN D	4.47	9.2
423088	NM_006687	Hs.123530	actin-like 7A	15.07	8.9
426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	18.55	8.9
421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	13.93	8.8
429877	W37337	Hs.103014	ESTs	6.97	8.7
413114	AI825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	3.78	8.6
412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	22.03	8.5
411844	AI807681	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	7.34	8.3
436868	AA974253	Hs.120319	Homo sapiens autoimmune infertility-rela	4.16	8.2
426599	AW183574		ESTs	6.29	8.1
426683	AI073430	Hs.146775	ESTs, Weakly similar to T30993 hypotheti	10.89	8.0
426930	AA393442		ESTs	5.06	8.0
427836	AA416642	Hs.116176	ESTs	4.79	8.0
407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	5.11	7.9
430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	21.26	7.6
434150	BE047007	Hs.116116	testis specific, 10	4.85	7.6
422789	AK001113	Hs.120842	hypothetical protein FLJ10251	10.29	7.5
422116	H64205	Hs.111850	mitochondrial capsule selenoprotein	9.12	7.5
433724	AI827749	Hs.144924	serine/threonine protein kinase SSTK	22.24	7.4
410187	AA860341	Hs.104680	ESTs	3.03	7.4
419584	AF053356	Hs.283764	F-box only protein 24	6.43	7.4
458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	9.90	7.3
418665	T19204	Hs.195685	ESTs	7.14	7.3
426646	AA382767	Hs.122713	ESTs	7.03	7.3
420349	NM_016611	Hs.97174	potassium inwardly-rectifying channel, s	14.90	7.3
428624	AI125222	Hs.98712	hypothetical protein DKFZp434H0311	3.71	7.1
420710	NM_007009	Hs.99875	zona pellucida binding protein	20.78	7.1
434317	AI674095		ESTs	3.98	7.1
443432	AI056863	Hs.339871	ESTs	3.46	7.0
425709	AA383076	Hs.159274	outer dense fibre of sperm tails 1	23.21	7.0
426670	AA383047	Hs.310210	ESTs	6.92	7.0
408613	AW242086	Hs.253967	ESTs	5.77	6.8
452235	AL039743	Hs.28514	testes development-related NYD-SP21	9.23	6.7
434133	AI655275	Hs.236635	ESTs, Weakly similar to ATHUB actin beta	7.46	6.7
427294	AA412594	Hs.125902	ESTs	3.44	6.7
427262	AA448509	Hs.128652	ESTs	5.66	6.5
429851	AA459835	Hs.120573	hypothetical protein DKFZp434K1172	9.01	6.5
406378			NM_021247*:Homo sapiens protamine 3 (PRM	3.96	6.4
425865	AA393491	Hs.183740	ESTs	9.15	6.4
428665	NM_017481	Hs.189184	ubiquilin 3	11.07	6.4
439379	AA835002	Hs.125611	ESTs	5.06	6.3
427520	BE467881	Hs.97489	ESTs, Weakly similar to B28096 line-1 pr	9.29	6.2
458940	BE149824	Hs.132888	KIAA1674	3.11	6.2
426620	AW450252		ESTs	12.27	6.2
429516	AI653299	Hs.99354	ESTs, Weakly similar to hyperpolarizatio	9.15	6.1

426736	AA431615	Hs.130722	ESTs	3.58	6.1
427843	AC005622	Hs.180943	hypothetical protein R30953_1	6.34	6.1
426639	AI799059	Hs.112807	ESTs	6.93	6.0
438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein	3.04	6.0
433795	AI216683	Hs.122599	ESTs, Weakly similar to ALU7_HUMAN ALU S	10.45	5.9
441232	AI656050	Hs.7086	hypothetical protein MGC12435	4.27	5.9
433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	6.87	5.8
426955	AA393669	Hs.238094	ESTs	4.75	5.8
428918	AL036967	Hs.2324	protamine 2	38.40	5.8
427851	AA846543	Hs.98257	ESTs	15.87	5.8
428208	AA442327	Hs.104854	ESTs	6.34	5.7
422207	AI828862	Hs.10964	ESTs	6.43	5.7
431153	AW972342	Hs.77823	hypothetical protein FLJ21343	9.24	5.7
419350	AC005328		Homo sapiens chromosome 19, cosmid R2666	14.94	5.6
427107	AA889586	Hs.180346	ESTs	6.25	5.6
429461	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	3.92	5.6
432512	NM_003284	Hs.3017	transition protein 1 (during histone to	22.03	5.6
434451	AW445179	Hs.121438	ESTs	7.89	5.5
420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	11.26	5.5
427214	AA442240	Hs.178213	ESTs	8.41	5.5
458658	AI301117	Hs.122055	ESTs	4.35	5.5
457034	AA398061	Hs.296587	Homo sapiens chromosome 21 segment HS21C	11.29	5.4
423120	AW160551	Hs.124021	soggy-1 gene	8.88	5.4
438983	AF085884	Hs.20029	proacrosin binding protein sp32 precurso	22.69	5.4
426619	AI357194	Hs.119284	ESTs	7.07	5.4
440822	AI554897		Homo sapiens clone 191B7 placenta expres	3.60	5.4
416205	AA176396	Hs.169624	ESTs	10.26	5.4
426712	AW173177	Hs.197755	hypothetical protein MGC5356	8.17	5.3
427840	AI216654	Hs.98251	ESTs	6.44	5.3
439314	AA382413	Hs.178144	ESTs	8.35	5.3
426943	BE551631	Hs.20969	ESTs	6.31	5.2
409209	AA460160	Hs.73217	ESTs	7.85	5.2
441710	AI187883	Hs.127510	ESTs, Weakly similar to ENC1_HUMAN ECTOD	7.73	5.1
420571	AA442366	Hs.98952	Human DNA sequence from clone RP1-39G22	9.39	5.1
428563	AA431616	Hs.98660	ESTs	14.94	5.1
433994	AL042483	Hs.335499	ESTs	6.84	5.0
441856	AI674774	Hs.128014	ESTs	3.74	5.0
427789	AA412428	Hs.48642	hypothetical protein FLJ23093	4.29	5.0
418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	4.14	4.9
430232	AA469940	Hs.105324	ESTs, Moderately similar to FRHUH ferrit	10.66	4.9
421850	AW274576	Hs.121021	ESTs	12.27	4.9
449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	4.50	4.9
426699	AA383337	Hs.121269	ESTs	5.67	4.9
426627	AF012359	Hs.195685	ESTs	20.66	4.9
427285	AA401664	Hs.97784	ESTs	4.72	4.8
423693	AL133633	Hs.131779	Homo sapiens mRNA; cDNA DKFZp434E2118 (f	6.03	4.8
457019	AA421844	Hs.12630	hypothetical protein	3.87	4.8
405264			NM_030813*:Homo sapiens suppressor of po	4.48	4.8
450606	AI668605	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	3.76	4.8
421378	L77564	Hs.103978	serine/threonine kinase 22B (spermiogene	7.35	4.8
431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	8.66	4.7
427423	BE267041	Hs.177926	exonuclease NEF-sp	19.27	4.7
438756	AW081754	Hs.303923	hypothetical protein DKFZp434L1717	12.05	4.7
424197	AF096834	Hs.142989	germ cell specific Y-box binding protein	17.70	4.7
423284	AC005764	Hs.126496	Homo sapiens chromosome 19, cosmid R3134	7.50	4.7
432117	AL036195	Hs.2909	protamine 1	55.33	4.7
424426	AI476416	Hs.132888	KIAA1674	5.41	4.6
437387	AI196874	Hs.28847	AD026 protein	5.04	4.6
420718	NM_002301	Hs.99881	lactate dehydrogenase C	9.18	4.6
420768	AI468780	Hs.292503	ESTs, Weakly similar to T47142 hypotheti	5.70	4.6
423677	M66808	Hs.131361	pyruvate dehydrogenase (lipoamide) alpha	10.93	4.5
436661	AI125270	Hs.128069	ESTs, Weakly similar to T19142 hypotheti	3.82	4.5
427749	BE045979	Hs.98095	Homo sapiens cDNA: FLJ23052 fis, clone L	6.45	4.5
441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	11.29	4.5
427877	AW138725	Hs.178067	ESTs	4.09	4.5
426623	AA382826	Hs.132793	ESTs	26.62	4.5
429965	AL040379	Hs.99551	Homo sapiens cDNA FLJ11789 fis, clone HE	13.25	4.5
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.88	4.4
417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosom	3.46	4.4
421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	4.69	4.4
424144	AA454033	Hs.41644	AKAP-associated sperm protein	19.15	4.4
426710	BE041517	Hs.143893	ESTs	5.57	4.4
428710	AI890919	Hs.126780	ESTs, Weakly similar to T12519 hypotheti	11.86	4.4
438641	AW138484	Hs.190653	ESTs	6.19	4.4
420614	AL110291	Hs.99364	putative transmembrane protein	6.86	4.4
422705	NM_006686	Hs.119287	actin-like 7B	9.73	4.4
421805	AL042716	Hs.130947	hypothetical protein DKFZp434N1415	5.89	4.4
446963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610712, mRNA,	6.77	4.3
426738	AA421097	Hs.291902	ESTs	3.49	4.3
440403	AW665135	Hs.130531	ESTs	6.97	4.3
456085	AI184560	Hs.130352	ESTs, Weakly similar to A47582 B-cell gr	6.30	4.3
439594	AI245026	Hs.111099	hypothetical protein MGC10974	7.85	4.3
428909	AI190714	Hs.98945	ESTs	7.79	4.3

	426735	T78716	Hs.120446	ESTs	5.10	4.3
	438653	AW188099	Hs.131813	ESTs	5.29	4.3
	443038	AI968058	Hs.209206	ESTs, Weakly similar to S38782 actin bet	7.29	4.2
	428677	AI657119	Hs.120036	troponin I, cardiac	10.73	4.2
5	424220	AK000869	Hs.143251	hypothetical protein	9.13	4.2
	426299	H93373	Hs.169222	acrosomal vesicle protein 1	4.87	4.2
	428871	AA913840	Hs.98903	ESTs	3.76	4.2
	410163	AF151977	Hs.59260	NTT5 protein	7.29	4.2
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.29	4.2
10	427757	AI142295	Hs.129794	ESTs	3.57	4.1
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	11.13	4.1
	401692			C16000122*:gi|5689527|db|BAA83047.1| (A	6.37	4.1
	403783			NM_031956:Homo sapiens NYD-SP14 protein	3.74	4.0
	421611	AA459841	Hs.97309	ESTs	11.51	4.0
15	404271			ENSP00000244792*:Phosphoglycerate kinase	4.02	4.0
	441800	AW027571	Hs.7973	hypothetical protein DKFZp434G156; KIAA1	8.86	4.0
	423000	AF049615	Hs.122959	Huntingtin interacting protein M	3.60	4.0
	423118	AL035460	Hs.124009	Human DNA sequence from clone RP5-860F19	4.84	4.0
	420419	AA397796	Hs.11614	HSPC065 protein	4.07	3.9
20	435897	AF269223	Hs.128322	t-complex 11 (a murine tcp homolog)	23.29	3.9
	428516	R38137	Hs.156469	ESTs, Moderately similar to KIAA0940 pro	5.28	3.9
	427179	AA400590	Hs.97543	ESTs	6.18	3.9
	426609	AL040604	Hs.99344	hypothetical protein PRTD-NY3	10.07	3.9
	452579	AA131657	Hs.23830	ESTs	5.24	3.9
25	441443	BE465999	Hs.129293	ESTs	4.60	3.9
	427709	AI631811	Hs.180403	STRIN protein	3.82	3.9
	435484	AA682756	Hs.88051	ESTs	5.10	3.9
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.61	3.8
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	7.14	3.8
30	421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214 salivary	5.20	3.8
	427086	AA436131	Hs.188781	ESTs	5.76	3.8
	420475	AW408407	Hs.187018	ESTs	3.99	3.8
	441357	AI240184	Hs.343487	ESTs	4.63	3.8
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	8.04	3.8
35	441806	AI024442	Hs.346385	ESTs	5.48	3.8
	413209	AW083791	Hs.21263	suppressor of potassium transport defect	9.02	3.8
	414544	AA149285	Hs.115659	hypothetical protein MGC5521	10.15	3.8
	427251	AI026844	Hs.98843	ESTs, Highly similar to GRA2_HUMAN GLYCI	7.69	3.8
	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	3.46	3.7
40	442589	BE409869		protein kinase, cAMP-dependent, regulato	4.50	3.7
	425841	BE262951	Hs.99052	ESTs	8.26	3.7
	410350	AA446395	Hs.62595	chromosome 9 open reading frame 9	7.64	3.7
	440487	AI203685	Hs.135763	ESTs	5.90	3.7
	419455	AW172570	Hs.14600	ESTs	4.23	3.7
45	436588	AA759233		ESTs	5.04	3.7
	421610	AA393168	Hs.90034	hypothetical protein FLJ21916	5.53	3.7
	441982	AI216902	Hs.48802	ESTs	4.79	3.6
	427288	AI139000	Hs.97792	hypothetical protein DKFZp434I099	5.17	3.6
	414439	W45387	Hs.100007	regulatory factor X, 2 (influences HLA c	4.43	3.6
50	401798			Target Exon	4.83	3.6
	433395	AF039442	Hs.160881	Homo sapiens colon cancer antigen NY-CO-	3.17	3.6
	438064	AI476330	Hs.234934	ESTs	3.56	3.6
	426658	AA397912	Hs.115366	Human DNA sequence from clone RP4-803K15	7.26	3.6
	431986	AA536130		Novel human gene mapping to chomosome 20	6.13	3.6
55	427872	AA835058	Hs.9622	Human DNA sequence from clone RP1-261G23	4.04	3.6
	437896	AA813689	Hs.123436	ESTs, Weakly similar to KIAA1205 protein	4.69	3.6
	420431	AB007131		Homo sapiens cDNA FLJ12825 fis, clone NT	4.24	3.5
	409467	Z22780	Hs.307358	cylicin, basic protein of sperm head cyl	5.13	3.5
	422770	AL117544	Hs.120021	DKFZP434I092 protein	8.02	3.5
60	437399	AI808626	Hs.121188	ESTs, Weakly similar to T29922 hypotheti	5.03	3.5
	428448	AA625766	Hs.98609	ESTs, Weakly similar to A Chain A, Coagu	4.30	3.5
	426705	AL042749	Hs.97714	ESTs	10.45	3.5
	427312	AA400657	Hs.135283	ESTs	4.47	3.5
	423329	AF054910	Hs.127111	teklin 2 (testicular)	4.40	3.5
65	439290	AI638094	Hs.236896	ESTs	3.29	3.4
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	6.18	3.4
	420500	AC005261	Hs.98338	serine/threonine kinase 13 (aurora/IPL1-	6.24	3.4
	441168	AI198850	Hs.131654	DMRT-like family B with proline-rich C-t	10.39	3.4
	420482	X57655	Hs.98243	serine protease inhibitor, Kazal type, 2	20.38	3.4
70	426988	AI208684	Hs.163960	Homo sapiens heat shock transcription fa	5.02	3.4
	444968	AW628609	Hs.148653	ESTs	5.10	3.4
	429210	AA448011	Hs.131918	ESTs	4.22	3.4
	442970	R28215	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	4.20	3.4
	422782	AL133054	Hs.120369	hypothetical protein DKFZp434H2215	4.72	3.4
75	436601	AA969884		ESTs	4.84	3.4
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	7.83	3.4
	415705	U06632	Hs.966	coilin	6.30	3.4
	435587	AF215924	Hs.97899	putative allantoicase	3.48	3.3
	427572	AA417291	Hs.97978	hypothetical protein MGC4766 similar to	3.54	3.3
80	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.33	3.3
	429404	NM_005738	Hs.201672	ADP-ribosylation factor-like 4	3.57	3.3
	415014	AW954064	Hs.24951	ESTs	4.03	3.3
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	10.76	3.3

412092	H43229	Hs.125201	ESTs, Weakly similar to I38022 hypotheli	5.27	3.3
441579	AW468847	Hs.127194	ESTs	7.13	3.3
420619	AF130255	Hs.99430	testis zinc finger protein	5.19	3.3
425368	AB014595	Hs.155976	cullin 4B	3.07	3.3
425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.52	3.3
429938	BE296804	Hs.226377	phosphate cytidylyltransferase 2, ethano	3.03	3.3
453017	R84301	Hs.31387	DKFZP564J0123 protein	3.30	3.3
424466	AL040420	Hs.148250	Homo sapiens mRNA; cDNA DKFZp434N1535 (f	4.81	3.3
442084	H81173	Hs.34596	ESTs	4.78	3.3
423196	AK001866	Hs.125139	hypothetical protein FLJ11004	4.63	3.3
434183	AW104257	Hs.123426	ESTs, Weakly similar to SN1L_HUMAN PROBA	5.73	3.3
428093	AW594506	Hs.104830	ESTs	6.95	3.3
433982	AA724720	Hs.112941	ESTs	5.11	3.2
429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (fr	4.04	3.2
408415	AW418788		ESTs, Weakly similar to S43569 R01H10.6	3.49	3.2
407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.77	3.2
402857			Target Exon	3.19	3.2
416667	AK000526	Hs.79457	hypothetical protein FLJ20519	3.69	3.2
435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	14.29	3.2
427748	AA421041		ESTs	4.57	3.2
422794	AJ011733	Hs.120857	synaptogyrin 4	4.23	3.2
417488	AL046052	Hs.321046	hypothetical protein FLJ11743	3.57	3.2
440115	R41808		ESTs, Weakly similar to B Chain B, Solut	4.67	3.2
437143	AW204056	Hs.8917	ESTs	4.16	3.2
417473	M55268	Hs.82201	casein kinase 2, alpha prime polypeptide	4.02	3.2
426594	AA884317	Hs.97130	ESTs	3.45	3.2
428733	AA346824	Hs.191996	Homo sapiens organic cation transporter	6.29	3.2
440864	AI382142	Hs.132104	ESTs	8.48	3.2
427141	AW628007	Hs.97643	testis-specific protein TSP-NY	5.60	3.2
431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp434F0919 (f	5.10	3.2
438670	AI275803	Hs.123428	ESTs	4.08	3.2
412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.26	3.2
452251	R37132	Hs.65009	ESTs	4.01	3.1
444141	AW629475	Hs.8977	ESTs, Weakly similar to RED1_HUMAN DOUBL	4.89	3.1
428254	AK000542	Hs.183362	hypothetical protein FLJ20535	5.23	3.1
421621	AL045589	Hs.180197	ESTs	7.09	3.1
451017	BE391847	Hs.181173	hypothetical protein MGC10771	3.57	3.1
457138	AW140059	Hs.98579	ESTs	13.17	3.1
428524	AA429772		ESTs	4.40	3.1
428726	AA432195	Hs.98694	ESTs	6.47	3.1
431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fis, clone TH	4.07	3.1
428076	AA420979	Hs.234895	ESTs, Weakly similar to Lysozyme [H.sapi	5.97	3.1
427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.45	3.1
424450	AL137526	Hs.147472	dynein intermediate chain 2	6.01	3.1
433963	AI218808	Hs.187778	ESTs	5.68	3.1
424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.20	3.1
440933	AI208217		ESTs	3.44	3.1
441854	AA215990	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.s	4.03	3.1
423313	NM_014269	Hs.126838	a disintegrin and metalloproteinase doma	6.36	3.1
428630	AA431270	Hs.140646	ESTs	3.59	3.1
448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	5.63	3.0
434720	AI208541	Hs.189160	ESTs, Weakly similar to cytochrome c-lik	6.04	3.0
436328	AI201145	Hs.122042	Human DNA sequence from clone RP4-576H24	7.10	3.0
429293	AI767879	Hs.99214	ESTs	5.69	3.0
427255	AA400082	Hs.343593	ESTs, Weakly similar to TD54_HUMAN TUMOR	5.37	3.0
440713	AA904448	Hs.126368	ESTs	6.26	3.0
418499	AI627392	Hs.302023	hypothetical protein FKSG25	7.88	3.0
423218	NM_015896	Hs.167380	BLu protein	6.68	3.0
444644	AW070634	Hs.144794	ESTs	5.00	3.0
430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.75	3.0
427829	AI188225		ESTs	7.36	3.0
426879	AI969340	Hs.115437	hypothetical protein MGC3048	7.24	3.0
427362	AA625582	Hs.97752	EST	4.38	3.0
441973	T60072	Hs.10688	ESTs, Weakly similar to HRIHFB2157 [H.sa	4.06	2.9
428989	AF104260	Hs.194712	piwi (Drosophila)-like 1	4.45	2.9
438735	M76676		ESTs	3.81	2.9
432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	11.37	2.9
427586	AA609661	Hs.190592	ESTs, Moderately similar to WASP-family	6.26	2.9
427306	AI476743	Hs.229275	ESTs	3.00	2.9
418725	AL117637	Hs.306094	DKFZP434I225 protein	7.13	2.9
456748	AW137749	Hs.125902	ubiquitin specific protease 2	3.48	2.9
443162	T49951	Hs.9029	DKFZP434G032 protein	3.60	2.9
433836	AA610065	Hs.179646	ESTs	3.33	2.9
439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.22	2.9
437426	AW136558	Hs.125246	ESTs	4.49	2.9
405528			C2002647:gi|4507721|ref|NP_003310.1| tit	6.03	2.9
442977	AW291731	Hs.144090	ESTs	4.23	2.9
433330	AW207084	Hs.132816	hypothetical protein MGC14801	13.24	2.8
424275	AW673173	Hs.144505	DKFZP566F0546 protein	5.60	2.8
426667	AA770016	Hs.121192	ESTs	3.64	2.8
410202	AB023213	Hs.60177	KIAA0996 protein	3.00	2.8
428080	AI198656	Hs.98330	ESTs	4.09	2.8
427252	AA400069	Hs.97757	hypothetical protein FLJ13031	4.34	2.8

458255	AW140126	Hs.132357	ESTs	3.23	2.8
433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.95	2.8
440582	AA993337	Hs.129082	ESTs	5.29	2.8
435566	AI457958	Hs.80464	hepatitis B virus x-interacting protein	3.28	2.8
433771	AI028794	Hs.112684	ESTs	3.36	2.8
447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.30	2.8
426703	AI221893	Hs.121549	ESTs	3.93	2.8
430251	AA609246	Hs.181451	ESTs	4.04	2.8
427184	AI969361	Hs.180471	ESTs	6.78	2.8
439909	AW450062	Hs.187134	ESTs, Moderately similar to AF263742 1 g	3.65	2.8
448885	AW003686	Hs.30325	ESTs, Highly similar to AF200923 1 testi	3.34	2.7
450340	AA442322	Hs.60288	ESTs	5.39	2.7
428100	AW665592	Hs.190413	ESTs	5.32	2.7
449333	AI203021		ESTs	4.35	2.7
429861	AI989571	Hs.99510	ESTs	3.28	2.7
426622	AL044400	Hs.25371	ESTs, Weakly similar to A37232 mucin, tr	5.38	2.7
427256	AL042436	Hs.97723	ESTs	4.08	2.7
408407	AF214680	Hs.44685	C3HC4-like zinc finger protein	3.27	2.7
403328			Target Exon	4.26	2.7
436264	AA707457	Hs.120014	ESTs	3.58	2.7
427104	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial ci	3.68	2.7
426640	AI200961	Hs.98104	ESTs	4.60	2.7
428789	AW296167	Hs.91930	ESTs	4.23	2.7
435274	AA887547	Hs.150905	ESTs	4.25	2.7
426612	AA922067	Hs.184185	ESTs	7.17	2.7
435110	N42688	Hs.81001	F-box only protein 25	4.85	2.7
433792	AA778661		ESTs	4.06	2.7
423278	AL117627	Hs.126289	Homo sapiens mRNA; cDNA DKFZp434B115 (fr	3.04	2.7
427284	AA400298	Hs.144696	ESTs	5.81	2.6
423375	Z94277	Hs.127689	type 1 protein phosphatase inhibitor	3.36	2.6
422362	Z46967	Hs.115460	calicin	4.72	2.6
439993	T18864	Hs.144924	serine/threonine protein kinase SSTK	5.03	2.6
409364	AI480252	Hs.137368	ESTs	7.22	2.6
419224	NM_012189	Hs.314452	fibrousheathin II	13.86	2.6
428915	AI041278	Hs.87908	Snf2-related CBP activator protein	4.73	2.6
427181	AI183653	Hs.27888	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.21	2.6
442122	AI932330		ESTs	3.07	2.6
424812	AF059252	Hs.153299	DOM-3 (C. elegans) homolog Z	3.80	2.6
430956	AI183529	Hs.2706	glutathione peroxidase 4 (phospholipid h	3.19	2.6
427234	AA399667	Hs.104675	ESTs	3.43	2.6
423005	AL080148	Hs.123004	DKFZP434B204 protein	3.53	2.6
428214	AA936282	Hs.120397	ESTs	4.14	2.6
452613	AA461599	Hs.23459	ESTs	7.78	2.6
410380	AL133068	Hs.62880	novel protein similar to mouse MOV10	3.45	2.6
452537	AW247390	Hs.77735	hypothetical protein FLJ11618	3.43	2.6
401712			Target Exon	4.51	2.6
429186	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	5.90	2.6
438124	AA778610	Hs.122045	ESTs	3.43	2.6
422937	U03270	Hs.122511	centrin, EF-hand protein, 1	3.60	2.6
410279	BE271977	Hs.61809	hypothetical protein FLJ14117	4.36	2.6
428625	W87565	Hs.18566	ESTs	5.29	2.6
433439	AA431176	Hs.133230	ribosomal protein S15	3.50	2.5
433760	AW592321		ESTs	3.26	2.5
431219	AI190773	Hs.127204	ESTs, Weakly similar to similar to CR16,	5.10	2.5
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	8.07	2.5
453468	W00712	Hs.32990	DKFZP566F084 protein	3.56	2.5
445158	AI992108	Hs.127206	ESTs	3.60	2.5
440860	R10482	Hs.132876	ESTs	4.26	2.5
452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.95	2.5
433281	N48673	Hs.146037	hypothetical protein DKFZp434C135	5.68	2.5
429369	AI269514	Hs.129802	ESTs	3.49	2.5
433949	AI674766	Hs.112877	ESTs	5.15	2.5
427668	AA298760	Hs.180191	hypothetical protein FLJ14904	10.46	2.5
414708	AA393379	Hs.97415	ESTs, Weakly similar to T33068 hypotheti	3.87	2.5
408485	AW274294	Hs.144092	ESTs, Weakly similar to A Chain A, Sacch	6.10	2.4
412869	AA290712	Hs.82407	CXC chemokine ligand 16	5.64	2.4
426956	AA393673		ESTs, Weakly similar to ALU5_HUMAN ALU S	4.68	2.4
429152	AA447209	Hs.99099	Homo sapiens NYD-SP28 mRNA, complete cds	4.34	2.4
426247	U92992	Hs.98834	ESTs	5.40	2.4
427589	T19219	Hs.97978	hypothetical protein MGC4766 similar to	3.40	2.4
429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2 (testis)	5.85	2.4
453353	U33055	Hs.32959	G protein-coupled receptor kinase 2 (Dro	4.82	2.4
413372	H55532		tubulin, alpha 2	9.32	2.4
411737	AW160339	Hs.71791	hypothetical protein	5.26	2.4
453868	NM_014433	Hs.35984	rhabdoid tumor deletion region protein 1	3.05	2.4
427098	AA398161	Hs.97602	ESTs	3.21	2.4
427165	AA429709	Hs.99336	ESTs, Weakly similar to T15446 hypotheti	4.27	2.4
425808	AA364109	Hs.177990	ESTs	7.80	2.4
444790	AB030506	Hs.11955	B9 protein	3.32	2.4
426718	AA383555	Hs.126413	ESTs	4.20	2.4
411441	AL042355	Hs.70202	WD repeat domain 10	6.14	2.4
450852	AI983354	Hs.7740	oxysterol binding protein-like 1	4.97	2.3
427054	AA421240	Hs.97570	ESTs	3.10	2.3

438633	AI653327	Hs.123501	ESTs	3.46	2.3
427199	AW015836	Hs.292919	ESTs	4.31	2.3
440182	AA868919	Hs.250110	ESTs	3.03	2.3
435517	AA928626	Hs.130177	ESTs	3.64	2.3
446309	BE044261	Hs.149774	ESTs	3.52	2.3
420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	4.23	2.3
433829	AI190715	Hs.102021	ESTs	6.08	2.3
429485	AW197086	Hs.99338	ESTs	3.14	2.3
423058	AW964568	Hs.111591	ESTs	3.36	2.3
433822	AI218609	Hs.112772	ESTs	3.83	2.3
442268	BE278064	Hs.8179	hypothetical protein, clone 2746033	3.00	2.3
434298	AA860090	Hs.116290	ESTs	3.71	2.3
440720	AW662776	Hs.336943	Human DNA sequence from clone RP11-60H7	3.08	2.3
427554	AW246578	Hs.179615	hypothetical protein FLJ10058	3.39	2.3
414251	AL042306	Hs.97689	VASA protein	11.25	2.3
430254	AI809520		ESTs	3.27	2.3
437418	AI478954	Hs.59459	ESTs	3.43	2.2
437522	AA983844	Hs.121383	ESTs	4.15	2.2
422808	AA449014	Hs.121025	chromosome 11 open reading frame 5	3.09	2.2
436695	AA725655	Hs.120480	ESTs	5.26	2.2
422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	6.78	2.2
421625	AA405386	Hs.178004	ESTs	3.22	2.2
434807	AA364183	Hs.323443	hypothetical protein FLJ11806	5.51	2.2
428174	AA913321	Hs.126778	ESTs	3.09	2.2
409735	AL035295	Hs.56175	H.sapiens gene from PAC 106H8, similar t	3.11	2.2
444467	AI150368		ESTs	3.81	2.2
433832	AA918018	Hs.172516	ESTs	6.94	2.2
440036	AW593295	Hs.210956	ESTs	5.87	2.2
415240	AA161411	Hs.58668	chromosome 21 open reading frame 57	3.66	2.2
432538	BE258332	Hs.278362	male-enhanced antigen	3.58	2.1
440882	AI205777	Hs.129538	ESTs	3.83	2.1
436605	AI187742		ESTs	3.41	2.1
422990	AF035620	Hs.122764	BRCA1 associated protein	5.66	2.1
432174	AW590264	Hs.132806	ESTs	3.05	2.1
409267	NM_012453	Hs.52515	transducin (beta)-like 2	5.46	2.1
423021	AL036111	Hs.292767	ESTs	3.87	2.1
439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	5.25	2.1
433812	AA725026	Hs.97165	ESTs, Weakly similar to T31611 hypotheti	3.62	2.1
456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	4.38	2.1
437249	AA432202	Hs.103147	hypothetical protein FLJ21347	3.38	2.1
426038	AA368101	Hs.99052	ESTs	3.03	2.1
427065	AA397903	Hs.236635	gb:zt89f12.r1 Soares_testis_NHT Homo sap	3.23	2.1
428624	W23624	Hs.173059	ESTs	3.07	2.1
428224	X54017	Hs.183088	acrosin	3.18	2.1
436954	AA740151	Hs.130425	ESTs	3.20	2.1
444470	AA412195	Hs.13740	ESTs	4.27	2.1
457579	AB030816	Hs.36761	HRAS-like suppressor	5.30	2.1
427886	AA417083	Hs.104789	ESTs	3.49	2.1
439273	AW139099	Hs.269701	ESTs	3.83	2.1
434318	AW207552	Hs.116328	ESTs, Weakly similar to A39564 transcrip	4.01	2.1
427015	AA397520		ESTs	4.28	2.1
421598	AW630942	Hs.106061	RD RNA-binding protein	3.30	2.1
427236	AA399959	Hs.148271	ESTs	3.07	2.1
434520	AA205273	Hs.177011	hypothetical protein	3.19	2.0
456051	T85626	Hs.76239	hypothetical protein FLJ20608	3.11	2.0
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	8.41	2.0
451807	W52854		hypothetical protein FLJ23293 similar to	3.52	2.0
448984	AW751955	Hs.22753	hypothetical protein FLJ22318	4.73	2.0
420484	W32963	Hs.98289	VRK3 for vaccinia related kinase 3	3.86	2.0
414181	AK000476	Hs.75798	hypothetical protein	3.33	2.0
424558	AF038847	Hs.150490	FK506-binding protein 6 (36kD)	7.70	2.0

TABLE 54B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
428618	2668_1	BC017998 BI826643 BG715794 BG722697 BI460787 BG773459 H52859 AI652853 AI990773 AW665193 AW340601 AA913806 AI337099 BE045942 AW572790 AW515652 H15004 AA909115 BI465310 BI462024 BI561578 BI463075 BG722527 R86003 BG623286 H15003 BI562131 BG435272
426599	10110_1	BE736800 BM471423 AL557221 BG763302 BF742196 BF991016 BG200112 BF920027 BG576409 BG332214 BI830957 AI827504 AW183574 AI805171 AI126491 AA448257 AI090641 AW183329 AA994873 AI203663 BE041513 AA382260 AA382261 AL554887 BE273483
426930	1310779_1	AI809889 AA393442 AI150574 AI200886 AI221692 AA608977 AA813213
434317	599587_1	AI209094 AI377740 AW117382 AW182289 AI674095 AW188019 AA897352 AA931314 AA923336 AW665317 AA629314 AA776691 AA906846 AA974625 AA884357 AI808590
426620	142987_1	AL042392 AI147451 AA758821 AW450252 AA399310 AI656343 AI636668 AW515660 AI190733 AI025812 AA723645 AA709253 AA725709 AA398244 AA382463 AI139837
419350	13086_1	AI218809 BC014609 BG724383 AI024359 AA904573 AI138595 AA868685 AI768931 BI828436 BG717350 BG719800 AW182303 AA448181 BI826670 BI827131 BI830254 BI824155 BI831745 T19190 BI830415
440822	532606_1	BG207562 BG192113 AA977616 AW274024 AI554897 AI221379 AA969158 AA906867 AI873494 AI015039
421938	863689_1	AA412383 AA300675 BG773248 AA412243 AA405951

	442589	33097_2	NM_004157 X14968 BG480488 BE409869 BG723898 BG476313 AU121626 BE386516 AI969297 AW172340 AA889668 R23436 AI015037 BE250558 BF590945 AW385993 BF983000 AA070235 AL556082 M78388 AW504473 AW370139 BG913697 BE899096 BG827945 BE741233 AI015465 AW370169 BE297350 AA093249
	436588	2470836_1	AI122828 AA909991 AA759233
5	431986	76926_1	AL591713 BF197609 AI985094 AW448916 AI243277 AL449630 AL449629
	420431	29290_1	AW241405 AW205071 AI671586 AI652354 AI638465 AW590359 AW662771 AW594067 BE502532 AI218894 BE466416 BF056295 AI247366
	436601	10131_1	AI990484 AI917746 AW665925 AI216456 AW182169 AA969884 AA723888 AI018419
	408415	4581_6	BI602176 BI603138 BI459895 BI755030 AW418788 AA883999 AA724858 AI480311 AW196355 AI004813 AI651117 BE814363 AW589856 AA448124 AA447982 BI461166 AA405629
10	427748	1372622_1	AI208966 AA421041 AA815377 AA411954
	440115	34_3	BF980396 R51074 BF979883 AI539370 BM128735 AA993397 AI611039 AW593985 R41808
	428524	1382184_1	AI208080 AA442662 AA429772
	440933	980517_1	AI125404 AW593312 AI247364 AI208217 AA910021 AI915307
	427829	1373537_1	AI190292 AI188225 AA416673 AA416596 AA952888 AA972172 AA906874
15	438735	10316_1	M76676 NM_022571 BG772522 BF516449 AI537485 AW517245 BF762536 AA634446 AW196331 AI203035 BG722281
	449333	36378_1	AK056320 AL522040 BI793043 AW071691 AI433682 AA865414 AA702684 BI792794 H96879 R52351 AA211126 AA442875 N25725 AA482563 N33446 N25222 Z41110 N26507 N73447 N24077 N20492 AW275550 H99619 AL518306 AL522041 AW959849 AL518307 AA725907 AI655113 AI309906 F10184 BM451081 BE257595 BG721625 BI828509 BG700470 F12568 Z45396 BI829288 AA364618 AA364851 AA421448 T74231 R52350 AA482415 AI203021 T88948 AI565842
20	433792	2204621_1	AI024286 AA769898 AA778661 AA868972 AA609524
	442122	2684549_1	AI932330 AI190707 AI376782 AA976847
	433760	584982_1	AA609179 AW592321 AA758282 AI214437 AW072537 AA781937
	426956	657337_1	BI831486 AW190479 AI472793 AA460217 AA459937 BF082576 AA393673 AA398702
	413372	32896_1	NM_006001 L11645 AI205604 AI207994 AI187362 AA709190 BI462421 BG772170 BG722772 AA436991 BG771655 BI553260 BF126025
25			BF125857 BI462670 BG724164 BI562424 BG721652 BI559662 BG722455 BI596415 BG717561 BG722138 BG773507 BG720572 C03867 AI016802 AL042663 AA770436 AA435720 T19365 AA626698 AA759057 AI208021 BF507844 AI208058 AA412719 AA426374 AI208775 AA977217 AA758055 F34585 AA180062
	430254	13102_1	BG700885 AA868017 AW341719 AA971332 AI688794 Z20462 AI808145 AW665263 AA884952 AA906136
	444467	1008400_1	AW663704 AI150368 AI216464
30	436605	1008207_1	AI125340 AI125684 AI377949 AI126470 AI218351 AW665355 AI243952 AW663454 AI240603 AI187742 AA884214 AA723933
	427015	683123_1	AA857437 AI968733 AI968938 AA992784 AA397520 AW235244
	451807	17758_2	BM479185 AL552795 AL577722 BF038888 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 AI806539 AW449522 AA993634 AI827626 AA904788

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TABLE 54C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

40 Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401979	2828778	Minus	75693-75851,76977-77112
45 406409	9256364	Minus	141101-141256
401741	2982169	Plus	196686-196823,200241-200381
406378	9256142	Minus	126408-126800
405264	7329374	Plus	28556-28684
401692	3540172	Plus	26365-26510
50 403783	8081824	Plus	128412-128635
404271	9828129	Minus	56392-57645
401798	6730720	Plus	22831-23448
402857	9801539	Plus	13402-14133
405528	9581957	Minus	22418-22687
55 403328	8469086	Minus	120428-120703
401712	6682593	Minus	76410-76527,76692-76829,76737-78866,8024

60

TABLE 55A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

65 Unigene Title: Unigene gene title

R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
416680	AW245540	Hs.79516	brain abundant, membrane attached signal	48.80
70 423961	D13666	Hs.136348	periostin(OSF-2os)	43.30
412948	BE243313	Hs.334851	LIM and SH3 protein 1	42.50
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	36.80
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	29.80
414438	AI879277	Hs.76136	thioredoxin	29.40
75 406658	AI920965	Hs.77961	major histocompatibility complex, class	29.25
446899	NM_005397	Hs.16426	podocalyxin-like	28.70
411573	AB029000	Hs.70823	KIAA1077 protein	28.40
432730	AI066520	Hs.131358	ESTs	28.00
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	28.00
80 444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	27.90
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	26.80
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	25.00
418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	24.15

406856	AW515336	Hs.29797	ribosomal protein L10	23.66
414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	23.60
440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	23.60
417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.35
417426	NM_002291	Hs.82124	laminin, beta 1	21.60
407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	21.55
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	21.50
413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	21.50
408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	20.90
412636	NM_004415		desmoplakin (DPI, DPII)	20.90
414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	20.30
414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	19.45
412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	19.30
406648	AA563730	Hs.277477	major histocompatibility complex, class	19.10
412247	AF022375	Hs.73793	vascular endothelial growth factor	17.45
446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	17.40
424800	AL035588	Hs.153203	MyoD family inhibitor	17.20
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	16.90
415314	N88802	Hs.5422	glycoprotein M6B	16.80
406656	M16714	Hs.89643	major histocompatibility complex, class	16.75
426295	AW367283		zinc finger protein 6 (CMPX1)	16.25
406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	16.00
444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	15.85
417088	M54915	Hs.81170	pim-1 oncogene	15.60
449338	H73444	Hs.394	adrenomedullin	15.51
444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	15.33
414420	AA043424	Hs.76095	immediate early response 3	15.30
425543	R23313	Hs.334895	ribosomal protein L10a	15.10
452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	15.00
420754	W79431	Hs.346911	ribosomal protein L22	14.92
410397	AF217517	Hs.63042	DKFZp564J157 protein	14.86
417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	14.70
415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	14.60
406786	AW161678	Hs.111334	ferritin, light polypeptide	14.57
422105	AI929700	Hs.111680	endosulfine alpha	14.57
422714	AB018335	Hs.119387	KIAA0792 gene product	14.25
444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.05
426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.00
445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	14.00
429614	AI371172	Hs.211539	hypothetical protein MGC4248	13.95
410185	BE294068	Hs.737	immediate early protein	13.85
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	13.60
410611	AW954134	Hs.20924	KIAA1628 protein	13.60
448588	AI970276	Hs.156905	KIAA1676	13.40
421406	AF179897	Hs.104105	Meis (mouse) homolog 2	13.10
420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.00
425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	13.00
452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	13.00
454413	AI653672	Hs.40092	PNAS-123	12.90
415221	W07418	Hs.78225	annexin A1	12.89
425535	AB007937	Hs.158287	KIAA0468 gene product	12.48
450000	AI952797	Hs.10888	hypothetical protein FLJ21709	12.45
418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.40
414799	AI752416	Hs.77326	insulin-like growth factor binding prote	12.19
412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	12.12
445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	12.07
412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	11.90
408437	AW957744	Hs.278469	lacrimal proline rich protein	11.80
430542	AI557486	Hs.119122	ribosomal protein L13a	11.51
424670	W61215	Hs.116651	epithelial V-like antigen 1	11.50
432409	AA806538	Hs.130732	KIAA1575 protein	11.50
425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	11.44
425996	W67330		hypothetical protein AL110115	11.40
449961	AW265634	Hs.133100	ESTs	11.40
435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	11.25
407179	AA206465		thymosin, beta 4, X chromosome	11.21
412623	R28898	Hs.74170	metallothionein 1E (functional)	11.10
429978	AA249027		ribosomal protein S6	11.10
450377	AB033091		KIAA1265 protein	11.10
418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	11.10
440869	NM_014297	Hs.7486	protein expressed in thyroid	11.00
417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	11.00
451106	BE382701	Hs.25960	N-MYC oncogene	10.93
426552	BE297660	Hs.170328	moesin	10.91
433423	BE407127	Hs.8997	heat shock 70kD protein 1A	10.90
442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	10.80
407951	W77762	Hs.79015	antigen identified by monoclonal antibod	10.80
449944	AF290512	Hs.58215	Homo sapiens, Similar to rhotekin, clone	10.75
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.70
435056	AW023337	Hs.5422	glycoprotein M6B	10.70
406743	AA911568	Hs.279860	tumor protein, translationally-controlle	10.70
422627	BE336857	Hs.118787	transforming growth factor, beta-induced	10.65
420676	AI434780	Hs.4248	vav 2 oncogene	10.60

444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	10.60
420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	10.50
436075	BE090176	Hs.179902	transporter-like protein	10.30
450139	AK001838		serum/glucocorticoid regulated kinase	10.30
427691	AW194426	Hs.20726	ESTs	10.26
424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	10.15
448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	10.10
440528	BE313555	Hs.7252	KIAA1224 protein	10.06
423184	NM_004428	Hs.1624	ephrin-A1	10.05
450847	NM_003155	Hs.25590	stanniocalcin 1	9.90
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.90
436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	9.90
421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	9.89
435918	AF263536	Hs.86232	growth differentiation factor 3	9.89
411251	R19774	Hs.22835	HHGP protein	9.80
406791	AI220684	Hs.347939	hemoglobin, alpha 2	9.75
441187	AW195237	Hs.7734	hypothetical protein FLJ22174	9.75
425580	L11144	Hs.1907	galanin	9.60
420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	9.60
413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	9.60
434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.60
417944	AU077196	Hs.82985	collagen, type V, alpha 2	9.53
409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	9.51
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	9.42
416926	H03109	Hs.263395	HT018 protein	9.41
456236	AF045229	Hs.82280	regulator of G-protein signalling 10	9.40
428065	AI634046	Hs.157313	ESTs	9.40
441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.39
410325	AB023154	Hs.62264	KIAA0937 protein	9.30
415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.30
454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	9.29
452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	9.24
447211	AL161961	Hs.17767	KIAA1554 protein	9.22
422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	9.20
418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	8.93
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	8.90
429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.90
422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	8.90
449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.84
413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	8.80
447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	8.70
426215	AW963419	Hs.155223	stanniocalcin 2	8.70
446627	AI973016	Hs.15725	hypothetical protein SBBI48	8.60
431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	8.60
433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	8.50
445245	AB032973	Hs.12461	LCHN protein	8.50
448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.40
453856	AA804789	Hs.19447	PDZ-LIM protein mystique	8.35
410143	AA188169		KIAA1191 protein	8.35
414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.30
433208	AW002834	Hs.24095	ESTs	8.30
423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.25
432559	AW452948	Hs.257631	ESTs	8.20
450581	AF081513	Hs.25195	TGF-beta 4	8.10
450157	AW961576	Hs.60178	ESTs	8.10
444795	AI193356	Hs.160316	ESTs	8.10
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	8.05
430253	AK001514	Hs.236844	hypothetical protein FLJ10652	8.00
420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	8.00
419970	AW612022		ESTs	8.00
411975	AI916058	Hs.144583	ESTs	7.95
446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.90
451831	NM_001674	Hs.460	activating transcription factor 3	7.90
437103	AW139408	Hs.152940	ESTs	7.90
432636	AA340864	Hs.278562	claudin 7	7.87
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.84
419682	H13139	Hs.92282	paired-like homeodomain transcription fa	7.80
407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.80
450147	AW373713	Hs.146324	CGI-145 protein	7.75
447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.70
449571	AW016812	Hs.200266	ESTs	7.70
429355	AW973253	Hs.292689	ESTs	7.70
446488	AB037782	Hs.15119	KIAA1361 protein	7.70
414774	X02419	Hs.77274	plasminogen activator, urokinase	7.69
422424	AI186431	Hs.296638	prostate differentiation factor	7.67
428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	7.65
416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	7.65
451812	X81889	Hs.152151	plakophilin 4	7.65
410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	7.60
452874	AK001061	Hs.30925	hypothetical protein FLJ10199	7.60
422746	NM_004484	Hs.119651	glypican 3	7.60
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	7.57

	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.57
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	7.55
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.53
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	7.50
5	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	7.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	7.47
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.44
	401466			vesicle-associated membrane protein 4	7.43
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	7.40
10	413686	AI469213	Hs.71404	ESTs	7.40
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	7.40
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.30
	444838	AV651680	Hs.208558	ESTs	7.30
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	7.28
15	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	7.20
	452924	AW580939	Hs.97199	complement component C1q receptor	7.15
	436398	H87136	Hs.5174	ribosomal protein S17	7.15
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.10
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.10
20	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	7.10
	401192			Target Exon	7.08
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	7.08
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	7.00
	449567	AI990790	Hs.188614	ESTs	7.00
25	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	7.00
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	7.00
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	7.00
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	6.90
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	6.87
30	442492	AA528489	Hs.234518	ribosomal protein L23	6.84
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	6.80
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	6.80
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	6.80
	435684	NM_001290	Hs.4980	LIM domain binding 2	6.80
35	442685	AB033017	Hs.8594	KIAA1191 protein	6.79
	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	6.77
	411789	AF245505	Hs.72157	Adlican	6.76
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	6.75
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	6.74
40	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.72
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	6.70
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	6.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.70
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	6.70
45	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	6.70
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.70
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	6.66
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	6.65
	406858	AI865720	Hs.29797	ribosomal protein L10	6.65
50	435748	AA699756	Hs.117335	ESTs	6.63
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	6.62
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	6.62
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.61
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.60
55	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.55
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	6.50
	450294	H42587	Hs.238730	hypothetical protein MGC10823	6.45
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.45
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	6.43
60	402145			Target Exon	6.43
	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.42
	436860	H12751	Hs.5327	PRO1914 protein	6.40
	438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	6.40
	435937	AA830893	Hs.119769	ESTs	6.40
65	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	6.40
	446173	BE565849	Hs.14158	copine III	6.39
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	6.36
	412093	BE242691	Hs.14947	ESTs	6.34
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.30
70	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.30
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.30
	447519	U46258	Hs.339665	ESTs	6.30
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.30
	434423	NM_006769	Hs.3844	LIM domain only 4	6.30
75	434524	AA636931	Hs.249716	ESTs	6.30
	441970	AW959918	Hs.73737	ESTs	6.30
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	6.30
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	6.25
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	6.23
80	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.20
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.20
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	6.20
	417315	AI080042	Hs.180450	ribosomal protein S24	6.20

	418840	AI821614	Hs.185831	ESTs	6.20
	410668	BE379794	Hs.159651	hypothetical protein	6.16
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.13
	413840	AI301558		RNA binding motif protein, X chromosome	6.13
5	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	6.12
	450944	AA554989		sudD (suppressor of bimD6, Aspergillus n	6.10
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	6.10
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.10
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	6.10
10	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	6.10
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.09
	435812	AA700439	Hs.188490	ESTs	6.06
	432805	X94630	Hs.3107	CD97 antigen	6.06
15	441283	AA927670	Hs.131704	ESTs	6.06
	417632	R20855	Hs.5422	glycoprotein M6B	6.00
	435905	AW997484	Hs.5003	KIAA0456 protein	6.00
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	5.99
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.95
20	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	5.95
	425291	AA354572		gb:EST62857 Jurkat T-cells V Homo sapien	5.95
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	5.93
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	5.90
	447217	BE465754	Hs.17778	neuropilin 2	5.90
25	417228	AL134324	Hs.7312	ESTs	5.86
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.86
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.84
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.84
	414483	R25513	Hs.10683	ESTs	5.82
30	428570	AA430321	Hs.293945	ESTs	5.81
	443194	AI954968		matrix Gla protein	5.80
	429582	AI569068	Hs.22247	ESTs	5.80
	414405	AI362533		KIAA0306 protein	5.80
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	5.80
35	437739	AW579216	Hs.264610	ESTs, Moderately similar to Ibd1 [H.sapi	5.80
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	5.80
	442821	BE391929	Hs.8752	transmembrane protein 4	5.77
	434511	R28982	Hs.18106	ESTs	5.76
	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	5.70
40	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	5.70
	453115	AW772041	Hs.18439	ESTs, Moderately similar to JC5238 galac	5.70
	406857	AA613726	Hs.29797	ribosomal protein L10	5.69
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	5.68
	444273	AI903474	Hs.230	fibromodulin	5.65
45	441623	AA315805		desmoglein 2	5.63
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	5.63
	440099	AL080058	Hs.6909	DKFZP564G202 protein	5.60
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	5.60
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	5.60
50	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	5.60
	438278	BE409248	Hs.57988	hypothetical protein FLJ22357 similar to	5.58
	430451	AA836472	Hs.297939	cathepsin B	5.57
	406699	L06505	Hs.182979	ribosomal protein L12	5.53
	458965	AA010319	Hs.60389	ESTs	5.50
55	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	5.50
	433655	AL036559	Hs.3463	ribosomal protein S23	5.50
	428471	X57348	Hs.184510	stratifin	5.42
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	5.40
	417849	AW291587	Hs.82733	nidogen 2	5.40
60	408989	AW361666	Hs.49500	KIAA0746 protein	5.40
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	5.40
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	5.40
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	5.40
	406819	AA908472		gb:og82a10.s1 NCI_CGAP_Ov8 Homo sapiens	5.39
65	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.36
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.34
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.34
	427968	AI857607	Hs.181301	cathepsin S	5.32
	429307	AU076592	Hs.198951	jun B proto-oncogene	5.30
70	424950	AA602917	Hs.156974	ESTs	5.30
	410619	BE512730	Hs.65114	keratin 18	5.30
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.27
	425430	BE185921	Hs.98073	ESTs, Moderately similar to Z195_HUMAN Z	5.27
	411165	NM_000169	Hs.69089	galactosidase, alpha	5.26
75	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	5.26
	435631	BE254086	Hs.29647	uncharacterized hematopoietic stem/proge	5.24
	418905	BE539674		actinin, alpha 4	5.23
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	5.22
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	5.20
80	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	5.20
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	5.20
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	5.20

	409604	AW444448	Hs.49124	ESTs	5.20
	432581	AU076465	Hs.278441	KIAA0015 gene product	5.16
	430556	AW967807	Hs.13797	ESTs	5.16
	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5.16
5	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	5.15
	454227	AW963897	Hs.44743	KIAA1435 protein	5.15
	429367	AB007867	Hs.278311	plexin B1	5.12
	452191	AU076408	Hs.28309	UDP-glucose dehydrogenase	5.11
	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis, clone NT	5.11
10	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	5.10
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	5.10
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	5.10
	424875	AI187945	Hs.199310	ESTs	5.10
	427641	AI270591	Hs.146116	ESTs	5.10
15	442606	AW294522	Hs.149991	ESTs	5.10
	442495	AI184717		ESTs	5.10
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.10
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	5.09
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.07
20	418117	AI922013	Hs.83496	linker for activation of T cells	5.06
	431824	AW972842		gb:EST384937 MAGE resequences, MAGL Homo	5.06
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	5.06
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.03
	431805	NM_014053	Hs.270594	FLVCR protein	5.00
25	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	5.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	5.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	5.00
	443634	H73972	Hs.134460	ESTs	5.00
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	5.00
30	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	4.97
	422200	AA080895	Hs.347969	cytochrome c oxidase subunit IV	4.95
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	4.94
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	4.94
	452063	R53185	Hs.32366	ESTs, Weakly similar to TWST_HUMAN TWIST	4.93
35	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.93
	429558	AI391454	Hs.207251	nucleolar autoantigen (55kD) similar to	4.92
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	4.92
	433162	AI025842		ESTs	4.92
	406797	AI432224		ribosomal protein L6	4.91
40	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	4.90
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	4.90
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	4.90
	447832	AI433357		ESTs	4.90
	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	4.90
45	413593	AA205248		gb:zq78c12.r1 Stratagene hNT neuron (937	4.90
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	4.90
	441224	AU076964	Hs.7753	calumenin	4.90
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	4.90
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.90
50	417308	H60720	Hs.81892	KIAA0101 gene product	4.90
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	4.89
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.89
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	4.88
	421748	NM_014718	Hs.107809	KIAA0726 gene product	4.87
55	427486	AA974433		fibroblast growth factor 4 (heparin secr	4.86
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	4.82
	406867	AA157857	Hs.182265	keratin 19	4.81
	449378	AW664026	Hs.59892	ESTs	4.81
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	4.80
60	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	4.80
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.80
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	4.79
	441321	H17182	Hs.7771	B-cell associated protein	4.75
65	448896	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr	4.75
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	4.73
	449317	AW293413	Hs.132906	19A24 protein	4.73
	436372	AW972301	Hs.310286	ESTs	4.71
	422082	AA016188	Hs.111244	hypothetical protein	4.70
70	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	4.70
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	4.70
	446659	AI335361	Hs.226376	ESTs	4.70
	414829	AA321568	Hs.77436	pleckstrin	4.70
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	4.70
75	417677	NM_016055	Hs.82389	CGI-118 protein	4.70
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.70
	423766	AA303799	Hs.300141	ribosomal protein L39	4.70
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	4.69
	453485	BE620712	Hs.33026	hypothetical protein PP2447	4.67
80	452973	H88409	Hs.40527	ESTs	4.67
	427816	AA159248	Hs.180909	peroxiredoxin 1	4.67
	406794	AI890243		ribosomal protein L6	4.66
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.65

	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.64
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	4.62
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	4.61
	417535	AA203569	Hs.191482	ESTs	4.61
5	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	4.61
	408491	AI088063	Hs.7882	ESTs	4.60
	428398	AI249368	Hs.98558	ESTs	4.60
	410295	AA741357		nidogen (enactin)	4.60
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	4.60
10	440327	R12581	Hs.191146	ESTs	4.60
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.60
	426141	C05886	Hs.293972	ESTs	4.60
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	4.59
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.58
15	416987	D86957	Hs.80712	KIAA0202 protein	4.57
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.57
	416581	H66276	Hs.108288	ESTs	4.56
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	4.56
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	4.56
20	413663	BE247585	Hs.75462	BTG family, member 2	4.55
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.54
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	4.53
	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	4.52
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	4.51
25	440774	AI420611	Hs.153934	ESTs	4.51
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	4.51
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	4.51
	449267	AI638640	Hs.220624	ESTs	4.51
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.50
30	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	4.50
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.50
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	4.50
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
35	406623	X69392	Hs.91379	ribosomal protein L26	4.49
	456642	AW451623	Hs.109752	putative c-Myc-responsive	4.47
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.47
	408307	AI761786	Hs.204674	ESTs	4.46
	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.46
40	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.45
	416801	X93834	Hs.79971	sal (Drosophila)-like 2	4.45
	406670	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	4.45
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.44
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondriat	4.44
45	428773	BE256238	Hs.193163	bridging integrator 1	4.43
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	4.43
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	4.43
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	4.43
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	4.42
50	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	4.41
	424868	AI568170	Hs.96886	ESTs	4.41
	408380	AF123050	Hs.44532	diubiquitin	4.40
	411960	R77776	Hs.18103	ESTs	4.40
	428782	X12830	Hs.193400	interleukin 6 receptor	4.40
55	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	4.40
	456629	AW891965		histone deacetylase 3	4.40
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	4.40
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	4.39
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	4.39
60	427779	AA906997	Hs.180780	TERA protein	4.38
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.37
	413276	Z24725	Hs.75260	mitogen inducible 2	4.36
	452651	AI218918	Hs.30209	KIAA0854 protein	4.35
	453467	AI535997	Hs.30089	ESTs	4.35
65	435961	BE293127	Hs.283722	GTT1 protein	4.35
	415691	AW963979	Hs.24723	ESTs	4.34
	435968	AW161481	Hs.111577	integral membrane protein 3	4.34
	420099	D80011	Hs.95140	KIAA0189 gene product	4.33
	421522	R48881	Hs.102991	hypothetical protein FLJ13956	4.33
70	457073	AA233210	Hs.179943	ribosomal protein L11	4.31
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	4.31
	420732	AA789133	Hs.63525	ESTs	4.30
	432731	R31178	Hs.287820	fibronectin 1	4.30
	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.30
75	408784	AW971350	Hs.63386	ESTs	4.30
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	4.30
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.30
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	4.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.30
80	413677	AW503116	Hs.301819	zinc finger protein 146	4.29
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.28
	408896	AI610447	Hs.48778	niban protein	4.26
	433550	AA989061	Hs.177376	ESTs	4.26

406230			Target Exon	4.25
435655	AW105663	Hs.6947	HSPC069 protein	4.25
448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.24
437386	W52452		ribosomal protein L10	4.24
416759	AK000978	Hs.79741	hypothetical protein FLJ10116	4.23
447341	AF106941	Hs.18142	arrestin, beta 2	4.22
410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	4.22
409453	AI885516	Hs.95612	ESTs	4.22
428453	AB011110	Hs.184367	GTPase activating protein-like	4.22
444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.21
416072	AL110370	Hs.79000	growth associated protein 43	4.20
450937	R49131	Hs.26267	ATP-dependant interferon response protei	4.20
447595	AW379130	Hs.18953	phosphodiesterase 9A	4.20
418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	4.20
430594	AK000790	Hs.246885	hypothetical protein FLJ20783	4.20
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.20
431560	BE244135	Hs.260238	hypothetical protein FLJ10842	4.20
439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN !!!!	4.20
409245	AA361037		tRNA isopentenylpyrophosphate transferas	4.18
437296	AA350994	Hs.20281	KIAA1700	4.17
406877	AA226392	Hs.179943	ribosomal protein L11	4.17
419652	AL157485	Hs.91973	hypothetical protein	4.15
406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.15
452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	4.14
448782	AL050295		KIAA0758 protein	4.14
407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	4.14
422960	AW890487		cadherin 13, H-cadherin (heart)	4.13
432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	4.12
415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	4.11
420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.11
419726	U50330	Hs.1274	bone morphogenetic protein 1	4.11
426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	4.10
430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.10
418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.10
443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	4.10
457415	AK000010	Hs.258798	hypothetical protein FLJ20003	4.10
412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	4.10
427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a l	4.10
444633	AF111713	Hs.286218	junctional adhesion molecule 1	4.10
441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	4.09
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.09
422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.08
439815	AA206079	Hs.6693	hypothetical protein FLJ20420	4.07
417930	H81136	Hs.334604	Homo sapiens mRNA for KIAA1870 protein,	4.06
418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.06
424464	R68537	Hs.17962	ESTs	4.06
417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.06
412627	BE391959	Hs.74276	chloride intracellular channel 1	4.06
414890	BE281095	Hs.77573	uridine phosphorylase	4.05
452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.05
450887	AA011518	Hs.271778	ESTs, Weakly similar to I38022 hypotheti	4.05
444224	AV648599	Hs.199438	ESTs	4.05
451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.04
439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.04
408745	AW936356	Hs.300925	ESTs, Weakly similar to A46010 X-linked	4.03
409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.01
410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.01
409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	4.01
426398	BE256390	Hs.169718	calponin 2	4.01
417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	4.01
446979	AI654443	Hs.197683	ESTs	4.00
416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	4.00
426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.00
436394	AA531187	Hs.126705	ESTs	4.00
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.00
414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	4.00
446013	AI360167	Hs.152774	ESTs	4.00
452404	AW450675	Hs.212709	ESTs	4.00
444736	AA533491	Hs.23317	hypothetical protein FLJ14681	4.00
438590	AA811465	Hs.123375	ESTs	4.00
451838	AW005866	Hs.193969	ESTs	4.00
449832	AA694264	Hs.60049	ESTs	4.00

TABLE 55B
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession

	413787	7612_1
	412636	1438_1
	426295	510_1
	425996	138046_1
	429978	35194_2
	450377	12109_1
	444060	6315_1
	450139	34017_1
	434280	1474904_1
	410143	MH1244_8

BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 AI082748 AI470204 BI711078 BF350700 BI496963 AI087141 AA720684 AA862331 AA605146 BM313650 AI089749 AI359738 N69107 AW995424 AI066917 AI083995 AW340217 N99662 AI829449 AI089839 AI608761 AI342365 AI199076 AA908944 AI248943 AU160053 AI191245 AI218477 AI077943 AA864930 AI310394 AA872478 AI279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 AI469689 BE464590 AW664539 H67097 AL534332 C21397 AI085941 AW028427 BG939820 AI697089 AI039008 AI125315 AI655561 AW150042 L20422 X57345 BI458375 AU142852 BI666601 BE888276 AU119302 BI603754 BG705953 BI598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AV683116 AV708195 AA127798 AI124697 D54224 F08031 AA340253 BF923383 BM467808 BI546644 BG777200 BG705941 BG468577 AU127209 AW403970 BI597630 BI458091 AV689560 BI669267 BG506219 BI837163 BI667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 BI869271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 BI493502 AW273118 AI473820 AA608688 AI359337 AV712091 AA084101 BF592036 H13301 AI864305 AA505883 AI423963 AW084401 AI917740 R69858 AA033631 N79982 BE885276 AI635674 AA096126 AA700018 AV707753 AI082545 AU145681 AA629032 AI421367 AA740589 AA150830 AI248541 AA988608 AA150478 W65437 BM310234 AA262704 T28031 AI811116 BM272753 H21979 T15405 AA938406 F04963 AI188296 AW152629 AA905196 BG223058 AI831016 AI766457 AI811102 AA776573 AI922133 AA775958 AI261476 AA219489 AI688035 AI872093 BE537084 AW189078 D82630 AI123121 AL583492 BE350791 R69901 W65436 BE155392 BI089081 BE155394 AL120538 AW166100 AI359620 AI174338 N20527 W47413 AA155615 AI272249 H25293 BE614558 H69864 AW383484 H78021 H11617 R56892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W46459 AI866231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AL537424 BE814866 BF823254 R82553 AI809817 AI559406

M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995515 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE665474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI856282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE705078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI536577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487

BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA668626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627

BM006551 AA367152 AW953705 AI631833 AW237429 AW027804 AA729038 BE503409 AI521935 BF739953 AA702982 AA557633 AA780065 AI218139 AW194264 D20120 AI082715 AI969980 BE857686 BE326711 AW953706 AI393749 AI383821 W67199 AI431759 AI796526 AI521794 AI796380 AW117545 AI749657 AI537634 N50122

BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963196 C06195 AI678018

AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164

AK055070 AK055612 AK000174 BG619806 BG108086 AI741949 AI004176 BF891936 BF378565 AW197163 BE856860 BE245124 AW674411 AA490531 AW674981 AA740788 AW274758 BF512523 AI521278 AA548759 AI802431 AW051682 AI628247 AI799606 AW088103 AA236549 AI191529 AW273168 AI168451 AW073612 AW090611 AW003593 AI215845 AI799616 AW474940 AA954927 BM193740 AW662704 AW090127 AA969444 AI080438 AA552500 AW237538 AA481060 AI246378 AA565227 AA398921 AA207051 AA721378 BF438508 AI086295 AI886630 AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766664 AI453279 AA435673 AI619515 AA879080 AA234592 AA890223 AA766824 BI259822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05809 N41323 T87376 R68544 H88711 BI087136

AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651865 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 AU135386 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI886459 AU155873 H04255 AW243986 AA557749 AI286227 R68691 R33453 AW388097

BE005398 AA628622 AA994155

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			AI581622 AI361357 AA468498 AW008694 AA903275 AI187724 AI187718 AA890505 BF092771 AI066655 BE714172 BG289028 AW080390 BE001197 BF132049
	419970	13569_1	AK055270 BE348291 AI190289 AW612022 AI269506 AI266578 AI269675 AW271406 BE879851 BF574163 BI497126 AW903775 BI917368 AW150900 BF244813 H79201
	409208	10117_2	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946
	430068	1177709_-2	AA947566
	444207	9172_3	BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI470335 AI247243 BG533994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658 AW393133 AW073060 AI707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658671 BG678060 AI565004 AW819026 BE843092 AV686437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AI962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497
	413497	1518002_1	BE177661 H06215 BE144709 BE144829
	438962	195763_1	AI207343 BF813684 BF928775 AA828585
	413840	38807_1	BC020284 AW953495 AW402677 BF890739 Z44378 AI660081 AI769242 T84954 C05886 AI224851 AI568340 AI024026 AW015010 AI032051 AA505095 AA830304 H98001 H63431 BG249610 AI284792 AA205732 AI598130 AW516813 AI123905 AA132557 AI140199 H53399 AA928496 AI200299 AI400044 BE940512 BE940609 H28028 BF913868 AI301558 D79095 AI762695 AA311547 AI673408 AI673002 N67358 AA885913 AI288094 N67347 Z40311 T94918 AV722693 AW170339 AW975566 AA452774 AA504759 AA370643 T79706 AA721603 BF858887 BG982917 AI343373 AW236167 BE568091 BF747959 BF241262 BE940663 AI435278 R05794 AW027091 AI860259 AI268890 T94871 AW182884 N67183 AW149083 H42473 AI678254 R26706 AI419684 R24905 AW388568 AW363261 N31299 H63489 AW195475 AA452592 BE844216 T91205 H64955 BF858811 AW962779 AW388295 BF857615 BF856552 BF856548 BF857611 AW866752
	450944	36100_1	BG926557 AW965540 R76280 AA335645 BF370246 BE835794 AA725102 AW152576 BF055494 AI743398 BE464853 AI391675 AI453078 BE017970 AI803141 AI417070 AA489486 BE835818 AW050475 BE835826 AI015220 AW300496 AA343881 H98062 AA554989 N32774 AA012825 BF989549 AL576463 W60527 AW576215 N32300 AA450065 AW137525 AI290944 T16431 T50379 AA830657 N78847 T51070 AW505288 AI446370 AA100986 AA824552 BE835780 AA770659 BF370223 H03890 R76557
	432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
	425291	298763_1	AI744949 AW062361 BF919486 AW813419 AW816041 AA354572
	443194	19335_1	BI754027 BF696071 AI351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA993445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733552 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568964 BF725590 AI004210 AI809799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AA155854 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 D57214 BE045265 AA541785 BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 F27562 AA614749 D56645 F20774 F30660 F25646 AW023542 AA827300 AA582214 AI701269 AA228293 AI906950 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518 AV704158 BE439643 AA910666 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA451625 AA916141 AL572719 AV707258 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553696 AA916094 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215
	414405	112689_1	AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545
	428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
	441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BG496559 BF248373 BG494800
	406819	0_0	AA908472
	418905	517_1	BM469076 AA533027 AI127512 AI368802 AA533141 AA700560 AW576028 AI610851 AI435361 BM129172 AW474544 BM128899 AI814292 AW502039 AA531243 BF941858 AW502037 AA702337 AI419854 AA662755 AA934364 AI300510 AI291136 AA505263 AI144527 AI076919 AI633534 AI242473 AA938561 BG055372 AA512894 AI671356 AA962403 BF808010 AA663911 AA847056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 AI305842 AW800873 AA302492 AA478427 AI817291 AW801104 AW801028 AA865744 BF155979 AI374743 AA478431 AI159846 AI369757 AI800672 BF435788 AA255451 AI937707 AW006198 AI280363 BF062434 AW801115 AI919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 AI302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 BI087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 AI142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605
	442495	928718_1	AI184717 AW518883 AF121173
	431824	1237125_1	AW972842 AA516061 AA630205
	433162	2167905_1	AI742311 AI025842 AA578843
	406797	0_0	AI432224 AW276890 AI499346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640
	447197	2176805_1	R36075 R36167 AI366546
	447832	1036795_1	AI628543 AI433357 AW772732
	413593	2949482_1	AA205248 AA204737 AA130658
	427486	684159_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
	406794	0_0	AI890243
	410295	2817_1	BG402852 BG545066 AA150252 AL036760 AA452480 AI033256 W68776 W93372 N31248 AI052219 AI367635 W69374 N88610 R58194 BI524854 BI497111 BF940043 AI129268 AI359798 AI056480 AA121421 AI042150 AW449003 AI418180 AI419420 AI356058 BF832243 AI349330 AI359448 W76647 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268

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	413703	376077_1	BG015794 BE158357 BE158353 BE158358 BE158360 BE158352 BE158351 BE158355
	406870	0_0	AA075144
	456629	207_22	AW891965 AW604749 BE080872 R15559 BE177623 AW883520 AW945343 AI246167 T07082 AW805679 W96278 AA135796 W32615 AW995418 AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239 BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AI378548 AW890438 AA077172 AI288683 AA229639 AA091945 AW945454 AA063629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399 AW885686 BE244086 BE005035 AW861913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408,AI907428 BE067491 AW861939 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI248811 BE179917 BE002200 AW607506 AW392889 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW601420 AI695314 BE083790 AW858568 AW945550 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW885979 AW794240 AW945566 AI688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW664582 AW877775 AW838449 BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099 BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 AI904717 AW610318 AW996909 AW610296 AW901923 AW880003 AI762171 AW062582 AW368713 AW062593 AW176663 AW842064 AW842089 AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577 AI909628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835656 AW606765 AW606770 AW835678 AW606758 AW606778 AI907484 BE172821 AW606768 AW999517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA090510 AW844117 BE173367 AW999878 AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629 BE089008 BE178350 BE178214 BE063291 AW820236 AW999653 BE089486 BE173126 BE171775 BE185787 AA558280 AI174840 AW999112 BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998972 AA767189 AW044272 H50689 AA768399 AA767764 AI087888 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945 AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI681913 AI759983 N69591 N69276 BE467722 AW392780 BE172467 H92861 AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H87220 AW374781
	437386	5541_2	BM476605 BI545004 BI834636 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AI734997 AA931168 AA429766 N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI889031 N98464 AI820039 AI459034 AV652512 AA622990 BE857200 AA932998 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895 AA535689 BF806025 BF806061 BF805985 BF746099 BF746097 AI309259 AI597603 BF806066 AI090653 AI129205 AI248410 H72993 AW615341 BF805990 BF805982 AA993819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76371
	439403	4937_10	AK056692 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145
	409245	3199_2	AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830 AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024 BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752 BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845 AI693426 AI652147 AI435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897 AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245 AA884954 AI125702 AI382934 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69061 AI768667 AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062 D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848 H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
	448782	34980_1	AB018301 AL050295 BF513128 AW385080 AL551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768 AI453845 AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099 AA995178 AW050649 AW026140 AI796309 AI584012 BE166666 AI767991 AI309041 AA724059 AI695284 AI245095 T63971 Z40627 BE166681 BG570071 BF921915 BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 H40993 R43277 AI352281 BG540263 BG538901 N95226 AI356752 AI221152 Z28777 R16574 AW965449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361 N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285
	422960	11862_2	BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260

TABLE 55C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401466	6682292	Plus	28748-29023
401192	9719502	Minus	69559-70101
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402145	8018280	Plus	113086-114800
406230	4760409	Plus	71716-72515

TABLE 56A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of seminomatous testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
414438	AI879277	Hs.76136	thioredoxin	47.30

	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	44.80
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.10
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	34.90
	417088	M54915	Hs.81170	pim-1 oncogene	31.10
5	430542	AI557486	Hs.119122	ribosomal protein L13a	29.60
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	29.10
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	28.15
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	28.13
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	28.10
10	406658	AI920965	Hs.77961	major histocompatibility complex, class	27.85
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	27.70
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	27.20
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.30
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	25.80
15	429978	AA249027		ribosomal protein S6	25.40
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	24.60
	440207	AI371978	Hs.128326	ESTs	24.50
	425543	R23313	Hs.334895	ribosomal protein L10a	24.30
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	24.10
20	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	24.05
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	24.00
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	22.90
	420367	AA259090	Hs.257028	ESTs	22.90
	406856	AW515336	Hs.29797	ribosomal protein L10	22.77
25	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.75
	412636	NM_004415		desmoplakin (DPI, DPII)	22.40
	420676	AI434780	Hs.4248	vav 2 oncogene	22.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	21.40
	446627	AI973016	Hs.15725	hypothetical protein SBBI48	21.20
30	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	21.10
	420754	W79431	Hs.346911	ribosomal protein L22	20.98
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	20.90
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	20.80
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.40
35	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	19.50
	422714	AB018335	Hs.119387	KIAA0792 gene product	19.15
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.00
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	18.50
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.50
40	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.00
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	17.90
	448588	AI970276	Hs.156905	KIAA1676	17.70
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	17.50
	428782	X12830	Hs.193400	interleukin 6 receptor	17.40
45	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	17.20
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	17.15
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	17.10
	440528	BE313555	Hs.7252	KIAA1224 protein	17.06
	410143	AA188169		KIAA1191 protein	17.05
50	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.90
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	16.70
	429183	AB014604	Hs.197955	KIAA0704 protein	16.70
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	16.60
	449571	AW016812	Hs.200266	ESTs	16.50
55	432730	AI066520	Hs.131358	ESTs	16.20
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.15
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	15.90
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	15.80
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	15.80
60	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	15.50
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	14.90
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	14.90
	406656	M15714	Hs.89643	major histocompatibility complex, class	14.85
65	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	14.71
	450377	AB033091		KIAA1265 protein	14.70
	425996	W67330		hypothetical protein AL110115	14.60
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	14.60
	427691	AW194426	Hs.20726	ESTs	14.42
70	429614	AI371172	Hs.211539	hypothetical protein MGC4248	14.35
	451106	BE382701	Hs.25960	N-MYC oncogene	14.21
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.13
	436860	H12751	Hs.5327	PRO1914 protein	13.90
	446899	NM_005397	Hs.16426	podocalyxin-like	13.90
75	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	13.75
	408380	AF123050	Hs.44532	diubiquitin	13.70
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	13.40
	427521	AW973352		ESTs	13.30
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.25
80	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.23
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.23
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	12.70
	426552	BE297660	Hs.170328	moesin	12.69

415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.55
436398	H87136	Hs.5174	ribosomal protein S17	12.50
418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.30
453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.30
410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.28
414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	12.25
425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	12.25
415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	12.20
419384	AA490866	Hs.39429	ESTs	12.20
410185	BE294068	Hs.737	immediate early protein	12.15
407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	12.05
433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.00
406743	AA911568	Hs.279860	tumor protein, translationally-controlle	11.90
408989	AW361666	Hs.49500	KIAA0746 protein	11.80
430268	AK000737	Hs.237480	hypothetical protein FLJ20730	11.80
447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.80
410325	AB023154	Hs.62264	KIAA0937 protein	11.70
445817	NM_003642	Hs.13340	histone acetyltransferase 1	11.70
418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	11.61
445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	11.60
454413	AI653672	Hs.40092	PNAS-123	11.60
418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	11.40
428065	AI634046	Hs.157313	ESTs	11.40
432805	X94630	Hs.3107	CD97 antigen	11.36
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.35
444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	11.30
452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	11.30
409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	11.11
402474			NM_004079:Homo sapiens cathepsin S (CTSS	11.00
407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.00
406786	AW161678	Hs.111334	ferritin, light polypeptide	10.95
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	10.90
444656	AI277924	Hs.145199	ESTs	10.90
453856	AA804789	Hs.19447	PDZ-LIM protein mystique	10.85
440774	AI420611	Hs.153934	ESTs	10.82
408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	10.80
431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	10.80
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.80
418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	10.70
437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	10.65
415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	10.60
450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	10.43
424800	AL035588	Hs.153203	MyoD family inhibitor	10.40
446682	AW205632	Hs.211198	ESTs	10.40
447211	AL161961	Hs.17767	KIAA1554 protein	10.31
425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	10.30
422105	AI929700	Hs.111680	endosulfine alpha	10.21
417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	10.20
422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	10.20
452651	AI218918	Hs.30209	KIAA0854 protein	10.15
418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	10.11
426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	10.10
427761	AA412205	Hs.140996	ESTs	10.10
443523	AK001575	Hs.9536	hypothetical protein FLJ10713	9.90
402145			Target Exon	9.82
413686	AI469213	Hs.71404	ESTs	9.80
446488	AB037782	Hs.15119	KIAA1361 protein	9.80
449246	AW411209	Hs.23363	hypothetical protein FLJ10983	9.80
424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	9.80
407179	AA206465		thymosin, beta 4, X chromosome	9.72
413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	9.70
430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	9.70
446795	AI797713	Hs.156471	ESTs	9.70
435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	9.65
451864	N20370	Hs.69547	ESTs	9.65
419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	9.60
419904	AA974411	Hs.18672	ESTs	9.60
427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.60
409208	Y00093		integrin, alpha X (antigen CD11C (p150),	9.52
424950	AA602917	Hs.156974	ESTs	9.50
447534	AW953935	Hs.288655	ESTs	9.50
419223	X60111	Hs.1244	CD9 antigen (p24)	9.41
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.40
422960	AW890487		cadherin 13, H-cadherin (heart)	9.33
412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	9.32
408784	AW971350	Hs.63386	ESTs	9.30
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.30
432409	AA806538	Hs.130732	KIAA1575 protein	9.30
440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	9.30
407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.22
408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.20
434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.20
434524	AA635931	Hs.249716	ESTs	9.20

	450294	H42587	Hs.238730	hypothetical protein MGC10823	9.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.10
	434442	AA737415		ESTs	9.10
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.03
5	447519	U46258	Hs.339665	ESTs	9.00
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	8.98
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	8.90
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	8.90
	442806	AW294522	Hs.149991	ESTs	8.90
10	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	8.89
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	8.81
	408437	AW957744	Hs.278469	lacrimal proline rich protein	8.80
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	8.80
	431187	AW971146	Hs.293187	ESTs	8.80
15	421098	AI697901	Hs.192425	ESTs	8.70
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	8.70
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	8.70
	401091			decay accelerating factor for complement	8.62
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
20	438089	W05391		nuclear receptor subfamily 1, group I, m	8.60
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	8.60
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	8.59
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	8.56
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.50
25	414829	AA321568	Hs.77436	pleckstrin	8.50
	430162	AW450843	Hs.346348	ESTs	8.50
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	8.50
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.45
	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.43
30	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	8.40
	433208	AW002834	Hs.24095	ESTs	8.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.38
	425284	AF155568		NS1-associated protein 1	8.33
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.33
35	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	8.30
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	8.30
	453716	AA037675	Hs.152675	ESTs	8.30
	418840	AI821614	Hs.185831	ESTs	8.20
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	8.20
40	449656	AA002008	Hs.188633	ESTs	8.20
	425535	AB007937	Hs.158287	KIAA0468 gene product	8.17
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.13
	432559	AW452948	Hs.257631	ESTs	8.10
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.10
45	420099	D80011	Hs.95140	KIAA0189 gene product	8.01
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.00
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.00
	434423	NM_006769	Hs.3844	LIM domain only 4	8.00
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	8.00
50	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.92
	433655	AL036559	Hs.3463	ribosomal protein S23	7.89
	435968	AW161481	Hs.111577	integral membrane protein 3	7.89
	434511	R28982	Hs.18106	ESTs	7.88
	423523	AW299828	Hs.193580	ESTs	7.86
55	409327	L41162	Hs.53563	collagen, type IX, alpha 3	7.84
	411960	R77776	Hs.18103	ESTs	7.80
	434159	AW135214	Hs.191828	ESTs	7.80
	447500	AI381900	Hs.159212	ESTs	7.80
	406699	L06505	Hs.182979	ribosomal protein L12	7.75
60	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	7.68
	426759	AI590401	Hs.21213	ESTs	7.66
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.62
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	7.60
	444795	AI193356	Hs.160316	ESTs	7.60
65	406663	U24683		immunoglobulin heavy constant mu	7.59
	442821	BE391929	Hs.8752	transmembrane protein 4	7.56
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.52
	407252	AA659037	Hs.163780	ESTs	7.50
	414405	AI362533		KIAA0306 protein	7.50
70	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.50
	429999	AI761902	Hs.99597	ESTs	7.50
	441436	AW137772	Hs.185980	ESTs	7.50
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.50
	420943	AI718702	Hs.279930	major histocompatibility complex, class	7.46
75	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.43
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.42
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	7.41
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	7.40
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	7.40
80	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.40
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	7.40
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	7.40
	432598	AI341227	Hs.157106	ESTs	7.38

	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.34
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.30
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.30
5	437103	AW139408	Hs.152940	ESTs	7.30
	442495	AI184717		ESTs	7.30
	445929	AI089660	Hs.323401	dpy-30-like protein	7.30
	446013	AI360167	Hs.152774	ESTs	7.30
	436075	BE090176	Hs.179902	transporter-like protein	7.20
10	450139	AK001838		serum/glucocorticoid regulated kinase	7.20
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.17
	406819	AA908472		gb:og82a10.s1 NCI_CGAP_Ov8 Homo sapiens	7.16
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.12
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	7.10
15	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	7.10
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	7.10
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.10
	427254	AL121523	Hs.97774	ESTs	7.10
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.10
20	438980	AW502364		gb:UI-HF-BR0p-aka-f-12-0-UI.r1 NIH_MGC_5	7.10
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	7.10
	441878	AI801869	Hs.127982	ESTs	7.09
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.04
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	7.00
25	417315	AI080042	Hs.180450	ribosomal protein S24	7.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.00
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.00
	445245	AB032973	Hs.12461	LCHN protein	7.00
	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.00
30	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	6.97
	410397	AF217517	Hs.63042	DKFZp564J157 protein	6.96
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	6.96
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	6.95
	418134	AA397769	Hs.86617	ESTs	6.90
35	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	6.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	6.90
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.89
	451838	AW005866	Hs.193969	ESTs	6.88
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	6.87
40	453485	BE620712	Hs.33026	hypothetical protein PP2447	6.85
	401466			vesicle-associated membrane protein 4	6.84
	457073	AA233210	Hs.179943	ribosomal protein L11	6.83
	412093	BE242691	Hs.14947	ESTs	6.83
	442492	AA528489	Hs.234518	ribosomal protein L23	6.83
45	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	6.83
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	6.82
	416401	N80139	Hs.268916	ESTs	6.80
	426501	AW043782	Hs.293616	ESTs	6.80
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	6.80
50	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	6.80
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.80
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.79
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	6.77
	425277	NM_001241	Hs.155478	cyclin T2	6.72
55	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	6.70
	428728	NM_016625	Hs.191381	hypothetical protein	6.70
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	6.70
	433735	AA608955	Hs.109653	ESTs	6.70
	430556	AW967807	Hs.13797	ESTs	6.69
60	417535	AA203569	Hs.191482	ESTs	6.69
	418117	AI922013	Hs.83496	linker for activation of T cells	6.67
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.65
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	6.62
	447341	AF106941	Hs.18142	arrestin, beta 2	6.61
65	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	6.60
	442460	NM_014135	Hs.8345	PRO0641 protein	6.60
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	6.59
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (defline not ava	6.57
	415221	W07418	Hs.78225	annexin A1	6.56
70	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.54
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	6.51
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	6.50
	441224	AU076964	Hs.7753	calumenin	6.50
	443749	R38828	Hs.143463	ESTs	6.50
75	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	6.50
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	6.40
	418259	AA215404		ESTs	6.40
	421633	AF121860	Hs.106260	sorting nexin 10	6.40
	435937	AA830893	Hs.119769	ESTs	6.40
80	445612	N94126	Hs.12969	hypothetical protein	6.40
	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.40
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.40
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	6.39

	434817	AA082118	Hs.102737	goliath protein	6.38
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	6.35
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.34
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.33
5	435812	AA700439	Hs.188490	ESTs	6.31
	401113			solute carrier family 22 (organic cation	6.30
	408418	AW963897	Hs.44743	KIAA1435 protein	6.30
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.30
	426780	BE242284	Hs.172199	adenylate cyclase 7	6.30
10	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	6.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	6.30
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	6.30
	449576	AW014631	Hs.225068	ESTs	6.30
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	6.30
15	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.27
	411975	AI916058	Hs.144583	ESTs	6.26
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	6.25
	433162	AI025842		ESTs	6.23
	449322	AI638616	Hs.196566	ESTs	6.22
20	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	6.20
	440327	R12581	Hs.191146	ESTs	6.20
	442832	AW206560	Hs.253569	ESTs	6.20
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	6.20
	427968	AI857607	Hs.181301	cathepsin S	6.18
25	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.16
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.16
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	6.15
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.15
	445493	AI915771		metallothionein 1E (functional)	6.15
30	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.14
	427477	AW973119	Hs.178391	ribosomal protein L44	6.14
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	6.13
	443441	AW291196	Hs.92195	ESTs	6.12
	413677	AW503116	Hs.301819	zinc finger protein 146	6.11
35	406797	AI432224		ribosomal protein L6	6.10
	406857	AA613726	Hs.29797	ribosomal protein L10	6.10
	410387	AI277367	Hs.47094	ESTs	6.10
	410503	AW975746	Hs.188662	KIAA1702 protein	6.10
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	6.10
40	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.08
	406877	AA226392	Hs.179943	ribosomal protein L11	6.07
	407784	AW139585	Hs.12708	ESTs	6.05
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.05
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	6.01
45	412949	AI471639	Hs.71913	ESTs	6.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	6.00
	435756	AI418466	Hs.33665	ESTs	6.00
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.00
	441623	AA315805		desmoglein 2	5.98
50	416926	H03109	Hs.263395	HT018 protein	5.96
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	5.95
	441244	BE612935	Hs.184052	PP1201 protein	5.95
	421305	BE397354	Hs.324830	diptheria toxin resistance protein requi	5.95
	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	5.94
55	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	5.92
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	5.91
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	5.90
	406542			C19000728*:gi|12585552|sp|Q9Y2Q1|Z257_HU	5.90
	406858	AI865720	Hs.29797	ribosomal protein L10	5.90
60	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.90
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	5.90
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.90
	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	5.90
	441321	H17182	Hs.7771	B-cell associated protein	5.88
65	429083	Y09397	Hs.227817	BCL2-related protein A1	5.87
	406806	AW088535		ribosomal protein, large, P0	5.87
	416987	D86957	Hs.80712	KIAA0202 protein	5.86
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	5.83
	428773	BE256238	Hs.193163	bridging integrator 1	5.83
70	406794	AI890243		ribosomal protein L6	5.82
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	5.82
	435511	AA683336	Hs.189046	ESTs	5.81
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.80
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	5.80
75	412528	AI123478	Hs.32112	ESTs	5.80
	424875	AI187945	Hs.199310	ESTs	5.80
	426981	AL044675	Hs.173081	KIAA0530 protein	5.80
	447711	AI459554	Hs.161286	ESTs	5.80
	449961	AW265634	Hs.133100	ESTs	5.80
80	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	5.80
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	5.79
	422773	AB028962	Hs.301552	KIAA1039 protein	5.78
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	5.78

	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.77
	449317	AW293413	Hs.132906	19A24 protein	5.75
	425787	AA363867	Hs.155029	ESTs	5.73
	414890	BE281095	Hs.77573	uridine phosphorylase	5.72
5	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	5.71
	435961	BE293127	Hs.283722	GTT1 protein	5.71
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	5.70
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	5.70
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	5.70
10	446659	AI335361	Hs.226376	ESTs	5.70
	457250	AA811987	Hs.125779	ESTs	5.70
	414150	AA136026		gb:zn88d07.r1 Stratagene lung carcinoma	5.68
	439924	AI985897	Hs.125293	ESTs	5.67
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.66
15	451812	X81889	Hs.152151	plakophilin 4	5.65
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	5.63
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	5.63
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	5.60
	431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	5.60
20	436511	AA721252	Hs.291502	ESTs	5.60
	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	5.60
	406623	X69392	Hs.91379	ribosomal protein L26	5.60
	452362	N38902	Hs.211539	hypothetical protein MGC4248	5.57
	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	5.56
25	437296	AA350994	Hs.20281	KIAA1700	5.56
	453985	N44545	Hs.251865	ESTs	5.56
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	5.55
	448877	AI583696	Hs.253313	ESTs	5.53
	435748	AA699756	Hs.117335	ESTs	5.52
30	420732	AA789133	Hs.63525	ESTs	5.51
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	5.50
	430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GCB1 Homo sapiens	5.50
	436716	AI433540		gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien	5.50
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	5.50
35	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	5.50
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	5.50
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	5.50
	433701	AW445023	Hs.15155	ESTs	5.49
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	5.47
40	420552	AK000492	Hs.98806	hypothetical protein	5.45
	449338	H73444	Hs.394	adrenomedullin	5.42
	427176	AW381569	Hs.40334	ESTs	5.42
	409945	AW015935	Hs.122642	ESTs	5.40
	421568	W85858	Hs.99804	ESTs	5.40
45	423961	D13666	Hs.136348	periostin(OSF-2os)	5.40
	440719	AA150869	Hs.26267	ATP-dependant interferon response protei	5.40
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	5.40
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	5.40
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	5.40
50	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TiT3 co	5.39
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
	439815	AA206079	Hs.6693	hypothetical protein FLJ20420	5.37
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	5.37
	457465	AW301344	Hs.122908	DNA replication factor	5.37
55	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.36
	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	5.35
	430283	BE391688		RAB7, member RAS oncogene family	5.33
	406814	AA642947	Hs.119122	ribosomal protein L13a	5.33
	409019	AW385412		myosin regulatory light chain 2, smooth	5.30
60	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	5.30
	412623	R28898	Hs.74170	metallothionein 1E (functional)	5.30
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	5.30
	418702	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	5.30
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.30
65	422900	AA641201	Hs.222051	ESTs	5.30
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	5.30
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.30
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	5.30
	430177	AW969233	Hs.302746	MSTP028 protein	5.30
70	430835	AI240006	Hs.192326	ESTs	5.30
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	5.30
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	5.30
	447082	T85314	Hs.54629	thioredoxin-like	5.30
	415995	NM_004573		phospholipase C, beta 2	5.29
75	424578	AK001973	Hs.150890	hypothetical protein	5.27
	441303	AW293081	Hs.241801	ESTs	5.27
	427816	AA159248	Hs.180909	peroxiredoxin 1	5.27
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.26
	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	5.24
80	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	5.23
	415121	D60971	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	5.21
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.21
	405086			NM_006662*:Homo sapiens Snf2-related CBP	5.20

	413401	AI361861	Hs.118659	ESTs	5.20
	418459	R85436	Hs.268814	ESTs	5.20
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.20
	426496	D31765	Hs.170114	KIAA0061 protein	5.20
5	431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	5.20
	434372	AA631373		gb:np86c01.s1 NCI_CGAP_Thy1 Homo sapiens	5.20
	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Su	5.20
	441390	AI692560	Hs.131175	ESTs	5.20
	449419	R34910	Hs.119172	ESTs	5.20
10	453127	AI696671	Hs.294110	ESTs	5.20
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.20
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	5.19
	451814	AA847992	Hs.137003	ESTs	5.18
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	5.18
15	406799	AA908548		gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens	5.16
	413963	R84282	Hs.75643	nuclear factor (erythroid-derived 2), 45	5.15
	422293	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	5.14
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	5.12
	414768	AW376989	Hs.259855	elongation factor-2 kinase	5.12
20	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	5.12
	430478	NM_014349	Hs.241535	apolipoprotein L, 3	5.11
	420151	AA255931	Hs.186704	ESTs	5.11
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	5.10
	419317	AA236282	Hs.172318	ESTs	5.10
25	424699	AW206227	Hs.287727	hypothetical protein FLJ23132	5.10
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	5.10
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	5.10
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	5.10
	436137	AI056769	Hs.133512	ESTs	5.10
30	440948	AW188311	Hs.128619	ESTs	5.10
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	5.09
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.09
	417228	AL134324	Hs.7312	ESTs	5.09
	424668	AI568170	Hs.96886	ESTs	5.08
35	418905	BE539674		actinin, alpha 4	5.08
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.07
	442618	R56222	Hs.26514	ESTs	5.06
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.06
	406813	AW276131		ribosomal protein L13a	5.06
40	454128	AL031259	Hs.41639	programmed cell death 2	5.05
	440709	AW797724	Hs.130350	ESTs	5.05
	436372	AW972301	Hs.310286	ESTs	5.05
	446173	BE565849	Hs.14158	copine III	5.05
	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	5.04
45	418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	5.03
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	5.00
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.00
	410800	BE280421	Hs.94499	ESTs	5.00
	431451	AA761378	Hs.192013	ESTs	5.00
50	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
	435655	AW105663	Hs.6947	HSPC069 protein	5.00
	435919	AI052189	Hs.114104	ESTs	5.00
	436394	AA531187	Hs.126705	ESTs	5.00
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	5.00
55	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	5.00
	442685	AB033017	Hs.8594	KIAA1191 protein	5.00
	444454	BE018316	Hs.11183	sorting nexin 2	5.00
	444670	H56373	Hs.332938	hypothetical protein MGC5370	5.00
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.00
60	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.00
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	5.00
	450887	AA011518	Hs.271778	ESTs, Weakly similar to I38022 hypotheti	5.00
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	5.00
	457068	X69391		ribosomal protein L6	5.00
65	406793	AW264291	Hs.5662	guanine nucleotide binding protein (G pr	4.97
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.95
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.94
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	4.92
	400281			Eos Control	4.91
70	414420	AA043424	Hs.76095	immediate early response 3	4.90
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.90
	434666	AF151103	Hs.112259	T cell receptor gamma locus	4.90
	449057	AB037784	Hs.22941	KIAA1363 protein	4.90
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.90
75	451598	N29102	Hs.118078	ESTs	4.90
	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	4.88
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.88
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.86
	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	4.86
80	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.85
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	4.85
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	4.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	4.84

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406781	AA639388		gb:nq88b06.s1 NCI_CGAP_Co9 Homo sapiens	4.83
449810	AB008681	Hs.23994	activin A receptor, type IIB	4.82
410323	AI241708	Hs.296322	Homo sapiens cDNA: FLJ22844 fis, clone K	4.81
444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	4.81
422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.81
400424	AJ276316	Hs.287374	zinc finger protein 304	4.80
411573	AB029000	Hs.70823	KIAA1077 protein	4.80
421045	BE144608	Hs.55533	ESTs	4.80
425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.80
430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.80
438590	AA811465	Hs.123375	ESTs	4.80
442071	BE048433	Hs.276043	ESTs	4.80
449567	AI990790	Hs.188614	ESTs	4.80
453213	AA082650	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	4.80
440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	4.78
437802	AI475995	Hs.122910	ESTs	4.77
409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.77
421932	W51778	Hs.323949	kangai 1 (suppression of tumorigenicity	4.74
428453	AB011110	Hs.184367	GTPase activating protein-like	4.74
413441	AI929374	Hs.75367	Src-like-adapter	4.74
446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	4.73
435541	AA687361	Hs.221318	ESTs	4.71
410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	4.70
412766	BE544475	Hs.54347	ESTs	4.70
415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.70
418973	AA233056	Hs.191518	ESTs	4.70
421433	AI829192	Hs.22380	ESTs	4.70
432925	AA878324	Hs.264750	ESTs	4.70
438869	AF075009		gb:Homo sapiens full length insert cDNA	4.70
442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypotheti	4.70
447198	D61523	Hs.283435	ESTs	4.70
448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.70
444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.66
414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	4.66
447817	BE620775	Hs.4866	Homo sapiens cDNA FLJ14387 fis, clone HE	4.65
416062	AA724811	Hs.334791	Homo sapiens cDNA FLJ14609 fis, clone NT	4.65
406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.64
424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	4.64
411165	NM_000169	Hs.69089	galactosidase, alpha	4.63
435905	AW997484	Hs.5003	KIAA0456 protein	4.63
445776	NM_001310	Hs.13313	cAMP responsive element binding protein-	4.62
424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	4.62
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin	4.62
410668	BE379794	Hs.159651	hypothetical protein	4.61
406774	AW518383	Hs.177592	ribosomal protein, large, P1	4.60
406648	AA563730	Hs.277477	major histocompatibility complex, class	4.60
407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.60
415682	AI347128	Hs.191870	ESTs	4.60
417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	4.60
419970	AW612022		ESTs	4.60
420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	4.60
431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	4.60
432586	AA568548		ESTs	4.60
437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	4.60
441355	AI822034	Hs.137097	ESTs	4.60
444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	4.60
458965	AA010319	Hs.60389	ESTs	4.60
406655	M21533	Hs.277477	major histocompatibility complex, class	4.60
414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	4.60
414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59
423766	AA303799	Hs.300141	ribosomal protein L39	4.59
451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
450043	AA885699	Hs.24332	CGI-26 protein	4.56
447742	AF113925	Hs.19405	caspase recruitment domain 4	4.54
433339	AF019226	Hs.8036	glioblastoma overexpressed	4.54
426395	BE151985		hypothetical protein FLJ23316	4.53
418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	4.53
423799	AW026300	Hs.132906	19A24 protein	4.53
445093	AI207197		ESTs	4.52
428044	AA093322	Hs.301404	RNA binding motif protein 3	4.52
453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	4.51
414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	4.50
427747	AW411425	Hs.180655	serine/threonine kinase 12	4.50
406745	AW511970	Hs.279860	tumor protein, translationally-controlle	4.50
407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	4.50
407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	4.50
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	4.50
429687	AI675749	Hs.211608	nucleoporin 153kD	4.50
436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	4.50
437634	AW293046	Hs.255158	ESTs	4.50
439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	4.50
442485	BE092285	Hs.29724	hypothetical protein FLJ13187	4.50
445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	4.50

	450497	H64159	Hs.15328	ESTs	4.50
	417497	AW402482	Hs.82212	CD53 antigen	4.50
	447667	AL117611	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (f	4.49
	413856	D13639	Hs.75586	cyclin D2	4.49
5	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.49
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.48
	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.48
	446021	BE389213	Hs.286	ribosomal protein L4	4.47
	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.46
10	412819	T25829	Hs.24048	FK506 binding protein precursor	4.46
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.45
	401846			NM_000988*:Homo sapiens ribosomal protei	4.44
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	4.43
	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	4.43
15	436623	AI417073	Hs.107265	ESTs	4.42
	412146	M92444	Hs.73722	APEX nuclease (multifunctional DNA repai	4.42
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	4.42
	416754	H07145	Hs.6799	ESTs, Weakly similar to T12483 hypothetl	4.41
	436671	AW137159	Hs.183291	ESTs	4.40
20	410079	U94362	Hs.58589	glycogenin 2	4.40
	420150	AA648712	Hs.29798	KIAA1712 protein	4.40
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.40
	428931	AA994979	Hs.98967	ATPase, H()-transporting, lysosomal, non	4.40
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	4.40
25	430280	AA361258	Hs.237868	interleukin 7 receptor	4.40
	438330	AW450572	Hs.257316	ESTs	4.40
	438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	4.40
	444794	AI419991	Hs.145225	ESTs	4.40
	445100	AW188205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	4.40
30	449659	R60031	Hs.198899	eukaryotic translation initiation factor	4.40
	449832	AA694264	Hs.60049	ESTs	4.40
	452404	AW450675	Hs.212709	ESTs	4.40
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.39
	425097	NM_014247		PDZ domain containing guanine nucleotide	4.37
35	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.37
	406742	AI468091	Hs.279860	tumor protein, translationally-controlle	4.35
	425095	AW014160	Hs.182585	KIAA1276 protein	4.34
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.34
	442333	AI650877	Hs.129302	ESTs	4.33
40	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.32
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.32
	437386	W52452		ribosomal protein L10	4.31
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	4.30
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	4.30
45	409604	AW444448	Hs.49124	ESTs	4.30
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.30
	419423	D26488	Hs.90315	KIAA0007 protein	4.30
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	4.30
	422797	AB033064	Hs.236463	KIAA1238 protein	4.30
50	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.30
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	4.30
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	4.30
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	4.30
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	4.30
55	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.30
	452994	AW962597	Hs.31305	KIAA1547 protein	4.30
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.30
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.29
	440910	H97875	Hs.117974	ESTs	4.29
60	406853	AA614553	Hs.252259	hypothetical protein FLJ23059	4.28
	432295	BE091049	Hs.343665	ribosomal protein S15a	4.28
	400244			Eos Control	4.28
	413518	BE149455	Hs.75415	beta-2-microglobulin	4.28
	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.27
65	406746	AA580395	Hs.279860	tumor protein, translationally-controlle	4.26
	400395	AF111167		v-fos FBJ murine osteosarcoma viral onco	4.26
	443229	AI057129	Hs.133396	ESTs	4.26
	450201	T97838	Hs.25722	ESTs	4.25
	409636	AA305729	Hs.18272	amino acid transporter system A1	4.25
70	422082	AA016188	Hs.111244	hypothetical protein	4.24
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	4.24
	453902	BE502341	Hs.3402	ESTs	4.24
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	4.22
	404854			Target Exon	4.21
75	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.20
	400440	X83957	Hs.83870	nebulin	4.20
	415049	N67334	Hs.50158	ESTs	4.20
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	4.20
	423180	AF068302	Hs.125031	choline/ethanolaminephosphotransferase	4.20
80	424684	AW752714	Hs.5174	ribosomal protein S17	4.20
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.20
	438141	AW946871		gb:RC2-ET0022-080500-012-d02 ET0022 Homo	4.20
	438607	AW080237	Hs.252884	ESTs	4.20

	451952	AL120173	Hs.301663	ESTs	4.20
	455397	AW936332		gb:QV4-DT0021-281299-070-g01 DT0021 Homo	4.20
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287 similar to	4.19
	453247	T80198	Hs.111806	ESTs	4.19
5	430451	AA836472	Hs.297939	cathepsin B	4.19
	414283	AW960011	Hs.154993	ESTs	4.18
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.18
	450746	D82673	Hs.278589	general transcription factor II, i	4.16
	444797	AB018333	Hs.12002	KIAA0790 protein	4.16
10	445718	H79791	Hs.15227	ESTs	4.15
	425783	AI026740	Hs.1948	ribosomal protein S21	4.15
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family, member	4.15
	406710	AI708347	Hs.184014	ribosomal protein L31	4.15
	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	4.14
15	422343	AI628633	Hs.346823	gb:ty77d05.x1 NCI_CGAP_Kid11 Homo sapien	4.13
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	4.13
	406724	C14071	Hs.234518	ribosomal protein L23	4.12
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.12
	413828	L19067		v-rel avian reticuloendotheliosis viral	4.11
20	416819	U77735	Hs.80205	pim-2 oncogene	4.11
	436674	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr	4.11
	405266			Target Exon	4.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	4.10
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	4.10
25	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.10
	423096	AA732684	Hs.278428	progestin induced protein	4.10
	426328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypotheti	4.10
	429355	AW973253	Hs.292689	ESTs	4.10
	433308	AA582718	Hs.291650	ESTs	4.10
30	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.10
	450850	AA648886	Hs.151999	ESTs	4.10
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.10
	406854	AA613705	Hs.252259	ribosomal protein S3	4.10
	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	4.09
35	419612	AI498267	Hs.110613	KIAA0421 protein	4.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.08
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	4.08
	441374	AA043696	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	4.08
	443415	AI056523	Hs.133472	ESTs	4.08
40	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	4.07
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.07
	400233			Eos Control	4.06
	421959	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.06
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	4.06
45	424795	AW102850	Hs.153177	ribosomal protein S28	4.05
	446231	NM_002163	Hs.14453	interferon consensus sequence binding pr	4.05
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	4.05
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfami	4.05
	409061	AI204994	Hs.7874	Homo sapiens cDNA: FLJ21435 fis, clone C	4.03
50	413891	BE271020		tumor suppressor deleted in oral cancer-	4.03
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	4.02
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.02
	410584	AB011112		KIAA0540 protein	4.01
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.00
55	423645	AI215632	Hs.147487	ESTs	4.00
	430048	T65054	Hs.73605	ESTs	4.00
	431113	AK000673	Hs.274337	hypothetical protein FLJ20666	4.00
	434170	AA626509	Hs.122329	ESTs	4.00
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	4.00
60	435391	AA704588	Hs.58934	ESTs	4.00
	446768	AV660305	Hs.110286	ESTs	4.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.00
	451831	NM_001674	Hs.460	activating transcription factor 3	4.00

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TABLE 56B
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552

75

80

		BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
429978	35194_2	BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AW682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963196 C06195 AI678018
442562	39593_1	AK056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 AI653056 AW973709 AI653173 BG054997 AI266043 BI054879 AI656750 AI492830 AW021142 AI472184 AW170056 AI082443 AI167921 D59940 BI492088 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832
412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE162164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487
413787	7612_1	BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 AI082748 AI470204 BI711078 BF350700 BI496963 AI087141 AA720684 AA862331 AA605146 BM313650 AI089749 AI359738 N69107 AW995424 AI086917 AI083995 AW340217 N99662 AI829449 AI089839 AI608761 AI342365 AI199076 AA908944 AI248943 AU160053 AI191245 AI218477 AI077943 AA864930 AI310394 AA872478 AI279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 AI469689 BE464590 AW664539 H67097 AL534332 C21397 AI085941 AW028427 BG939820 AI697089 AI039008 AI125315 AI655561 AW150042 L20422 X57345 BI458375 AU142852 BI666601 BE888276 AU119302 BI603754 BG705953 BI598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AW683116 AV708195 AA127798 AI124697 D54224 F08031 AA340253 BF923383 BM467808 BI546644 BG777200 BG705941 BG468577 AU127209 AW403970 BI597630 BI458091 AV689560 BI669267 BG506219 BI837163 BI667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 BI869271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 BI493502 AW273118 AI473820 AA608688 AI359337 AV712091 AA084101 BF592036 H13301 AI864305 AA505883 AI423963 AW084401 AI917740 R69858 AA033631 N79982 BE885276 AI635674 AA096126 AA700018 AV707753 AI082545 AU145681 AA629032 AI421367 AA740589 AA150830 AI248541 AA988608 AA150478 W65437 BM310234 AA262704 T28031 AI811116 BM272753 H21979 T15405 AA938406 F04963 AI188296 AW152629 AA905196 BG223058 AI831016 AI766457 AI811102 AA776573 AI922133 AA775958 AI261476 AA219489 AI688035 AI872093 BE537084 AW189078 D82630 AI123121 AL583492 BE350791 R69901 W65436 BE155392 BI089081 BE155394 AL120538 AW166100 AI359620 AI174338 N20527 W47413 AA155615 AI272249 H25293 BE614558 H69864 AW383484 H78021 H11617 R56892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W46459 AI866231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AL537424 BE814866 BF823254 R82553 AI809817 AI559406
410143	MH1244_8	AK000357 AI571830 AA579613 AA668790 BF939495 BF196886 AI990982 BF591561 AI809189 AW410232 BF739769 AI144392 BF438721 AI707495 AI423359 N52503 BE855784 N94367 AI023931 AA563662 AI744624 AI221298 AI299523 AI299520 BI491312 AI452711 AI360730 AA622643 AW195955 AA470473 AW392767 AI218127 AA873430 AA906005 AA748160 H89523 AW020252 AW664988 AA970424 AA879079 AI581622 AI361357 AA468498 AW008694 AA903275 AI187724 AI187718 AA890505 BF092771 AI066655 BE714172 BG289028 AW080390 BE001197 BF132049
426295	510_1	BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA668626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627
450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164
425996	138046_1	BM006551 AA367152 AW953705 AI631833 AW237429 AW027804 AA729038 BE503409 AI521935 BF739953 AA702982 AA557633 AA780065 AI218139 AW194264 D20120 AI082715 AI969980 BE857686 BE326711 AW953706 AI393749 AI383821 W67199 AI431759 AI796526 AI521794 AI796380 AW117545 AI749657 AI537634 N50122
427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
444060	6315_1	AK055070 AK055612 AK000174 BG619606 BG108086 AI741949 AI004176 BF891936 BF378565 AW197163 BE856860 BE245124 AW674411 AA490531 AW674981 AA740788 AW274758 BF512523 AI521278 AA548759 AI802431 AW051682 AI628247 AI799606 AW088103 AA236549 AI191529 AW273168 AI168451 AW073812 AW090611 AW003593 AI215845 AI799616 AW474940 AA954927 BM193740 AW662704 AW090127

			AA969444 AI080438 AA552500 AW237536 AA481060 AI246378 AA565227 AA398921 AA207051 AA721378 BF438608 AI086295 AI886630 AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766664 AI453279 AA435673 AI619515 AA879080 AA234592 AA890223 AA766824 BI259822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05809 N41323 T87376 R68544 H88711 BI087136
	413497	1518002_1	BE177661 H06215 BE144709 BE144829
	430068	1177709_2	AA947566
	409208	10117_2	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946
	422960	11862_2	BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260
	434280	1474904_1	BE005398 AA628622 AA994155
	434442	111738_1	AA662701 AA633929 AA737415
	410730	114639_1	BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823
	438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701
	425284	3834_5	BM476120 BE672181 AI697653 AA938187 AI280879 AW340123 AI912727 AI081775 AI089556 AI191349 AI871604 AI631607 AI890800 AI701917 AW771624 AA663041 AI991576 AI160622 AA771763 BE089784 BE089788 AI222942 AW418516 AA329211 AI095736 BE550294 AA738345 BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634
	422689	874209_1	AW954733 AA315006 AW856665
	414405	112689_1	AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545
	442495	928718_1	AI184717 AW518883 AF121173
	450139	34017_1	AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 AU135386 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI886459 AU155873 H04255 AW243986 AA557749 AI286227 R68691 R33453 AW388097
	406819	0_0	AA908472
	424677	2518_37	U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708
	438980	917280_1	AW502384 AA828822 AI982587
	451129	1495511_1	BE072881 AI762181 BE072946
	432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
	418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
	451653	MH115364_1	BG119563 AW975776 BG498478 BE245304 AW450934 BF508792 AA599489 AA599477 AI805268 AA055489 AI128758 AA761425 AA731858 AI302271 BE219432 AA687294 AA018972 AW629429 Z45675 AW961626 T30940 R34554 T84712 BG986694
	433162	2167905_1	AI742311 AI025842 AA578643
	406870	0_0	AA075144
	445493	423456_1	AV711317 AI809938 AI808768 AI240593 AI915771
	406797	0_0	AI432224 AW276890 AI499346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640
	441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179588 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129622 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BG496559 BF248373 BG494800
	430504	5477_6	BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575 AW300064 AW262133 H21568 AI363015 AI884914 H86948
	433891	647290_1	AW182329 AA613792 T05304 AW858385
	455263	26143_1	BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 BI596425 AA115605 AI589156 BF439839 BG188832 AI359615 BG190473 AI024233 BF439574 AW118065 AI672797 AA610042 BG212008 AI204382 R70913 AA033534 AA781036 AI627278 AA307285 AA034218 BG482749 AW162429 BI602460 AA721969 AA476516 AA476416 AA903019 BF110884 AA307286 AA115471 AW964555 AA423826 AA115129 AI419107
	406806	0_0	AW088535 AI889321 AA954221 AI337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA857965 AI625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 AI149335 AA936925 AA581684 AA954198 AW238461 AI281504 AI265812 AA583267 AW236162 AA876535 AW304286 AW474334 AI559415 AI589241 AI660952 AA641137 AI431696 AI688844 AA552513 AA564954 AW090553 AI205612 AI245753 AA954883 AA947909 AI866014
	406794	0_0	AI890243
	431155	1235742_1	AW971213 AA493925 AA493567 AA876839 AA934462
	414150	2305332_1	T40644 AA136139 AA136026
	430915	197844_1	BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
	436716	2472838_1	AI433540 AA804981 AA728984
	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
	430283	1418_1	BC013728 BI084032 BF090365 BE410706 N36391 W80436 BF813124 R90857 R62778 H00591 H02329 AA355285 AK000826 BC008721 BG744004 BG479141 BG823656 BG479061 AU121103 AU138176 BG702567 BI599840 BG422775 BG700944 BE280747 AU138529 BE269929 BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AU139772 BG714385 BF568538 BE304393 BF971755 BE267965 BE272012 AU135396 AU124535 BI551682 BG700612 AI815488 BG475195 BE388273 BE391517 BM148991 BF929247 AV653435 AW250299 AW249189 BF093150 BF093173 AW205325 BF057101 BF000551 AI341108 AL162009 AK026136 BE907957 W73238 BI711467 BG926027 AI816428 AA837518 AI754405 BG179142 AA481485 AW023435 BE855747 AI885101 N52163 AI016096 AI090204 BE677045 AI523320 AI126855 N26501 AA043680 AA976459 AI039590 AI937917 AI361000 W94866 AI375797 AI079801 AI168236 AA599882 AA084368 AI342635 AI190294 N26093 AI085234 AI298169 BF939715 AI223164 H98704 BE218925 N29394 AI918735 N41520 AI147784 AI918796 AA854317 N22193 AA199850 AI149728 AA121263 AI051074 AA565116 AI097349 N22209 AA552917 N33151 D52422 BF477483 AA476599 AA525787 AI279198 D53353 AA738063 AA558406 BI496334 AA999948 AA425847 BI496335 AA909624 BF197591 AW023259 AI652819 T31424 AA088213 T31115 AI206650 AA976796 AI948989 AW248762 AA449265 AA290687 AI682521 AA310227 Z38743 AA935369 AW119141 BF941087 AI470657 AI349451 AW079338 D45665 N21640 T30071 AI446705 R60220 BE833481 R49680 R70049 R41223 R32402 R69984 R70111 BM476906 BE293615 BE382443 BF155692 BE720638 BE931983 BE720594 BF085890 AA336953 BF081638 AA359915 AA384116 AA360142

			BI667664 BG823235 BE315559 BE301958 BE891114 BG826267 BE253680 BG979094 AV722757 N57629 BG997927 BI915769 BG680692 R62777 BE251116 H56358 AW369586 BG677759 BI044604 R75787 BE770960 H69529 R69983 AA259238 R97827 AA310379 W01103 AI873384 AL554578 BF038102 H87182 H87517 H01574 T52573 N28881 AA301397 T92375 R68401 AW800466 AI268172 BE876949 D54019 AI909769 AW798415 BI222383 AI393171 C15260 N26959 H17129 T53095 T52494 R68602 AI364765 BF687869 AI817035 AW105354 BE293820 H14206 BI093066 C14063 AL534349 BE255883 BE254068 AA428399 AW579360 AW579381 N53144 D60748 D54020 BG292106 H96705 D52423 T36174 D54161 R73016 D55021 BI857200 H83444 BI016954 D54163 R15563 BI818664 BE152207 BI048502 BF885667 BE613212 BE165773 BF149332 AW607045 BE305200
	409019	32320_4	BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA489668 AW968806 AW085196 AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285
	433009	2142268_1	AA761668 AA573621 R09670 R92814
	415995	2117_1	M95678 NM_004573 AL530754 AI439623 AW374413 BF898880 AW630959 BF875526 AW402206 BF818690 BF893068 AW504110 AW408049 BG002913 AL530753 AI524064 AW769231 AA464970 AA293723 AI095051 AI953375 AI982938 BM146050 AW575804 AA962489 AI655426 BM146046 T28538 BE241936 T89023 BI910963 AI416986 AI767111 AI422290 AW468260 BE676853 AI656771 AI961755 F04675 AA682826 AA737606 BM194382 AA912021 AW183098 BE676682 AI952227 AI591366 AA621765 AA293724 R51642 F10194 BI909727 BF892632 AW950600 AW950138 BG258587 BF892649 AI800647 BF892710 AA353176 BF894726 AA465038 BI040869 BI837749 BE244320 H18054 T74300 AW797026 AA926790 F32814 AW751282 AI933994 AA578823 T78372 BF899896 BF882808 BF974969
	434372	858779_1	BG622121 AA631424 AA988296 AA631373
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
	406799	0_0	AA908548
	430968	1237115_1	AW972830 AA489820 AA527647 AA570362
	418905	517_1	BM469076 AA533027 AI127512 AI368802 AA533141 AA700560 AW576028 AI610851 AI435361 BM129172 AW474544 BM128899 AI814292 AW502039 AA531243 BF941858 AW502037 AA702337 AI419854 AA662755 AA934364 AI300510 AI291136 AA505263 AI144527 AI076919 AI633534 AI242473 AA938561 BG055372 AA512894 AI671356 AA962403 BF808010 AA663911 AA847056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 AI305842 AW800873 AA302492 AA478427 AI817291 AW801104 AW801028 AA865744 BF155979 AI374743 AA478431 AI159846 AI369757 AI800672 BF435788 AA255451 AI937707 AW006198 AI280363 BF062434 AW801115 AI919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 AI302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 BI087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 AI142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605
	406813	0_0	AW276131
	418876	121279_1	AA740616 AA654854 AA229923
	447197	2176805_1	R36075 R36167 AI366546
	457068	1196_1	BC022444 BC004138 NM_000970 BC020679 X69391 D17554 BC013863 BG779630 BG574189 BG571986 BG494603 BG575713 AV702244 AU145720 AI568177 BE350654 BG943995 AA730918 AA634024 AV744673 AI611573 AI613381 AI613403 AI250148 AW301759 AI312307 AI376488 BE139682 AV743357 AI371951 AI613376 AI613570 AI345719 AI312458 AI612697 AI334453 AW268747 AW268318 AI343026 AI335454 AI313096 AI308011 AW075176 AI348782 AI334479 AW268332 AI611433 AI371906 AI312459 AI371647 AI370051 AI335217 AI312262 AI610971 AI348798 AI613378 AI612698 AI348772 AI345434 AI345283 AI312292 AA775853 AI611363 AI345286 AI318305 BF054854 AI613384 AI348808 AI802857 AI609452 AI583301 AI349258 AI345645 AI345011 AI340442 AI335410 AI310907 BF055880 BF055774 BF055754 BF054712 AI583261 AI309664 BF054905 AI370092 AI349212 AI345583 AI334554 AI312242 BF055856 AI612686 AI611382 AI610952 AI345301 AI312235 AI610936 AI609836 AI340650 AI312472 BF054840 AI802838 AI345448 AI336508 AI313098 AI312293 AI312277 AI254912 AW302091 AW074788 AI611968 AI611948 AI583362 AI583284 AI583245 AI379398 AI371935 AI340564 AW301840 AI862239 AI612025 AI611869 AI609852 AI345449 AI312375 AI312318 AI311993 AI310895 BF057960 BE178604 AI802860 AI612115 AI611886 AI370059 AI313286 AI802856 AI611438 AI311967 AI802821 AI312997 BF054711 AI611889 AI376483 AI252445 AI611577 AI349139 BF054925 AI802840 AI583286 AI340739 AI612041 AI345196 BF054833 AI308909 AI611883 AI313275 BF477097 AI609466 AI348792 AI340468 BG944254 BG941457 AW302007 BG944413 BG941475 D58042 AA328428 BG429596 BE395392 BM424161 BF663310 AV727364 BM473884 BG531178 AA307591 BF965435
	440638	371165_1	BG009500 AI376551 AA897445 T87714
	400281	9758_4	BE564506 Z47727 BF028489 BI597545 AA152273 AA730753 W07504 AA406507 AA316220 AA424683 N35844 N72473 AA442109 W01788 AA747605 AA235894 N41438 AA382786 AI906934 AI906935 BF091197 N85572 N75678 AV758098 BE719745 BE719744 BE719735
	406781	0_0	AA639388 AA584945 AA776364 AA776365 AA865528
	440129	2607882_1	AI732997 AA977633 AA865818
	438869	52134_1	AF075009 R63109 R63068
	419970	13569_1	AK055270 BE348291 AI190289 AW612022 AI269506 AI266578 AI269675 AW271406 BE879851 BF574163 BI497126 AW903775 BI917368 AW150900 BF244813 H79201
	432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
	426395	22291_3	AK057067 BF111915 AW249706 AI222199 AI887251 AI818753 AI244687 AW135782 BF476693 BF060935 AI197928 AW251092 AI685636 AI685630 BE673458 AA932894 AW205200 AA720784 BG236866 AI583152 BE677464 AW149338 AI926439 BG031285 BF915924 BG982583 BI060025 BG991393 BE830027 BE151985 BE152208 BE152002 BE818337 BE717581 BE818354 BE830030 AA377477 T51255 BF920761 BG170636 N90052
	445093	175963_1	AI207197 BF773544 AW196462
	438962	195763_1	AI207343 BF813684 BF928775 AA828585
	425097	23175_2	AF070570 BF439282 BF109960 AI480268 AI038060 AW082339 BF516290 BE218214 AI469956 AA039955 BE644674 AI861871 AA766231 AA845840 W85716 AA676253 AI087188 AA022908 AW953178 T33195 BF594711 AA488969 R55652 D81245 D80778 D81560 AW960933 BF930897 BE698103 AA040024 BF515960 BE168475 AA453247 AI267601 R60894 R44223 T33194 AA114936 W31640 W38829 W39109 AA004849 H41952 W88634 BF031932 BM423354 AL041825 H29654 AI908178 W85754 AI905762 AA309860 C04540 AA340246 H84669
	437386	5541_2	BM476605 BI545004 BI834636 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AI734997 AA931168 AA429766 N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI166232 AI889031 N98464 AI820039 AI459034 AV652512 AA622990 BE857200 AA932998 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895 AA535689 BF806025 BF806061 BF805985 BF746099 BF746097 AI309259 AI597603 BF806066 AI090653 AI129205 AI248410 H72993 AW615341 BF805990 BF805982 AA993819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76371
	418866	245947_1	T65754 AA229658 AA229857
	400244	12188_1	X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 AI074589 AI523475 BE890249 AW406263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 AI460106 AA740411 AI499168 AI078223 AI682923 BE696559 AW375385 AA786739 BG984978 Z40874 T17054 F09669 AW844043 U10439 BI711870 AW245957 AU158567 AA679305 AA679316 W72510 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172 AW192891 AI707980 AI094937 AI042115 AI200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826 AI422774 AW873114 AW073597 AW664483 AI218710 AW020550 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655 AI554424 AI274187 BE465703 AW512940 AW241366 AI923954 AA576649 AW168294 AA813181 AA912168 AI049738 AW514073 AA548255 AI569630 BE710031 AA244182 AI341697 AA563904 AI537990 AW517908 AW172943 Z39498 AI750294 AW150414 AI253293 BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 BI021048 BM048783 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 BI919250 BI253018 AW130996 BE074249 BE895428 BI034862 BE083277 BF952166
	418304	1093209_1	BE883520 BI057842 AA215702 AA215703 AA368006 BE006876 BE066555

	438141	1173217_1	AA778849 AW946871 AW946782 AW946955
	455397	1163606_1	AW936332 AW936341
	413828	9453_1	BC011603 BG479117 AU124990 BG829759 AU143705 BG701663 BG699781 AU131718 BE515064 AU121812 BG898850 AL558461 BM151887 AU128758 BM263692 AU099013 AI241350 U88316 AW058398 AW469340 BF683967 AI470140 AU150993 AA633376 AW150821 AA536142 AU148749 AI620647 AU151769 AU153404 AW070666 AI457758 AU153077 N99966 AW050940 BG055674 AA506657 AW301529 AI918646 AI611235 AI266081 AI334542 AW071277 AI312434 AW303114 AI436544 AI436466 R22972 AI472987 N77886 AW072883 AA318683 D19761 AW050566 AI312433 AA328444 R72435 AA430721 AI142599 AA582290 AU148896 AA721233 AW628132 R93935 AA100710 BI520773 AI934172 BG222461 H85359 AW074639 AA017117 BI026412 AL582142 AA443547 AA586793 AA777535 AA693844 AI018661 AA577422 AA522800 BF054818 AA102378 AA757993 AA687769 R55540 AA505784 BI820705 BI767939
	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523 BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866 AW840571
	400233	11259_1	BC004324 NM_001020 BC007977 M60854 BM050628 BG829809 BE385504 BG744451 BI826914 BE440007 BI260656 BE395117 BE389334 BE255792 BI194169 BI668218 BI194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM424171 BI828267 AW958606 BG831252 BE392943 BE394033 BI858915 BI668334 BE621019 BG706995 BE791985 BF967484 BI193635 BG761859 BM466537 BG747165 BG827488 AI133550 BM011511 BI227282 BG489212 BG478368 BE727789 BI160880 BG831707 BG324692 BM470427 BI083889 BG831605 BG754114 BG420536 BF308210 BE384213 BG832271 BG828032 BG481641 BF205675 BE899041 BE271558 BI193807 BI159866 BG473786 BG397178 BI194428 BI117210 BG768326 BG759507 BF975645 BF343657 BM020598 BG831082 BG829943 BG829501 BF306557 BE562511 BM050145 BM017978 BI193934 BI160764 BI160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 BI192794 BG831002 BG830459 BG764737 BG761808 BG481705 BG104314 BM464565 BI261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762 BG480900 BG419627 BG248771 BF975542 BM042233 BI161149 BG831302 BG830033 BG829626 BM050064 BI193014 BI161360 BG822729 BG110091 BG106500 BI258369 BG831982 BM458301 BM019513 BI161350 BI114178 BG481969 BG474870 BF974048 BF971122 BE741405 BE395269 BG832027 BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG666284 BG337575 BG336551 BF206677 BI258301 BI160946 BG105893 BF183072 BM459542 BI193881 BG832043 BG831323 BI194545 BI160968 BG755930 BG706018 BE743865 BM465145 BG831227 BG774290 BF683451 BE907161 BM045391 BI194396 BI161269 BG747091 BG546643 BF984863 BI160206 BI226402 BI226336 AW328236 BG339458 BF972634 BE909808 BI160988 BI160251 BG828764 BG826860 BG758360 BF568228 BI818282 BI457127 BG831491 BG759864 AI830010 BF568381 BE907238 BI161172 BI116773 BG827153 BG825088 BG335419 BG109404 AI929068 BE906354 BE408564 BM045000 BG339617 BG282794 BG335767 BE907263 BF568921 BG829961 BG479305 BG260397 AI922228 BE301975 AW516055 BG480919 BG480626 AW196817 BG336261 BE906157 BE395717 BE391427 BI192954 BG829757 BG476379 BE301536 BE394727 BE257695 BE905344 AI433577 BE894416 BE886992 BE409223 BF034756 BE904077 BG830886 BE909153 BE907998 BE395767 AI871751 BE744523 BI192663 BG831669 AI000225 BE743836 BE272515 AA628078 BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297 BE391448 BE390780 BE388821 BE258477 BE905970 BE901567 BE898833 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542 BE744156 BE394125 BE742207 BE395265 BE392942 BE894336 BE378222 BE906926 BE904650 BE393704 BE620999 BE515162 BE378753 BE272370 BE907458 BE612801 BE392484 BE907636 BE907353 BE910491 BE909796 BE905331 AW248173 AI683576 BE908826 BE620180 BF037570 BE908312 BE615015 BE256977 BE746875 BE394133 BE391478 BE910068 BE907185 BE742109 AA995746 BE561195 BE908825 BE906472 BE906509 BE906017 BE910442 BE514657 BI261969 BE741707 BE392216 BM042793 BF570283 BI262119 BE395707 BE378298 AW327827 BE394422 BF569178 BE263240 AI700512 BG830290 BF569308 BF569156 BI194587 BE390831 BG745096 AI681675 BE395674 AA136372 BE279892 AA442622 BE384898 AA313519 AI878866 AA305904 F33366 BE394852 F29153 F33618 AI133637 AA300009 F34063 F29455 AU099691 AI905085 AI906656 AA343249 BE388691 AW404280 AA379888 F29022 BF089981 F31013 F24305
	413891	823_1	BE271020 AI925430 AI806151 AW129911 AA626002 AW003539 BE042625 AI287859 AW778973 AI621173 AI991000 AA846016 AW150029 AW169748 AA649945 AI358496 AI470921 BF434211 AW513748 AW451232 AI953739 AI249448 AI040580 AI655280 AI637976 AW194345 AW611997 AI367197 BF064039 F29558 AI537342 BF593207 AW879538 AA973211 AI674328 AW879559 BF061961 AA481914 AA426532 AA426653 AA480106 AW243290 BF513102 BF346057 AI763358 AW003726 AI139045 AI570748 AW237602 T57492 BE887212 AI969311 AA133045 F23464 AA576416 T15590 AI650891 AI950958 AI983931 AW515101 AI650820 H81989 AA508473
	410584	35319_1	BF828833 AI968217 AI651409 AI760574 AI147562 AW001418 AI146791 AI650589 AI952939 AI432373 AI964094 AI963870 AI420438 AI336803 AA809634 BF590826 AA741075 BI712639 AL134637 BM264338 AA527993 AI867208 AI439038 AI684987 AI631696 AI587126 AI637622 AI651931 AI867525 AI783674 AI638281 AI825752 AI339197 AI653411 AI341372 AI673213 AI673191 AW779768 AI627934 AI921836 AI741634 AI382284 AI741624 AI401569 AW190430 AW196390 AI829182 AI523816 AI760522 BE505014 AI917343 BG818909 AW009307 AA927544 AA825621 AA829400 AA527307 AI887999 AI865022 AA885063 AA653458 AA483816 AA836167 AA505879 AA421004 AA252626 AI380678 AW196980 AA649133 AI742276 AW015700 AA595019 AA877835 AI701658 AA729793 AA535004 AA926792 AA505113 AA603726 W68390 N90130 AA489461 AA830462

TABLE 56C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402145	8018280	Plus	113086-114800
401091	9958240	Plus	94760-94898
401466	6682292	Plus	28748-29023
401113	9966541	Minus	19419-19959
406542	7711499	Plus	117335-118473
405086	8072509	Plus	73664-73841,74081-74217,74610-74779,7492
401846	7712190	Minus	82775-82823,82912-83022
404854	7143420	Plus	14260-14537
405266	4156171	Minus	63337-63552

TABLE 57A: 703 genes upregulated in testicular cancer relative to normal body tissues

Table 57A lists about 703 genes upregulated in testicular cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 95th percentile of testicular cancer AIs divided by the 50th percentile of normal tissues AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1

424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase); matrix metalloproteinase 9 (gelatinase B; 31.23
440119; AA865455; Hs.125331; ESTs, Moderately similar to unknown [H.sapiens]; ESTs, Moderately similar to unknown [H.s; 27.37
421241; X91817; Hs.102866; transketolase-like 1; transketolase-like 1; 26.89
431840; AA534908; Hs.2860; POU domain, class 5, transcription factor 1; POU domain, class 5, transcription facto; 25.03
435918; AF263538; Hs.86232; growth differentiation factor 3; growth differentiation factor 3; 19.88
432666; AW204069; Hs.351118; ESTs, Weakly similar to unnamed protein product [H.sapiens]; ESTs, Weakly similar to unnamed protein ; 17.74
419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); chitinase 1 (chitotriosidase); 17.64
452838; U65011; Hs.30743; preferentially expressed antigen in melanoma; preferentially expressed antigen in mela; 17.06
417886; AA214584; ; ESTs; ESTs; 15.95
412265; AA101325; Hs.86154; hypothetical protein FLJ12457; hypothetical protein FLJ12457; 15.93
425572; AB011076; Hs.158307; undifferentiated embryonic cell transcription factor 1; undifferentiated embryonic cell transcri; 15.82
423905; AW579960; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 15.11
419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; ubiquitin carrier protein E2-C; 15.08
427584; BE410293; Hs.179718; v-myb avian myeloblastosis viral oncogene homolog-like 2; v-myb avian myeloblastosis viral oncogen; 14.17
418696; AW959433; Hs.326290; hypothetical protein FLJ12581; hypothetical protein FLJ12581; 13.58
416819; U77735; Hs.80205; pim-2 oncogene; pim-2 oncogene; 13.20
414034; U89277; Hs.305985; early development regulator 1 (homolog of polyhomeotic 1); early development regulator 1 (homolog o; 12.93
454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); insulin-like 3 (Leydig cell); 12.90
432730; AI066520; Hs.131358; ESTs; ESTs; 12.84
446293; AI420213; Hs.149722; LIM domain transcription factor LIM-1 (hLIM-1) mRNA; LIM domain transcription factor LIM-1 (h; 12.74
423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; calcium channel, voltage-dependent, alph; 12.46
450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta 4; 12.42
450719; AI096837; Hs.21349; ESTs, Weakly similar to RB8B_HUMAN RAS-RELATED PROTEIN RAB-8B [H.sapiens]; ESTs, Weakly similar to RB8B_HUMAN RAS-R; 12.26
431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precursor; granin-like neuroendocrine peptide precu; 11.96
431354; BE046956; Hs.251673; DNA (cytosine-5-)-methyltransferase 3 beta; DNA (cytosine-5-)-methyltransferase 3 be; 11.91
402199; ; ; Target Exon; Target Exon; 11.85
424578; AK001973; Hs.150890; hypothetical protein; hypothetical protein; 11.81
416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholipase A2, group IID; 11.67
439979; AW600291; Hs.6823; hypothetical protein FLJ10430; hypothetical protein FLJ10430; 11.57
410048; W76467; Hs.343874; proline oxidase homolog; proline oxidase homolog; 11.42
442573; H93366; Hs.7567; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 11.42
414812; X72755; Hs.77367; monokine induced by gamma interferon; monokine induced by gamma interferon; 11.38
421917; AB028943; Hs.109445; KIAA1020 protein; KIAA1020 protein; 11.15
440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; NALP2 protein; PYRIN-Containing APAF1-li; 10.92
414683; S78296; Hs.76888; hypothetical protein MGC12702; hypothetical protein MGC12702; 10.91
423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage elastase); matrix metalloproteinase 12 (macrophage ; 10.74
433800; AI034361; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 10.68
429120; AK001673; Hs.196530; hypothetical protein FLJ10811; hypothetical protein FLJ10811; 10.48
444371; BE540274; Hs.239; forkhead box M1; forkhead box M1; 10.46
441553; AA281219; Hs.121296; ESTs; ESTs; 10.37
426534; U58096; Hs.2051; testis specific protein, Y-linked; testis specific protein, Y-linked; 10.28
441878; AI801869; Hs.127982; ESTs; ESTs; 10.06
432117; AL036195; Hs.2909; protamine 1; protamine 1; 10.01
425427; AI652662; Hs.317432; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 9.97
416201; AA467752; Hs.195161; ESTs; ESTs; 9.97
410929; H47233; Hs.30643; ESTs; ESTs; 9.91
427486; AA974433; Hs.362432; fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene); fibroblast growth factor 4 (heparin secr; 9.81
427239; BE270447; Hs.356512; ubiquitin carrier protein; ubiquitin carrier protein; 9.68
402680; ; ; Target Exon; Target Exon; 9.68
409208; Y00093; Hs.172631; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); integrin, alpha X (antigen CD11C (p150),; 9.46
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; chromosome 20 open reading frame 1; 9.42
440207; AI371978; Hs.128326; ESTs; ESTs; 9.41
433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; clone HQ0310 PRO0310p1; 9.41
447534; AW953935; Hs.288655; ESTs; ESTs; 9.33
442333; AI650877; Hs.129302; ESTs; ESTs; 9.28
421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425); Homo sapiens mRNA; cDNA DKFZp434B0425 (f; 9.24
423458; AI204212; Hs.351113; ESTs; ESTs; 9.23
431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placental); cadherin 3, type 1, P-cadherin (placenta; 9.23
422938; NM_001809; Hs.1594; centromere protein A (17kD); centromere protein A (17kD); 9.21
411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 9.21
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); topoisomerase (DNA) II alpha (170kD); 9.18
428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosophila)-like; similar to SALL1 (sal (Drosophila)-like; 9.17
428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabotropic glutamate family GPCR; retinoic acid induced 3 (RAIG1); metabo; 9.11
447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient, yeast, homolog)-like 2; MAD2 (mitotic arrest deficient, yeast, h; 9.11
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 9.10
449722; BE280074; Hs.23960; cyclin B1; cyclin B1; 8.86
441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 8.86
440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; solute carrier family 2 (facilitated glu; 8.86
409342; AU077056; Hs.54089; BRCA1 associated RING domain 1; BRCA1 associated RING domain 1; 8.83
420367; AA259090; Hs.257028; ESTs; ESTs; 8.82
415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1); mutS (E. coli) homolog 2 (colon cancer, ; 8.73
418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase kinase 1; mitogen-activated protein kinase kinase ; 8.71

417407; AA923278; Hs.290905; ESTs, Weakly similar to protease [H.sapiens]; ESTs, Weakly similar to protease [H.sapi; 8.64
407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 8.58
436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-conjugating enzyme; HSPC150 protein similar to ubiquitin-con; 8.55
412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkinesin 6); RAB6 interacting, kinesin-like (rabkines; 8.52
438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 8.51
424800; AL035588; Hs.153203; MyoD family inhibitor; MyoD family inhibitor; 8.45
447186; H65423; Hs.17631; hypothetical protein DKFZp434E2135; hypothetical protein DKFZp434E2135; 8.45
430056; X97548; Hs.228059; KRAB-associated protein 1; KRAB-associated protein 1; 8.42
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); midkine (neurite growth-promoting factor; 8.40
430676; AF084866; Hs.372585; gb:Homo sapiens envelope protein RIC-3 (env) gene, complete cd; gb:Homo sapiens envelope protein RIC-3 (; 8.38
420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.38
406621; X57809; Hs.181125; immunoglobulin lambda locus; immunoglobulin lambda locus; 8.37
453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; fructose-1,6-bisphosphatase 1; 8.25
423198; M81933; Hs.1634; cell division cycle 25A; cell division cycle 25A; 8.19
418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin, beta 2 (antigen CD18 (p95), ly; 8.17
453968; AA847843; Hs.62711; High mobility group (nonhistone chromosomal) protein 4; High mobility group (nonhistone chromoso; 8.16
453985; N44545; Hs.251865; ESTs; ESTs; 8.14
451106; BE382701; Hs.25960; N-MYC oncogene; N-MYC oncogene; 8.10
420347; AL033539; Hs.97124; Human DNA sequence from clone RP1-309H15 on chromosome 6p22.1-22.3 Contains a gene similar to HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)), ESTs, STSs, GSSs and a CpG Isl; Human DNA sequence from clone RP1-309H15; 8.03
415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.02
425601; AW529485; Hs.140720; GSK-3 binding protein FRAT2; GSK-3 binding protein FRAT2; 7.90
421016; AA504583; Hs.101047; transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47); transcription factor 3 (E2A immunoglobul; 7.89
432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;, mRNA sequence; gb:zr03f12.r1 Stratagene NT2 neuronal pr; 7.83
422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); neutrophil cytosolic factor 1 (47kD, chr; 7.80
433228; F28212; Hs.14953; KIAA1491 protein; KIAA1491 protein; 7.73
446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); nucleolar protein 1 (120kD); 7.71
447350; AI375572; Hs.172634; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 7.71
448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; nudix (nucleoside diphosphate linked moi; 7.71
430253; AK001514; Hs.236844; hypothetical protein FLJ10652; hypothetical protein FLJ10652; 7.70
444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1); ectonucleotide pyrophosphatase/phosphodi; 7.62
443537; D13305; Hs.203; cholecystokinin B receptor; cholecystokinin B receptor; 7.57
446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; interferon, gamma-inducible protein 30; 7.55
410006; AW732308; Hs.57783; eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD); eukaryotic translation initiation factor; 7.53
430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551 protein, partial cds; Homo sapiens mRNA for KIAA1551 protein, ; 7.52
411975; AI916058; Hs.144583; 3'UTR of: dead ringer (Drosophila)-like 1; 3'UTR of: dead ringer (Drosophila)-like ; 7.50
439864; AI720078; Hs.291997; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 7.47
440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4669, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 2700; 7.47
417705; AW134952; Hs.175220; hypothetical protein FLJ14541; hypothetical protein FLJ14541; 7.47
425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; protein tyrosine phosphatase, receptor t; 7.47
407710; AW022727; Hs.23616; ESTs; ESTs; 7.45
445093; AI207197; Hs.374149; ESTs; ESTs; 7.41
418113; AI272141; Hs.83484; SRY (sex determining region Y)-box 4; SRY (sex determining region Y)-box 4; 7.39
417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae, homolog); CDC20 (cell division cycle 20, S. cerevi; 7.37
429469; M64590; Hs.111801; glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P); glycine dehydrogenase (decarboxylating; ; 7.33
422726; U11690; Hs.1572; faciogenital dysplasia (Aarskog-Scott syndrome); faciogenital dysplasia (Aarskog-Scott sy; 7.33
430504; H52761; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 7.32
448981; AI968719; Hs.195387; ESTs; ESTs; 7.28
413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); FK506-binding protein 4 (59kD); 7.26
435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; Homo sapiens mRNA; cDNA DKFZp761E13121 (; 7.25
434414; AI798376; ; gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;, mRNA sequence; gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens; 7.24
428977; AK001404; Hs.194698; cyclin B2; cyclin B2; 7.19
434274; AA628539; Hs.57783; ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Moderately similar to ALU1_HUMAN A; 7.19
446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc f; Human DNA sequence from clone RP11-145L2; 7.16
420524; AB010575; Hs.98547; amiloride-sensitive cation channel 3, testis; amiloride-sensitive cation channel 3, te; 7.15
439053; BE244588; Hs.6456; chaperonin containing TCP1, subunit 2 (beta); chaperonin containing TCP1, subunit 2 (b; 7.14
445076; AI206888; Hs.154131; ESTs; ESTs; 7.14
448588; AI970276; Hs.156905; KIAA1676; KIAA1676; 7.13
429486; AF155827; Hs.203963; hypothetical protein FLJ10339; hypothetical protein FLJ10339; 7.10
441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E coli RecA homolog); RAD51 (S. cerevisiae) homolog (E coli Re; 7.04
433914; AF108136; Hs.112160; Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds; Homo sapiens DNA helicase homolog (PIF1); 7.02
413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; interferon-stimulated protein, 15 kDa; 7.02
423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840937, mRNA, partial cds; Homo sapiens, clone IMAGE:3840937, mRNA,; 6.96
416658; U03272; Hs.79432; fibrillin 2 (congenital contractural arachnodactyly); fibrillin 2 (congenital contractural ara; 6.92
438450; AI050866; Hs.65853; nodal, mouse, homolog; nodal, mouse, homolog; 6.90
415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); neutrophil cytosolic factor 2 (65kD, chr; 6.90
444381; BE387335; Hs.283713; hypothetical protein BC014245; hypothetical protein BC014245; 6.89
447582; BE293520; Hs.18910; prostate cancer overexpressed gene 1; prostate cancer overexpressed gene 1; 6.89
424779; AL046851; Hs.153053; CD37 antigen; CD37 antigen; 6.89
443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; TYRO protein tyrosine kinase binding pro; 6.84
427298; AA400495; ; ESTs; ESTs; 6.82
414732; AW410976; Hs.77152; minichromosome maintenance deficient (S. cerevisiae) 7; minichromosome maintenance deficient (S.; 6.81
424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; activated p21cdc42Hs kinase; 6.81
426866; U02330; Hs.172816; neuregulin 1; neuregulin 1; 6.80
418203; X54942; Hs.83758; CDC28 protein kinase 2; CDC28 protein kinase 2; 6.80
427521; AW973352; ; ESTs; ESTs; 6.75
430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; bicarbonate transporter related protein ; 6.75
427719; AI393122; Hs.134726; ESTs; ESTs; 6.74

439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72
453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71
446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein, ; 6.70
445363; NM_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70
433701; AW445023; Hs.15155; ESTs; ESTs; 6.69
418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63
441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59
424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58
414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58
418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57
414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57
437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55
425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete ; 6.55
452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55
422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51
409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin); minichromosome maintenance deficient (S.; 6.50
418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell ; 6.49
417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A (; 6.44
427747; AW411425; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42
430280; AA361258; Hs.237868; interleukin 7 receptor; interleukin 7 receptor; 6.42
432938; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42
422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40
427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3_HUMAN TUBBY; 6.40
417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39
428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (Cy; 6.39
441384; AA447849; Hs.288660; retinoic acid induced 3; retinoic acid induced 3; 6.38
438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34
416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34
451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; 6.31
444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright ; 6.31
425274; BE281191; Hs.155462; minichromosome maintenance deficient (mis5, S. pombe) 6; minichromosome maintenance deficient (mi; 6.31
434649; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcrip; 6.30
420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30
415829; AW450198; Hs.163742; ESTs; ESTs; 6.28
410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26
446839; BE091926; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25
457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25
428918; AL036967; Hs.2324; protamine 2; protamine 2; 6.24
443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19
424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19
407245; X90568; Hs.172004; titin; titin; 6.18
458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18
421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (Cy; 6.16
435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13
424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12
430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10
444823; BE262989; Hs.12045; putative protein; putative protein; 6.10
428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino ; 6.09
402260; ; ; NM_001436*:Homo sapiens fibrillarin (FBL), mRNA. transcript) (F8A), mRNA.; NM_001436*:Homo sapiens fibrillarin (FBL; 6.09
441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05
422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04
431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); interferon, alpha-inducible protein (clo; 6.04
402678; ; ; Target Exon; Target Exon; 6.03
453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01
439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 2168212; hypothetical protein from EUROIMAGE 2168; 6.01
420596; NM_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01
420676; AI434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00
418756; AA252254; Hs.226949; ESTs; ESTs; 5.99
454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98
407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98
413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96
424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95
417777; AI823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/th; 5.94
449569; AI656634; Hs.195389; ESTs; ESTs; 5.92
436576; AI458213; Hs.77542; ESTs; ESTs; 5.90
438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89
420005; AW271106; Hs.133294; ESTs; ESTs; 5.89
417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88
403171; ; ; C2001472*:gi|5809678|gb|AAB41848.2| (U64675) sperm membrane protein BS-63 [Homo sapiens][; C2001472*:gi|5809678|gb|AAB41848.2| (U64; 5.87
448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87
406137; ; ; NM_000179*:Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM_000178.1 GI; NM_000179*:Homo sapiens mutS (E. coli) h; 5.85
423787; AJ295745; Hs.236204; nuclear pore complex protein; nuclear pore complex protein; 5.85
425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84
452796; AB011100; Hs.30656; KIAA0528 gene product; KIAA0528 gene product; 5.84
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80
447359; NM_012093; Hs.18268; adenylate kinase 5; adenylate kinase 5; 5.79
420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78
420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1_HUMAN ALU S; 5.75
414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5_HUMAN LEUKE; 5.74
436251; BE515065; Hs.296585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73
421535; AB002359; Hs.105478; phosphoribosylformylglycinamidine synthase (FGAR amidotransferase); phosphoribosylformylglycinamidine syntha; 5.71
414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69
425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspart; 5.69
401704; ; ; NM_021195*:Homo sapiens claudin 6 (CLDN6), mRNA. VERSION NM_020982.1 GI; NM_021195*:Homo sapiens claudin 6 (CLDN6; 5.66
425358; AL079658; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin assoc; 5.65
402677; ; ; NM_000478:Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase), polypeptide 1 (CYP7B1), mRNA.; NM_000478:Homo sapiens alkaline phosphat; 5.64
409264; NM_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63
432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63
409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63
430252; AI638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61
419359; AL043202; Hs.90073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61
452816; AA131789; Hs.61509; ESTs; ESTs; 5.60
402679; ; ; NM_000478:Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase), polypeptide 1 (CYP7B1), mRNA.; NM_000478:Homo sapiens alkaline phosphat; 5.59
414291; AI289619; Hs.13040; G protein-coupled receptor 86; G protein-coupled receptor 86; 5.58
453028; AB006532; Hs.31442; RecQ protein-like 4; RecQ protein-like 4; 5.58
453905; NM_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-assoc; 5.55
419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino ; 5.55
446979; AI654443; Hs.197683; ESTs; ESTs; 5.54
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kin; 5.53
418962; AA714835; Hs.271863; ESTs; ESTs; 5.53
447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 5.52
427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); integrin, alpha L (antigen CD11A (p180),; 5.52
449322; AI638616; Hs.196566; ESTs; ESTs; 5.51
428450; NM_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51
415141; AA189099; Hs.268171; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7_HUMAN ALU S; 5.48
454048; H05626; Hs.6921; ESTs; ESTs; 5.46
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; interleukin 1 receptor antagonist; 5.45
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304; Homo sapiens cDNA FLJ11980 fis, clone HE; 5.44
414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44
452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisi; 5.44
438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class ; 5.44
427668; AA298760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43
449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 5.41
453633; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40
450746; D82673; Hs.278589; general transcription factor II, i; general transcription factor II, i; 5.40
425966; NM_001761; Hs.1973; cyclin F; cyclin F; 5.39
418134; AA397769; Hs.86617; ESTs; ESTs; 5.38
432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37
417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, m; 5.36
428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.; 5.35
406811; U82979; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 5.34
415819; AU077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII),; 5.33
448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33
424762; AL119442; Hs.183684; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor; 5.32
421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 5.32
429271; AF039850; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32
456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A; 5.30
414907; X90725; Hs.77597; polo (Drosophia)-like kinase; polo (Drosophia)-like kinase; 5.30
422997; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29
440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosop; 5.28
418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26
416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer anti; 5.21
450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20
409670; AI368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20
429083; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20
408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); lymphocyte cytosolic protein 2 (SH2 doma; 5.19
438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 5.16
437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-asso; 5.15
448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15
436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor t; 5.14
426752; X69490; Hs.172004; titin; titin; 5.13
415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2 ; 5.13
400263; ; Hs.75309; Eos Control; Eos Control; 5.13
437099; N77793; Hs.48659; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin a; 5.12
427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10
407347; AA829847; ; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element;, mRNA sequence.; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens; 5.10
458933; AI638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10
450431; AW136797; Hs.266041; ESTs; ESTs; 5.09
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08
410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-recept; 5.08
417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05
412723; AA648459; Hs.335951; hypothetical protein AF301222; hypothetical protein AF301222; 5.05

447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03
410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02
433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog) ; 5.02
425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha 2 (RAG cohort 1, impor; 5.00
425237; U07695; Hs.155227; EphB4; EphB4; 5.00
414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99
402145; ; ; Target Exon; Target Exon; 4.99
432126; AA865239; Hs.37196; ESTs; ESTs; 4.99
408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 4.98
419525; T79257; Hs.1259; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97
424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97
427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96
457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96
448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94
426427; M86699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91
440129; AA865818; Hs.369523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-lik; 4.91
453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1 ; 4.90
435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89
452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88
445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88
437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87
441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG51) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIG; 4.87
421350; AW301608; Hs.278188; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 4.87
409093; BE243834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86
424304; NM_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86
437696; Z83844; Hs.5790; hypothetical protein dJ37E16.5; hypothetical protein dJ37E16.5; 4.86
417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; solute carrier family 23 (nucleobase tra; 4.84
416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83
448939; BE267795; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82
413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82
424081; NM_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81
425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81
412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor (; 4.81
422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80
409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79
412760; AW379030; Hs.41324; ESTs; ESTs; 4.79
447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79
429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78
448950; AF288687; Hs.9275; CGI-152 protein; CGI-152 protein; 4.78
412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C ; 4.78
412541; M16650; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76
420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 4.76
421905; AI660247; Hs.32699; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H; 4.75
413880; AI660842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75
424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74
418355; L42563; Hs.1165; ATPase, H? transporting, nongastric, alpha polypeptide; ATPase, H? transporting, nongastric, alp; 4.74
435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74
428024; Z29067; Hs.2236; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74
421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72
419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72
437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70
450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (bamacan); chondroitin sulfate proteoglycan 6 (bama; 4.70
421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69
449475; AI348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69
420062; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69
429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIIB (25-hy; 4.69
436856; AI469355; Hs.127310; ESTs; ESTs; 4.68
406937; U14622; ; gb:Human transketolase-like protein gene, partial cds.; gb:Human transketolase-like protein gene; 4.67
411296; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67
426726; AA488915; Hs.171955; trophinin associated protein (tastin); trophinin associated protein (tastin); 4.67
409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67
449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66
431681; AK000378; Hs.267566; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.65
443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent, ; 4.65
441595; AW206035; Hs.356457; ESTs; ESTs; 4.64
423419; R55336; Hs.23539; ESTs; ESTs; 4.64
415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63
435045; BE297155; Hs.143698; ESTs; ESTs; 4.62
424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62
414972; BE263782; Hs.77695; KIAA0008 gene product; KIAA0008 gene product; 4.62
436685; W28661; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62
449515; AI653378; Hs.302012; ESTs; ESTs; 4.61
425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61
420027; AF009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61
436469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61
413441; AI929374; Hs.75367; Src-like-adapter; Src-like-adapter; 4.60
456847; AI360456; Hs.86088; ESTs; ESTs; 4.58
421506; BE302796; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57
426935; NM_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57
428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56
409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56
412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L OR; 4.55

443068; AI188710; Hs.374480; ESTs; ESTs; 4.55
441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54
453227; AW135862; Hs.243991; ESTs; ESTs; 4.52
438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51
422565; BE259035; Hs.118400; singed (Drosophila)-like (sea urchin fascin homolog like); singed (Drosophila)-like (sea urchin fas; 4.51
453613; F06838; Hs.374476; ESTs; ESTs; 4.50
413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H; 4.50
412507; L36645; Hs.73964; EphA4; EphA4; 4.50
419034; NM_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49
413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo; 4.49
406547; ; ; Target Exon; Target Exon; 4.49
443216; W80487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48
417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47
448595; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47
445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46
446236; NM_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46
429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46
420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TiT3 complex); CD3Z antigen, zeta polypeptide (TiT3 com; 4.46
413426; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt; 4.44
421819; NM_013403; Hs.108665; zinedin; zinedin; 4.44
409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44
428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, Dr; 4.43
434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; ESTs, Highly similar to A35661 DNA excis; 4.43
418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42
409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42
437103; AW139408; Hs.152940; ESTs; ESTs; 4.42
413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic; 4.42
456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40
424078; AB006625; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39
448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi; 4.37
410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36
435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35
400440; X83957; Hs.83870; nebulin; nebulin; 4.35
437218; AL117497; Hs.58185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifera; 4.34
430478; NM_014349; Hs.241535; apolipoprotein L, 3; apolipoprotein L, 3; 4.34
432744; AA988835; Hs.38664; ESTs; ESTs; 4.33
423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33
415995; NM_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33
408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30
431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re; 4.30
427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfami; 4.29
426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29
427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, receptor for (CD16); Fc fragment of IgG, low affinity IIIb, r; 4.29
434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29
412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled recepto; 4.28
447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28
426108; AA622037; Hs.166468; programmed cell death 5; programmed cell death 5; 4.28
428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component ; 4.27
437908; AI082424; Hs.351043; ESTs; ESTs; 4.27
444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27
429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26
439334; AI148976; Hs.112062; ESTs; ESTs; 4.26
425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25
413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25
453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24
447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24
447528; AI612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23
452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22
449810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22
447198; D61523; Hs.283435; ESTs; ESTs; 4.22
416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated; 4.22
425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 145kD; inositol polyphosphate-5-phosphatase, 14; 4.22
422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21
444535; AF011466; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21
417088; M54915; Hs.81170; pim-1 oncogene; pim-1 oncogene; 4.20
421707; NM_014921; Hs.107054; lectomedin-2; lectomedin-2; 4.20
408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20
438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19
419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18
418755; Y14443; Hs.88219; zinc finger protein 200; zinc finger protein 200; 4.18
417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17
413686; AI469213; Hs.71404; ESTs; ESTs; 4.17
419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16
418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); chemokine (C-X-C motif), receptor 4 (fus; 4.16
408482; NM_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16
422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15
409421; AA199883; Hs.67624; ESTs; ESTs; 4.15
415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14
415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14
424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to; 4.13
423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbon; 4.13
433436; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitoch; 4.13
420253; AI656055; Hs.96200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 9; 4.12
412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12
400205; ; Hs.81848; NM_006265*:Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA. (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA.; NM_006265*:Homo sapiens RAD21 (S. pombe); 4.12
425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11
419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10
459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31611 hypotheti; 4.10
432512; NM_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to ; 4.10
452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09
423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); interferon-stimulated transcription fact; 4.09
413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09
442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G pr; 4.09
425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/apyrimidinic endonuclease(APEX ; 4.08
421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08
432841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-recept; 4.08
452069; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08
425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker-; 4.07
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic; 4.07
424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; Homo sapiens cDNA FLJ12169 fis, clone MA; 4.07
434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe co; 4.06
446791; AI632278; Hs.195922; ESTs; ESTs; 4.06
432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), cata; 4.06
431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta; 4.06
418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory su; 4.06
425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, de; 4.05
408692; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04
446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrat; 4.04
439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 pr; 4.04
417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule; 4.04
410068; AI633888; Hs.58435; FYN-binding protein (FYB-120/130); FYN-binding protein (FYB-120/130); 4.03
410639; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03
427716; L38951; Hs.180446; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03
451050; AW937420; Hs.351869; ESTs; ESTs; 4.02
449667; AB023227; Hs.23860; KIAA1010 protein; KIAA1010 protein; 4.02
448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01
437527; AI241019; Hs.145644; ESTs; ESTs; 4.01
425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; methylene tetrahydrofolate dehydrogenase; 4.00
451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fis, clone COLF1210; Homo sapiens cDNA FLJ20201 fis, clone CO; 4.00
412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor; 4.00
409581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99
433577; AW007080; Hs.284192; ESTs; ESTs; 3.99
439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD); platelet-activating factor acetylhydrola; 3.99
418629; BE247550; Hs.66859; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99
448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin, gamma 1; 3.98
402398; ; ; C19000263:gi|3108023|gb|AAC15755.1| (AC004659) BC62940_2 [Homo sapiens]||66335; C19000263:gi|3108023|gb|AAC15755.1| (AC0; 3.97
406414; AI114686; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.97
415012; NM_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97
416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kin; 3.95
422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial ; 3.95
447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine pr; 3.95
430770; AA765694; Hs.123296; ESTs; ESTs; 3.94
442994; AI026718; Hs.16954; ESTs; ESTs; 3.94
420333; AJ001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46); lymphocyte antigen 94 (mouse) homolog (a; 3.94
438456; AA913381; Hs.279763; ESTs; ESTs; 3.94
422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A) ; 3.93
420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93
424829; NM_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR super; 3.93
447574; AF162666; Hs.18695; tousled-like kinase 1; tousled-like kinase 1; 3.93
425797; AF002986; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93
421910; NM_014586; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associa; 3.92
413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenas; 3.92
434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fis, clone NT; 3.92
400262; ; Hs.75309; Eos Control; Eos Control; 3.90
424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 3.90
409799; D11926; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90
435206; AI432364; Hs.160594; ESTs; ESTs; 3.90
439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90
413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90
426265; AA421069; Hs.97896; ESTs; ESTs; 3.89
451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89
407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89
437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88
400261; ; Hs.1802; Eos Control; Eos Control; 3.88
450447; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88
422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glut; 3.87
414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87
417767; BE242241; Hs.82542; acyloxyacyl hydrolase (neutrophil); acyloxyacyl hydrolase (neutrophil); 3.87
414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor,; 3.87

444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86
419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86
427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86
443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86
408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86
410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 3.85
450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85
418978; T85295; Hs.268606; ESTs; ESTs; 3.84
429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84
442980; AA857025; Hs.8678; kinesin-like 1; kinesin-like 1; 3.84
447232; AW499834; Hs.327; interleukin 10 receptor, alpha; interleukin 10 receptor, alpha; 3.84
434689; AF154115; Hs.4076; CTD (carboxy-terminal domina, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domina, RNA polyme; 3.83
432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83
415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83
451598; N29102; Hs.79658; ESTs; ESTs; 3.82
449433; AI672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bindi; 3.82
426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81
435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80
443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80
422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79
421508; NM_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79
414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79
421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; suppressor of var1 (S.cerevisiae) 3-like; 3.79
439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; frizzled (Drosophila) homolog 8; 3.79
411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78
425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78
423909; AJ223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78
429687; AI675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77
414177; AI351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77
414135; NM_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77
445817; NM_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77
410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76
412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repai; 3.76
413011; AW068115; Hs.821; biglycan; biglycan; 3.76
428157; AI738719; Hs.198427; hexokinase 2; hexokinase 2; 3.76
400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor, alpha polypeptide); integrin, alpha 5 (fibronectin receptor,; 3.75
427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75
405484; ; ; C3002124*:gi|12737280|ref|XP_006682.2| keratin 18 [Homo sapiens]|6633; C3002124*:gi|12737280|ref|XP_006682.2| k; 3.75
450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75
432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75
428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74
431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU8_HUMAN ALU S; 3.74
453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.74
426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74
438330; AW450572; Hs.257316; ESTs; ESTs; 3.74
419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74
452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73
442233; AW957149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypotheti; 3.73
451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73
410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Homo sapiens clone 24675 mRNA sequence; 3.73
426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72
449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpo; 3.71
423523; AW299828; Hs.193580; ESTs; ESTs; 3.71
413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71
448336; R53848; Hs.44976; ESTs; ESTs; 3.70
422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70
416087; AF045184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70
442200; AW590572; Hs.235768; ESTs; ESTs; 3.70
414280; BE410769; Hs.75873; zyxin; zyxin; 3.69
409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69
415276; U88666; Hs.78353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69
439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69
446522; NM_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.69
422785; AI824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68
401083; ; ; NM_016582*:Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM_016579.1 GI; NM_016582*:Homo sapiens peptide transpor; 3.68
413048; M93221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68
452690; AI536070; Hs.15085; ESTs; ESTs; 3.68
428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU2_HUMAN ALU S; 3.68
415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68
428579; NM_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68
446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.66
442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for cysteine desulfurase, two genes for novel proteins and the gene for the; Human DNA sequence from clone RP11-353C1; 3.66
416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65
441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610; 3.65
413076; U10564; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65
429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to S65657 alpha-1C-; 3.65
452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN20), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1; 3.65
414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65
417426; NM_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65
450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyros; 3.64
437669; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA667999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64
414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep; 3.64
444388; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64
425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63
451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63
444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63
447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc; 3.62
408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62
424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62
411165; NM_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62
422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62
453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61
438795; AA825792; Hs.377119; gb:od84b11.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:od84b11.s1 NCI_CGAP_Ov2 Homo sapiens ; 3.61
445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61
407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60
423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60
444985; AI677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60
433764; AW753676; Hs.39982; zinc finger protein RINZF (NM_023929); zinc finger protein RINZF (NM_023929); 3.59
427857; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59
415020; BE249915; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains the gene for a novel glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59
415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57
458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57
423576; NM_000383; Hs.129629; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57
440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57
434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57
404976; ; ; NM_014323*:Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA.; NM_014323*:Homo sapiens zinc finger prot; 3.57
449656; AA002008; Hs.188633; ESTs; ESTs; 3.56
413795; AL040178; Hs.142003; ESTs; ESTs; 3.56
406859; AI581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56
411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56
447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.sa; 3.56
424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55
413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high affi; 3.55
443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible IkappaB kinase; IKK-related kinase epsilon; inducible Ik; 3.55
426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55
450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfami; 3.55
425836; AW955696; Hs.90960; ESTs; ESTs; 3.54
441054; AA913591; Hs.126480; ESTs; ESTs; 3.54
440592; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54
458946; AA009716; Hs.42311; ESTs; ESTs; 3.53
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53
421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53
422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); transformer-2 alpha (htra-2 alpha); 3.53
424870; T15545; Hs.244624; ESTs; ESTs; 3.52
442794; AI744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52
417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51
419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A.i - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51
410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51
424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51
421921; H83363; Hs.355993; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50
454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50
434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil; 3.50
453641; AA444140; Hs.90960; ESTs; ESTs; 3.50
429592; AB029041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49
430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211_HUMAN ZINC ; 3.47
410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44
413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07
437224; AL117628; Hs.97808; ESTs; ESTs; 2.77
430439; AL133561; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76
435897; AF269223; Hs.128322; t-complex 11 (a murine tcp homolog); t-complex 11 (a murine tcp homolog); 2.53
417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosom; 2.46
412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35
422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33
426627; AF012359; Hs.195685; ESTs; ESTs; 2.12
436983; AF085884; Hs.20029; proacrosin binding protein sp32 precursor; proacrosin binding protein sp32 precurso; 2.07
425709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99
433724; AI827749; Hs.144924; serine/threonine protein kinase SSTK; serine/threonine protein kinase SSTK; 1.68
420710; NM_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession

417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
407347	810943_1	T23514 AI655785
430439	6750_2	AL133561 AL117481 AL122069 AW439292 AI968826 AL041090

TABLE 57C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
402678	8113438	Plus	37395-37514,37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3097841	Plus	24712-25374
402677	8113438	Plus	22135-22309,23063-23238
402679	8113438	Plus	132079-132216
402145	8018280	Plus	113086-114800
406547	7711513	Minus	172780-174358
402398	4092817	Minus	24019-24973
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
401083	3242744	Plus	33192-33360
404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UnigeneID; Unigene Title; Pred.Prot.Domains; R1

430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;; 35.25
422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExbB;TM=Y;SS=M; 33.25
414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip;TM=M;SS=Y; 31.68
415192; D17793; Hs.78183; aldo-keto reductase family 1, member C3 ; aldo_ket_red;TM=M;; 31.04
417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 28.50
439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 27.43
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 25.98
413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT,none; 25.38
418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT,none; 25.28
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisoIV,HATPase_c;SS=M; 23.58
421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig,pkinase;TM=Y;SS=M; 21.24
424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 20.45
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 19.78
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;; 18.90
427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M;; 18.75
410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 18.63
444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypotheti; Collagen;TM=M;SS=M; 18.60
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd_glycop;TM=Y;SS=M; 18.55
415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;; 18.25

413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalyti; PKI;SS=M; 17.73
427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, r; ig;TM=Y;SS=M; 17.68
450746; D82673; Hs.278589; general transcription factor II, i; none,SH3,PX; 17.12
416945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M;; 16.88
420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone_rec,zf-C4;TM=M;; 16.78
439941; AI392640; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y;; 16.75
431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 16.56
424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD_Synth,ldh,ldh_C,pkinase;SS=M; 16.43
414883; AA926960; ; CDC28 protein kinase 1; CKS;; 16.20
436091; AW373062; ; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 15.80
439963; AW247529; Hs.6793; platelet-activating factor acetylhydrola; PAF-AH_lb,Lipase_GDSL;TM=M;; 15.70
428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;; 15.63
422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 15.45
434293; NM_004445; Hs.3796; EphB6; EPH_lbd,fn3,pkinase,SAM;TM=Y;SS=M; 15.43
417880; BE241595; Hs.82648; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi;TM=M;SS=M; 15.28
443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 15.10
416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 14.90
432306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib; CBM_21;TM=M;; 14.80
413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;; 14.73
429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 14.58
449230; BE613348; Hs.211579; melanoma cell adhesion molecule; ig,isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 14.55
421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M;; 14.53
446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 14.35
429556; AW139399; Hs.98988; ESTs; none;TM=M;; 14.18
416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;SS=M; 14.13
429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ;SS=M; 13.90
426657; NM_015865; Hs.171731; solute carrier family 14 (urea transport; UT;TM=Y;; 13.83
428157; AI738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 13.80
400843; ; ; NM_003105*:Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 13.78
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;; 13.38
432314; AA533447; Hs.312989; ESTs; Xlink,none; 13.25
413109; AW389845; Hs.110855; ESTs; PHO4,none; 13.15
424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;; 13.13
426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M;; 12.93
426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 12.43
440249; AI246590; Hs.249175; ESTs; TatD_DNase,pkinase,death,none; 12.38
425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 12.38
404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36;TM=Y;SS=M; 12.03
439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 11.93
443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT; Aa_trans,none; 11.88
408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FliD,bZIP,Tropomyosin,Myc-LZ,M,ldh_C,CH,AIP3;TM=M;; 11.88
412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr;; 11.85
433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.80
425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M;; 11.69
418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 11.50
426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586I2022 (f; none;TM=Y;SS=M; 11.48
439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_lectin; 11.38
446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 11.23
436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.18
409960; BE261944; Hs.339673; hexokinase 1; none,none; 11.02
426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate_kin;TM=M;; 10.78
417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF;SS=M; 10.63
427654; AA410183; Hs.137475; ESTs; ion_trans,vwc,IGFBP,tsp_1; 10.58
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 10.53
447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (; SH3,PH,RhoGEF;TM=M;; 10.53
449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none,none; 10.52
436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;; 10.48
451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin_N;SS=M; 10.38
418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 10.35
431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subuni; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 10.34
440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 10.25
420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 10.18
437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365O12.1 [H.sa; GPS,7tm_2;TM=Y;; 10.13
400752; ; ; NM_003105*:Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 10.08
427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M;; 10.05
426728; NM_007118; Hs.171957; triple functional domain (PTPRF interact; SH3,ig,pkinase,PH,spectrin,RhoGEF;TM=M;; 10.05
400496; ; ; ENSP00000224716*:GTP-binding protein SAR; none;TM=Y;; 10.01
413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanylate_kin;TM=M;; 10.00
404568; ; ; NM_022071*:Homo sapiens hypothetical pro; SH2;TM=M;; 10.00
444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 9.93
421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm_1;TM=M;; 9.90
413441; AI929374; Hs.75367; Src-like-adapter; SH2,SH3;TM=M;; 9.90
424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,IRK;TM=M;; 9.88
452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase;TM=M;; 9.85
439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 9.83
429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y_phosphatase;TM=Y;SS=M; 9.80
414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M;; 9.73
452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none,none; 9.73
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;; 9.72
403912; ; ; C5000394*:gi|12737280|ref|XP_006682.2| k; none;TM=M;; 9.70
427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 9.70

428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xe; pkinase;TM=M;; 9.68
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;; 9.63
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;; 9.63
425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_PI4_kinase,FAT,FATC;TM=M;; 9.55
430259; BE550182; Hs.127826; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 9.50
428520; AA331901; Hs.184736; hypothetical protein FLJ10097; none;TM=M;; 9.50
418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;; 9.50
448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;; 9.50
414911; NM_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40,homeobox,LIM;TM=M;; 9.48
451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene ; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 9.45
402328; ; ; Target Exon; pkinase;TM=M;; 9.44
443710; AI928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha,none; 9.42
414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 9.42
434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin;SS=M; 9.40
418827; BE327311; Hs.47166; HT021; none;TM=M;; 9.40
440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase,none; 9.35
433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;SS=M; 9.28
410668; BE379794; Hs.65403; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 9.25
430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 9.23
452696; AI826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate_kin,PDZ,SH3; 9.13
434263; N34895; Hs.44648, ESTs; ig,none; 9.13
407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell ; Ribosomal_S14,ank,pkinase,death,none; 9.10
429332; AF030403; Hs.199263; Ste-20 related kinase; pkinase,metalthio;TM=M;SS=M; 9.08
417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,integrin_B;SS=M; 9.08
443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22_Claudin,none; 9.07
414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 8.98
451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;; 8.93
438000; AI825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M;; 8.90
446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.90
436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.88
437056; AI147061; ; gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S; none,spectrin,SH3,PH,CH; 8.78
445496; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArfGap;TM=M;; 8.78
418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 8.75
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 8.70
445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank;; 8.68
417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 8.65
432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y_phosphatase;SS=M; 8.65
430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;; 8.64
448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;; 8.60
442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 8.60
429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M;; 8.60
455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8_HUMAN ALU S; none,7tm_1; 8.55
437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 ; TIMP,pkinase,DAG_PE-bind,RBD; 8.43
417035; AA192455; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA se; none,none; 8.40
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 8.39
448209; AW160489; Hs.20709; tetraspan 5; transmembrane4;TM=Y;SS=M; 8.33
450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 8.33
445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M;; 8.31
427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a l; 7tm_1;TM=Y;SS=M; 8.30
445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 8.28
446719; W39500; Hs.301872; hypothetical protein MGC4840; AAA,SKI;TM=M;; 8.23
424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none,none; 8.20
427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 8.18
416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none,none; 8.15
419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS,zf-C2H2,SET; 8.15
417386; AL037228; Hs.82043; D123 gene product; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 8.13
431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 8.10
439656; AA332057; Hs.6639; hypothetical protein MGC15440; none;TM=M;SS=M; 8.09
425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;; 8.08
422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin_A,none; 8.05
408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 8.03
447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase;SS=M; 8.03
404891; ; ; Target Exon; none,none; 7.95
414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none,none; 7.93
452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 7.93
433211; H11850; Hs.12608; MARK; pkinase,UBA,KA1;SS=M; 7.91
438485; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase,ABC1,none; 7.90
413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.90
417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan_ur_permease,RA; 7.88
427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2,; Furin-like,pkinase,Recep_L_domain,YLP;TM=Y;SS=M; 7.86
405036; ; ; NM_021628*:Homo sapiens arachidonate lip; lipoxygenase,complex1_49Kd,PLAT;TM=M;; 7.83
418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 7.83
431912; AI660552; Hs.76549; ESTs, Weakly similar to A56154 Abl subst; none,Acyl-CoA_dh,Acyl-CoA_dh_M,Acyl-CoA_dh_N; 7.80
432981; NM_002733; Hs.3136; protein kinase, AMP-activated, gamma 1 n; CBS,Aa_trans;TM=M;; 7.78
422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo; Sec7,PH,ANF_receptor,lig_chan,WD40,IRK; 7.78
446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonin; CNH,DAG_PE-bind,PH,Involucrin,M;TM=M;; 7.78
431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 7.78
400845; ; ; NM_003105*:Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 7.73
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 7.73
437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ_con,Y_phosphatase,SH2; 7.70
403212; ; ; NM_019595:Homo sapiens intersectin 2 (IT; SH3,efhand,C2,PH,RhoGEF;TM=M;; 7.70
441190; H09073; Hs.25046; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,none; 7.68

409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 7.68
428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,pkinase;SS=M; 7.65
447898; AW969638; Hs.112318; 6.2 kd protein; none,none; 7.65
425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;SS=M; 7.63
401927; ; ; C17000914*:gi|8394367|ref|NP_058549.1| s; none;; 7.60
407347; AA829847; ; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens; RhoGAP,SH2,pkinase,POLO_box,none; 7.58
449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3,none; 7.57
429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 7.55
445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none,none; 7.55
421489; AI922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylatekinase,SRP54;TM=M;; 7.50
430570; AI417881; Hs.292464; ESTs; 7tm_2,Fz,Frizzled,none; 7.50
431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;; 7.48
420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 7.48
444252; R21135; Hs.54985; ESTs; none,none; 7.47
414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_PI4_kinase;TM=M;; 7.47
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;; 7.45
418546; AA224627; ; gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens ; vwa,integrin_A,FG-GAP,none; 7.45
437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 7.43
452007; AA426234; Hs.34906; ESTs, Weakly similar to T17210 hypotheti; none,pkinase; 7.40
432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 neuronal pr; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPc,tsp_1,Ribosomal_S21,rvp;TM=M;; 7.40
424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M;; 7.40
421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-li; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 7.38
430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y;; 7.38
422813; AV656571; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (; none,spectrin,SH3,PH,CH; 7.25
409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;; 7.24
444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M;; 7.23
452617; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M;; 7.19
407591; NM_000910; Hs.37125; neuropeptide Y receptor Y2; 7tm_1;TM=Y;; 7.18
427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M;; 7.18
403344; ; ; NM_000341:Homo sapiens solute carrier fa; alpha-amylase;TM=Y;; 7.15
427268; X78520; Hs.174139; chloride channel 3; CBS,voltage_CLC;TM=Y;; 7.14
442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 7.14
404875; ; ; NM_022819*:Homo sapiens phospholipase A2; phoslip;SS=M; 7.11
433618; AA602539; Hs.345494; ESTs; G-alpha,A_deaminase; 7.10
417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.08
413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 7.05
426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M;; 7.05
423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 7.03
400211; ; ; NM_003899*:Homo sapiens PAK-interacting ; SH3,PH,RhoGEF,Terpene_synth;TM=M;; 7.03
438150; AA037534; Hs.342874; transforming growth factor, beta recepto; zona_pellucida,none; 6.93
431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M;; 6.93
405275; AB028989; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
415392; Z44067; Hs.10957; ESTs; PIP5K,none; 6.89
429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadillo_seg,none; 6.88
429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, ; C2,PLA2_B;TM=M;; 6.85
427832; AF038362; Hs.180930; TBP-associated factor 172; SNF2_N,helicase_C,Armadillo_seg,HEAT;TM=M;; 6.83
447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;; 6.80
400158; ; ; ENSP00000244302*:CDNA FLJ11591 fis, clon; Sm;SS=M; 6.78
401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,ion_trans,PAC,PAS,none; 6.78
400844; ; ; NM_003105*:Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 6.73
457238; U07358; Hs.211601; mitogen-activated protein kinase kinase ; pkinase;; 6.73
404440; ; ; NM_021048:Homo sapiens melanoma antigen,; MAGE;TM=M;; 6.73
424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kina; Ets,SAM_PNT;TM=M;; 6.70
426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase;TM=M;; 6.70
429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65
450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin;SS=M; 6.64
408638; AW451353; Hs.173328; ESTs; B56,none; 6.63
408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
401057; BE563196; ; eukaryotic translation elongation factor; ion_trans,IQ;TM=Y;; 6.60
446526; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none,none; 6.60
400528; ; ; NM_020975*:Homo sapiens ret proto-oncoge; cadherin,pkinase;TM=Y;SS=M; 6.58
418562; R60669; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57
453826; AL138129; ; gb:DKFZp547F152_r1 547 (synonym: hfbr1) ; PK,PK_C,none; 6.55
437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC_tran,GTP_EFTU,ABC_membrane,none; 6.54
415088; AI077288; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 6.50
453489; AA300067; Hs.33032; hypothetical protein DKFZp434N185; F5_F8_type_C,pkinase,Ets,F5_F8_type_C,pkinase,Ets; 6.47
439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M;; 6.46
456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M;; 6.46
441712; AW391927; Hs.7946; KIAA1288 protein; AIP3;TM=M;; 6.44
414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; pkinase,7tm_1; 6.43
432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M;; 6.43
432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40
438941; AF075047; Hs.31864; ESTs; Ca_channel_B,SH3,arf,none; 6.40
441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB,none; 6.33
438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypotheti; lipoxygenase,PLAT,none; 6.33
433255; AI274270; Hs.96840; KIAA1527 protein; MHCK_EF2_kinase;TM=M;SS=M; 6.33
427801; AW979155; Hs.298275; amino acid transporter 2; Aa_trans;TM=M;SS=M; 6.32

407970; AW403814; Hs.41714; BCL2-associated athanogene; ubiquitin,BAG,Tropomyosin;; 6.30
438464; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none,none; 6.30
453977; AA886006; Hs.250427; ESTs; pkinase,P2X_receptor,E1-E2_ATPase,Hydrolase; 6.30
412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras,arf,PP2C;TM=M;; 6.30
413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180kD); DNA_gyraseB,DNA_topoisolV,HATPase_c,DNA_gyraseB,DNA_topoisolV,HATPase_c; 6.29
404342; ; ; C7002192*:gi|7299207|gb|AAF54404.1| (AE0; none;TM=M;; 6.27
409274; NM_003930; Hs.52644; SKAP55 homologue; SH3,PH;SS=M; 6.25
419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 6.23
405429; ; ; Target Exon; Y_phosphatase,none; 6.23
404975; AL042279; ; uncharacterized hypothalamus protein HT0; kringle;TM=Y;SS=M; 6.20
452929; AW954938; Hs.172816; neuregulin 1; Neuregulin,EGF,ig,Neuregulin,EGF,ig; 6.18
446883; AW452756; Hs.16364; hypothetical protein FLJ10955; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPc,tsp_1,Ribosomal_S21,rvp;TM=M;; 6.18
433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M;; 6.15
458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 6.15
421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none,none; 6.14
447727; AI421079; ; tumor necrosis factor receptor superfami; none,synaptobrevin; 6.13
401536; ; ; NM_002530*:Homo sapiens neurotrophic tyr; ig,pkinase,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.11
444317; AI140566; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H.; PAN,kringle,trypsin,PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN; 6.10
427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6,ET,PLA2_inh;SS=M; 6.08
450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;; 6.08
450107; AI873287; Hs.257812; ESTs; ICE_p20,DED;TM=M;; 6.05
418175; AW967054; Hs.206312; ESTs, Weakly similar to I38022 hypotheti; zf-C2H2,BTB,K_tetra,Syntaxin,none; 6.05
408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran,ABC_membrane,PRK,Bac_export_3;TM=Y;; 6.05
439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig),; Sema,PSI,integrin_B;TM=Y;; 6.03
427625; AF008216; Hs.285013; putative human HLA class II associated p; none,none; 6.03
409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.03
446650; AB016625; Hs.15813; solute carrier family 22 (organic cation; sugar_tr;TM=Y;SS=M; 6.03
405102; ; ; C15001220*:gi|4469558|gb|AAD21311.1| (AF; DAG_PE-bind,PH,RhoGEF,DC1;SS=M; 6.03
400121; ; ; Eos Control; SH3,PH,RhoGEF,Terpene_synth;TM=M;; 6.03
415327; H22769; ; gb:ym54c02.r1 Soares infant brain 1NIB H; SH3,PDZ,Guanylate_kin;SS=M; 6.03
404148; ; ; NM_002944*:Homo sapiens v-ros avian UR2 ; fn3,pkinase,DUF139;TM=Y;SS=M; 6.03
405531; ; ; Target Exon; PDZ,CARD,Guanylate_kin;TM=M;; 6.00
433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B) ; NDK,none; 6.00
427270; H47921; Hs.174139; chloride channel 3; voltage_CLC,CBS,none; 5.99
423774; L39064; Hs.1702; interleukin 9 receptor; none;TM=M;SS=M; 5.98
424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked ; pkinase,TBC; 5.98
411040; AF007393; Hs.177574; protein-kinase, interferon-inducible dou; HLH;TM=M;; 5.95
423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer,7tm_1,none; 5.88
453902; BE502341; Hs.3402; ESTs; none,none; 5.88
409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y;; 5.86
436154; AA764950; Hs.119898; ESTs; efhand,DAG_PE-bind,DAGKa,PHD,DAGKc,PSI,none; 5.85
455358; AW902641; ; gb:QV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase,Somatomedin_B,Phosphodiest,none; 5.83
414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;; 5.82
452547; AA335295; Hs.74120; adipose specific 2; LEA;TM=M;; 5.82
415204; T27434; ; gb:hbc2294 Human pancreatic islet Homo s; Na_Ca_Ex,Calx-beta,none; 5.80
435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;; 5.78
456097; C15702; Hs.288028; ESTs, Moderately similar to I54374 gene ; dsrm,FKBP; 5.78
422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle,; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase;TM=Y;; 5.77
436246; AW450963; Hs.119991; ESTs; none,DNA_gyraseB,DNA_topoisolV,HATPase_c; 5.75
422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC_tran,PRK;TM=Y;SS=M; 5.75
425854; AA749190; ; ESTs; RhoGAP,SH2,pkinase,POLO_box,none; 5.74
424160; T74062; ; gb:yc81f01.r1 Soares infant brain 1NIB H; ROK,none; 5.70
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 5.69
437613; R19892; Hs.10267; MIL1 protein; none,none; 5.68
410820; BE391493; Hs.16475; Human DNA sequence from clone RP5-852M4 ; TBC;SS=M; 5.68
423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M;; 5.66
426500; NM_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;; 5.63
406930; U04691; ; gb:Human olfactory receptor (OR17-219) g; none;TM=Y;SS=M; 5.60
401044; ; ; Target Exon; none,ICE_p20,ICE_p10,CARD,Peptidase_M1; 5.56
428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 5.55
421970; AF227156; Hs.110103; RNA polymerase I transcription factor RR; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;; 5.53
426248; T18988; Hs.293668; ESTs; pkinase,none; 5.50
418426; NM_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pkinase,death;TM=M;; 5.43
417086; AA194446; ; ESTs, Weakly similar to S55024 nebulin, ; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.43
447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupl; 7tm_1,SH2;TM=Y;SS=M; 5.40
412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF;SS=M; 5.40
434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, com; pkinase,TBC,Rhodanese;TM=M;; 5.38
419355; AA428520; Hs.90061; progesterone binding protein; heme_1;TM=Y;SS=M; 5.35
411188; BE161168; ; gb:PM0-HT0425-170100-002-a10 HT0425 Homo; adenylatekinase,none; 5.35
422461; NM_003417; Hs.117077; zinc finger protein 264; zf-C2H2,KRAB,TFIIS;TM=M;; 5.28
426348; BE466586; Hs.17433; hypothetical protein FLJ20967; none,none; 5.25
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;; 5.23
429592; AB029041; Hs.209646; KIAA1118 protein; Troponin,Exo_endo_phos,IQ;TM=M;; 5.22
434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER_lumen_recept,Ribosomal_L11,Ribosomal_L11_N;TM=Y;SS=M; 5.21
434368; AW519020; Hs.73893; dopamine receptor D2; pkinase,SH3,none; 5.15
405586; ; ; NM_000299:Homo sapiens plakophilin 1 (ec; Armadillo_seg;TM=M;; 5.13
408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase,none; 5.12
407443; AF227138; ; gb:Homo sapiens candidate taste receptor; none;TM=Y;SS=M; 5.11
416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recep_L_domain,fn3,none; 5.10
401886; ; ; NM_021783:Homo sapiens XEDAR (XEDAR), mR; TNFR_c6;TM=M;SS=M; 5.08
410314; AW360708; Hs.18851; hypothetical protein FLJ10675; myb_DNA-binding,PAH,BAH,bromodomain,PHD,SET;TM=M;; 5.08

401579; AL031447; ; Homo sapiens, clone IMAGE:4053044, mRNA,; Neur_chan_LBD,Neur_chan_memb,none; 5.05
445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-l; PABP,rrm,pkinase,14-3-3; 5.05
417529; AA203634; ; gb:zx58b09.r1 Soares_fetal_liver_spleen_; pkinase,UBA,KA1,none; 5.03
417527; AA203524; ; gb:zx56e10.r1 Soares_fetal_liver_spleen_; SH3;SS=M; 4.98
407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfkB;TM=M;; 4.96
431321; AW136372; Hs.1852; acid phosphatase, prostate; acid_phosphat,none; 4.93
404298; ; ; C6001238*:gi|121715|sp|P26697|GTA3_CHICK; none,GST_C,GST_N,pkinase; 4.85
407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA,; none;TM=M;; 4.82
424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;; 4.73
422366; T83882; Hs.97927; ESTs; pkinase,none; 4.64
424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M;; 4.48
426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone H; Esterase,enolase,Peptidase_S9;TM=M;; 4.45
439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 4.40
400749; ; ; NM_003105*:Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.38
425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4;TM=Y;SS=M; 4.33
444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_a,PKD,MHC_I;TM=M;SS=Y; 4.31
400751; ; ; NM_003105*:Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.18
408906; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;SS=M; 3.90
422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none,none; 3.88
458760; Al498631; Hs.111334; ferritin, light polypeptide; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.85
441218; BE327561; Hs.202345; ESTs; none,WD40,E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase; 3.78
419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death,ZU5;SS=M; 3.76
451385; AA017656; ; gb:ze39h01.r1 Soares retina N2b4HR Homo ; Atrophin-1,enolase,Atrophin-1,Y_phosphatase,SH2,fibrinogen_C,TIM; 3.60
412604; AW978324; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;; 3.30
409582; R27430; Hs.271565; ESTs; none,Neur_chan_LBD,Neur_chan_memb; 3.28
441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1_LC3;SS=M; 3.23
436740; AW975133; ; gb:EST387239 MAGE resequences, MAGN Homo; none,EPH_lbd,fn3,pkinase,SAM; 3.20
418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked ; none,IRK; 3.20
409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none;NA;NA; 3.13
418764; N30531; Hs.42215; protein phosphatase 1, regulatory subuni; none,none; 3.10
400846; ; ; sortilin-related receptor, L(DLR class) ; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 3.09
422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (fr; none,Na_H_Exchanger; 3.03
426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 3.02
424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 2.98
425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death,TNFR_c6;TM=Y;SS=M; 2.93
401279; ; ; C13000351*:gi|2494033|sp|Q64398|KDGD_MES; none,none; 2.88
406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema,pkinase,TIG,PSI,none; 2.83
447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK;TM=Y;; 2.80
453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase;TM=M;; 2.75
441699; AW511126; Hs.127572; ESTs; none,Aa_trans; 2.73
458781; Al444821; Hs.63085; ESTs, Weakly similar to MPP3_HUMAN MAGUK; SH3,PDZ,Guanylate_kin,L27;TM=M;; 2.73
446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tetr; transmembrane4;TM=Y;SS=M; 2.70
453487; R31770; Hs.56562; ESTs; 7tm_1,none; 2.68
421279; AW664878; Hs.106645; ESTs; pkinase,none; 2.68
419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none,none; 2.65
452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc;TM=M;; 2.63
422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF;TM=Y;; 2.62
425212; AW962253; Hs.171618; ESTs; pkinase,none; 2.60
427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 2.58
423629; AW021173; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage_CLC,CBS,none; 2.55
456737; BE247203; Hs.124831; CGI-67 protein; abhydrolase_2;TM=M;SS=M; 2.53
421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1;TM=Y;SS=M; 2.53
424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y7; none,none; 2.50
448324; Al571356; Hs.34174; ESTs, Moderately similar to ALU8_HUMAN A; ICE_p20,CARD,ICE_p10,none; 2.50
402256; ; ; Target Exon; pkinase,UBA,none; 2.43
452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI,7tm_1,none; 2.40
419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypotheti; none,spectrin,SH3,PH,CH; 2.40
420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP_binding,ion_trans;TM=Y;; 2.35
419630; W57756; ; gb:zd20g10.r1 Soares_fetal_heart_NbHH19W; zf-C3HC4,none; 2.35
426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1;TM=Y;SS=M; 2.35
400704; ; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor;TM=Y;SS=M; 2.33
400149; ; ; Eos Control; acid_phosphat;TM=Y;SS=M; 2.30
459327; AW149706; Hs.7859; gb:xf41d02.x1 NCI_CGAP_Bm50 Homo sapien; PHD,PWWP,SET,pkinase,ig; 2.30
452220; BE158006; Hs.212296; ESTs; integrin_A,FG-GAP,none; 2.25
416690; H84078; Hs.108551; ESTs; pkinase,none; 2.23
408354; Al382803; Hs.159235; ESTs; none,none; 2.23
452203; X57522; ; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 2.21
405093; ; ; C12001101*:gi|7522643|pir||T32733 AMPA g; none,none; 2.20
412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M;; 2.20
418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none,none; 2.18
417185; NM_002484; Hs.81469; nucleotide binding protein 1 (E.coli Min; ParA,fer4_NifH,ArsA_ATPase;TM=M;; 2.18
433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none,PHO4; 2.18
413627; BE182082; Hs.246973; ESTs; Armadillo_seg,IBB;TM=M;; 2.18
407415; AF073328; ; gb:Homo sapiens tetracyline transporter-; none,none; 2.15
450592; Al701555; Hs.202562; ESTs; pkinase,none; 2.15
426767; Al421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1 ; none,pkinase,ig; 2.15
429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm,BAG;SS=M; 2.15
419122; Al401360; Hs.44410; ESTs; ABC_tran,ABC_membrane,none; 2.10
446420; AW015693; Hs.135614; ESTs; ion_trans,none; 2.05
420076; AA827860; Hs.293717; ESTs; DUF59,pkinase; 2.05
409416; AW388359; Hs.10667; ESTs; transmembrane4;TM=Y;SS=M; 2.03
428766; AA477989; Hs.98800; ESTs; TPR,7tm_1; 2.03
427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;TM=M;; 2.03

453709; AL119133; ; protein kinase C substrate 80K-H; none,histone; 2.03
423341; AW242394; Hs.108660; ESTs; none,none; 2.00
456772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.88
427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7tm_1; 1.65
423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.00
447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 58B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA356689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H43870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
433470	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895

			AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
	437056	428504_3	AW976398 AI147061 AA765223 AA743380 AI803927
	422940	58443_1	BC012771 BG397153 BF366196 AA337277 AA319285 AW843252
	409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
	407347	810943_1	T23514 AI655785
	418546	242836_1	T59708 AA224827 T59843 BE156903
	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
	423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138
	400211	3532_1	NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
	400158	2166_1	BC000486 BC001930 U15008 NM_004597 BG326561 AV761269 BF212132 BG113313 BI838038 BG944198 BG255198 BG164334 BM013507 AV682717 BF028761 BG755489 BG030141 BG105499 BE440103 BF727449 BM454228 BG912181 BM015197 BG395995 AI126579 AW248204 BI857394 BI857319 BG944205 BG323958 BI092930 AV756576 AA280959 BF033078 BE539360 AW247174 BG107836 BE796975 BG170920 AI148142 AI092009 AI336349 AV713409 BF685591 BE616029 AV713166 BE909458 BE743868 BM018218 AI340153 BE792567 BE206806 AI159916 AI184271 BE208585 BI862286 C18760 BG219364 AI122677 BE207297 BF754798 AA314384 BE873951 BG207294 AI148198 AI336189 AI141094 AI308985 BF220098 AI143289 BE856397 AA644001 BE675402 AJ346708 AI052809 AI140082 BF081542 AI342428 AI479625 AA278456 AI750163 BE707501 BG944510 AA314616 AA315774 BF360721 BE738404 AA814194 AA477195 AA932107 F36858 AA363159 BE865458 AA354147 AW904224 AI055855 AA380365 F28474 D59140 AA341946 AA993339 AA323350 F24344 AA374436 BG942061 AA636015 AA852919 T31486 F36334 BG943190 T30319 BG943153 BG941836 T32569 T31160 AA311749 BE710086 BE709911 W23826 BG941639 BF769034 AA026407 AA229555 AV756340 AV714380
	453826	366136_1	AL138129 BG003205 AL138179 BI021773 BE064231
	447727	10123_14	AL520734 BI666852 BF870571 BF945361 BF945354 AI770086 BI861138 AI421079 AL043200 BG683612 AW946265
	400121	3532_1	NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
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	455358	1160035_1	AW902569 AW902557 AW902654 AW902641 AW902650 AW902741 AW902644
	415204	1865508_1	Z25288 R85077 F00323 D82802 T27434
	425854	2638_3	BF184345 AA364846 BI494468 AA775693 BF195801 AA749190 AI480223 BE327332 AI470017 AW628345 AI917472 AI972264 AI375571 AI652583 AI656167 AI983110 BE550378 AW015085 BE552318 AI631475 AI433447 AA534540 AI865480 AI468119 BF110875 AW512059 W58721 AA827482 R59357
	424160	5320_3	AW370493 AA923304 AI660828 AA502611 BI017370 AA039704 W65393 BE938514 W65295 BF919626 BI759440 BI838879 AA336207 F12441 BF171187 BE185031 T74062 AW904410 AA280078 BF919629
	417086	1154_2	AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176595 AA176955 AA194350 BC005933 BC017866 AA196396 Z24810 AA181361 AA193115 AA086465 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 AI620346 BG986374 BE706521 C02691 AL596834 F31902 F26078 AA670099 BF475555 F30818 F37524 AJ346558 F26050 F17933 F31637 C03413 AI092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546
	411188	1072487_1	AW821260 BE162466 BE161168
	417529	3302462_-1	AA203634
	417527	2431831_1	AA203524 W88451
	451385	85022_1	AA019761 AA017656 AA017374
	436740	1239008_1	AW975133 AA805813 AA729943
	419630	37310_5	BF223647 AA204668 AA256086 BF574707 W57756 AA249070 BI906494 AA248011
	400149	16458_1	BC003160 NM_001610 X12548 BG386685 BI760866 BI559619 BG323829 AU135543 BI834101 AU142120 AU124511 AU124889 AL558171 AU117286 BI824000 BG386610 BI753285 BI223475 AU134828 BM126369 BE206493 BF751498 AL544274 AY007137 BI828921 BE870130 BF771242 BI835451 BI765655 BI820955 BI223344 BG015924 BI759894 AL527413 BF310588 N31870 N23974 BE514914 T48863 AW860257 BF334625 AA883860 AU144168 AA442562 AU159491 AU148353 AA564123 AU148667 AI377256 AW664004 AI871712 AI141486 AI332351 AI339094 BE206109 AW519033 AI817729 AI332490 AI149455 AI857411 AI763154 AI751608 AI377222 AI081956 AW664229 AI275872 AW168546 AA975270 AI367408 AI687729 AI269164 AW105344 BM193081 BE550930 AI082116 AA854691 AI056249 AI221062 AI290113 D51818 AA732409 BG055125 N85878 AU156121

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	452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
	453709	59915_1	AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H80793 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239 AA074615 AI291059 AI681053 AA702355 BF439899 AW055166 AI096957 BF223853 AL119659 AI692209 BM312961 AI869297 BE466252 AI292024 AA402764 AI214620 AA765312 BF380770 AA442682 AL519746 AW295039 AI037878 AW473433 AI499437 AI401618 AI130831 AA427406 AI042138 BG272488 AI828769 AI828764 AI189390 W84635 AA398496 AA761672 AA699520 AI200406 N68093 AI143913 AA993133 AA613306 AI050971 AA661905 AA722687 AI749977 AA829345 BG057324 BF001339 AA910169 AA765133 AI360722 AI701849 AI365083 H95974 AI830377 AI312866 AI370491 BE858907 N62185 AA705746 BE379632 W93803 AI440333 AW367670 AW367640 N77131 BF993216 AI858263 W52329 N68106 R83113 R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 AI073567 AA004957 AI539585 N95093 H99798 H95072 H96853 AA215712 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 AI693577 BE181027 AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734 R58506

TABLE 58C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36461
400496	9743564	Plus	41515-41695
404568	9966995	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84974-85125
405036	7543748	Minus	121957-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 8.2. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420923	AF097021	Hs.273321	differentially expressed in hematopoieti	90.5
416854	H40164	Hs.80296	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	AI093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microseminoprotein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nel (chicken)-like 2	54.6
428398	AI249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.116258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7

	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	49.6
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
5	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	415314	N88802	Hs.5422	glycoprotein M6B	43.2
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
10	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	41.1
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	39.0
15	447726	AL137638	Hs.19368	matrilin 2	38.6
	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.5
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	37.0
20	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	35.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	35.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
25	415539	AI733881	Hs.72472	BMP-R1B	34.9
	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
	452114	N22687	Hs.8236	ESTs	34.0
30	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	33.8
	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AI918950	Hs.123642	EphA3	32.7
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
35	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	32.4
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
	408380	AF123050	Hs.44532	diubiquitin	31.6
40	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	31.4
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	31.2
	408001	AA046458	Hs.95296	ESTs	30.8
	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
45	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
50	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	29.2
	418827	BE327311	Hs.47166	HT021	29.0
	410330	AW023630	Hs.46786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	28.5
55	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
60	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	27.4
	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
	403047			NM_005656*:Homo sapiens transmembrane pr	27.2
65	407709	AA456135	Hs.23023	ESTs	27.0
	433444	AW975324	Hs.129816	ESTs	26.8
	415989	AI267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
	408221	AA912183	Hs.47447	ESTs	26.5
70	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	26.4
	437179	AA393508	Hs.300642	serologically defined colon cancer antig	26.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
	400292	AA250737	Hs.72472	BMP-R1B	26.0
75	433647	AA603367	Hs.222294	ESTs	26.0
	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448106	AI800470	Hs.171941	ESTs	25.5
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	25.5
80	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	418961	AW967646	Hs.23023	ESTs	24.8

451027	AW519204	Hs.40808	ESTs	24.5
413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	24.5
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	24.4
418396	AI765805	Hs.26691	ESTs	24.1
412088	AI689496	Hs.108932	ESTs	24.1
429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
411644	H92064	Hs.278626	Arg/Abl-interacting protein ArgBP2	24.0
409619	AK001015	Hs.55220	BCL2-associated athanogene 2	23.9
433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	23.6
440995	T57773	Hs.10263	ESTs	23.5
432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	22.9
440260	AI972867	Hs.7130	copine IV	22.5
443622	AI911527	Hs.11805	ESTs	22.2
426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	21.9
450642	R39773	Hs.7130	copine IV	21.9
417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
435981	H74319	Hs.188620	ESTs	21.8
450693	AW450461	Hs.203965	ESTs	21.7
444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
423242	AL039402	Hs.125783	DEME-6 protein	21.7
408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	21.6
408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
419526	AI821895	Hs.193481	ESTs	21.5
442799	AI564739	Hs.68505	ESTs	21.4
424846	AU077324	Hs.1832	neuropeptide Y	21.3
420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
431474	AL133990	Hs.190642	ESTs	21.2
430887	N66801	Hs.260287	KIAA1841 protein	21.1
416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
445133	AW157646	Hs.153506	ESTs	21.0
421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
446795	AI797713	Hs.156471	ESTs	20.7
440774	AI420611	Hs.127632	ESTs	20.7
407168	R45175	Hs.117183	ESTs	20.6
417511	AL049176	Hs.82223	chordin-like	20.6
431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	20.5
427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	20.5
424897	D63216	Hs.153684	frizzled-related protein	20.5
430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
401197			ENSP00000229263*:HSPC213.	20.3
452814	AI092790	Hs.334703	hypothetical protein FLJ14529	20.3
429918	AW873986	Hs.119383	ESTs	20.2
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	20.2
453469	AB014533	Hs.33010	KIAA0633 protein	20.2
444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
419440	AB020689	Hs.90419	KIAA0882 protein	20.0
429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
441690	R81733	Hs.33106	ESTs	19.9
423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	19.8
423044	AA320829	Hs.97266	protocadherin 18	19.8
410929	H47233	Hs.30643	ESTs	19.7
427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
431556	AF016028	Hs.183428	sarcospan (Kras oncogene-associated gene	19.6
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	19.6
444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	19.4
431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
430187	AI799909	Hs.158989	ESTs	19.3
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	19.3
434423	NM_006769	Hs.3844	LIM domain only 4	19.2
417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
436032	AA150797	Hs.109276	latexin protein	18.9
431548	AI834273	Hs.9711	novel protein	18.9
418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

445929	AI089660	Hs.323401	dpy-30-like protein	18.8
453160	AI263307	Hs.239884	H2B histone family, member L	18.8
439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	18.8
434987	AW975114	Hs.293273	ESTs	18.7
407690	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	18.7
418819	AA228776	Hs.191721	ESTs	18.7
450831	R37974	Hs.25255	ESTs	18.7
415691	AW963979	Hs.24723	ESTs	18.7
417124	BE122762	Hs.25338	ESTs	18.7
445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
436420	AA443966	Hs.31595	ESTs	18.4
427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
439569	AW602166	Hs.222399	CEGP1 protein	18.1
417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
424682	AW604804	Hs.151717	KIAA0437 protein	18.0
432435	BE218886	Hs.282070	ESTs	17.9
443547	AW271273	Hs.23767	hypothetical protein FLJ12666	17.8
431121	AW971157		gb:EST383245 MAGE resequences, MAGL Homo	17.8
410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	17.7
429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
427958	AA418000	Hs.98280	potassium intermediate/small conductance	17.6
421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
430487	D87742	Hs.241552	KIAA0268 protein	17.4
419355	AA428520	Hs.90061	progesterone binding protein	17.4
417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
434217	AW014795	Hs.23349	ESTs	17.3
439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
430177	AW969233	Hs.302746	MSTP028 protein	17.2
432473	AI202703	Hs.152414	ESTs	17.1
421823	N40850	Hs.28625	ESTs	17.1
418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
420092	AA814043	Hs.88045	ESTs	17.0
414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	17.0
417426	NM_002291	Hs.82124	laminin, beta 1	17.0
400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
401747			Homo sapiens keratin 17 (KRT17)	17.0
424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
442369	AI565071	Hs.159983	ESTs	16.9
432966	AA650114	Hs.325198	ESTs	16.9
426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	16.8
443745	AB039670	Hs.9728	ALEX1 protein	16.8
438899	AF085833	Hs.135624	ESTs	16.8
418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
442064	AI422867	Hs.88594	ESTs	16.8
409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	16.5
453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	16.4
443801	AW206942	Hs.253594	ESTs	16.3
437536	X91221	Hs.144465	ESTs	16.3
409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
416239	AL038450	Hs.48948	ESTs	16.3
448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	16.2
409060	AI815867	Hs.50130	neccin (mouse) homolog	16.1
442571	C06338	Hs.165464	ESTs	16.1
419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
450164	AI239923	Hs.30098	ESTs	16.0
429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	16.0
417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
436024	AI800041	Hs.190555	ESTs	16.0
412652	AI801777	Hs.6774	ESTs	16.0
456516	BE172704	Hs.222746	KIAA1610 protein	16.0
452576	AB023177	Hs.29900	KIAA0960 protein	15.9
430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
434792	AA649253	Hs.132458	ESTs	15.9
418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
5	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
10	426501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	15.6
	434988	AI418055	Hs.161160	ESTs	15.6
15	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.5
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	15.5
20	415672	N53097	Hs.193579	ESTs	15.5
	450325	AI935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	15.4
	443674	AI081330	Hs.145008	ESTs	15.4
	415263	AA948033	Hs.130853	ESTs	15.4
25	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
	418693	AI750878	Hs.87409	thrombospondin 1	15.3
30	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
	446091	AW022192	Hs.200197	ESTs	15.2
35	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	15.1
40	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	15.0
	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
45	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	tumican	15.0
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
50	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
	453510	AI699482	Hs.42151	ESTs	14.8
55	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	14.8
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
60	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	426044	AA502490	Hs.336695	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
65	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	14.7
	433226	AW503733	Hs.9414	KIAA1488 protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-l	14.6
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	14.6
70	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0966 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	14.5
	410339	AI916499	Hs.298258	ESTs	14.5
75	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.146858	protocadherin 10	14.5
	431933	AI187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	14.5
80	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413786	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
	416836	D54745	Hs.80247	cholecystokinin	14.4
5	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chai	14.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	14.2
10	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	AI927288	Hs.196779	ESTs	14.2
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	14.2
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	14.2
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
15	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	14.1
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
20	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbb2-interacting protein ERBIN	13.9
	418848	AI820961	Hs.193465	ESTs	13.9
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
25	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153026	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
	447384	AI377221	Hs.40528	ESTs	13.9
30	444880	AW118683	Hs.154150	ESTs	13.9
	433409	AI278802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
35	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
40	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	13.8
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
45	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96667	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
50	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
55	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
	410001	AB041036	Hs.57771	kallikrein 11	13.6
60	452242	R50956	Hs.159993	gycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021965*:Homo sapiens phosphoglucomuta	13.6
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfami	13.6
	414279	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	13.6
65	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
70	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
	447082	T65314	Hs.42644	thioredoxin-like	13.5
75	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypotheti	13.3
	433517	AW022133	Hs.189838	ESTs	13.3
80	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (	13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371145	Hs.226627	leptin receptor	13.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
5	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
	407938	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
10	409277	T05558	Hs.156880	ESTs	13.2
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
15	408495	W68796	Hs.237731	ESTs	13.1
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI362575	Hs.167133	ESTs	13.0
20	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
25	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
	448779	BE042877	Hs.177135	ESTs	12.8
30	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
	417315	AI080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW296451	Hs.24605	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
35	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA992480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	12.7
40	452512	AW363486	Hs.337635	ESTs	12.7
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
	442501	AA315267	Hs.23128	ESTs	12.7
45	434466	AB037829	Hs.3662	regulator of nonsense transcripts 2; DKF	12.7
	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AB040928	Hs.65366	KIAA1495 protein	12.6
	453830	AA534296	Hs.20953	ESTs	12.6
	409995	AW960597	Hs.30164	ESTs	12.6
50	414290	AI568801	Hs.71721	ESTs	12.6
	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
55	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
	427078	AI676062	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
60	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	12.5
65	420345	AW295230	Hs.25231	ESTs	12.4
	432205	AI806583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
70	404642			NM_021965*:Homo sapiens phosphoglucomuta	12.4
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI459306	Hs.24908	ESTs	12.4
75	441269	AW015206	Hs.178784	ESTs	12.3
	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
80	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165590	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

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	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	12.2
	400880			NM_000611*:Homo sapiens CD59 antigen p18	12.2
	425920	AL049977	Hs.162209	claudin 8	12.2
5	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
10	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449625	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	12.1
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
15	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
20	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AI085198	Hs.164226	ESTs	12.0
	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984625	Hs.9884	spindle pole body protein	12.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
25	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
	436746	AA730045	Hs.187866	ESTs	11.9
30	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206088	ESTs, Moderately similar to ALU8_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42683	ESTs	11.8
	431645	AF078849	Hs.266483	dynein light chain-A	11.8
35	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
	426981	AL044675	Hs.173081	KIAA0530 protein	11.8
40	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
	438032	BE045624	Hs.152992	ESTs	11.7
45	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
	423782	AI472209	Hs.323117	ESTs	11.6
50	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
	411096	U80034	Hs.58583	mitochondrial intermediate peptidase	11.5
55	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methenyltetrahydrofolate synthetase	11.5
	412677	AW029608	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
60	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
65	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674585	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
70	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	11.4
	456804	AI421645	Hs.139851	caveolin 2	11.4
75	422546	AB007969	Hs.301478	KIAA0500 protein	11.4
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
	433577	AW007080	Hs.8817	ESTs	11.4
80	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AI473827	Hs.31793	ESTs	11.3

	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
5	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476*:gi|12737279|ref|XP_012163.1|	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	11.2
10	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.116410	ESTs	11.2
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
15	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
20	434158	T86534	Hs.14372	ESTs	11.1
	414341	D80004	Hs.75909	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
25	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
30	433230	AW136134	Hs.220277	ESTs	11.0
	412622	AW664708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
35	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
40	450244	AA007534	Hs.125062	ESTs	11.0
	417169	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104696	KIAA1324 protein	10.9
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
45	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.156110	immunoglobulin kappa constant	10.9
	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
	441540	C01367	Hs.127128	ESTs	10.9
50	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	10.9
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI623752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcospan (Kras oncogene-associated gene	10.8
	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
55	447982	H22953	Hs.137551	ESTs	10.8
	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phosphodiesterase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	10.8
60	419326	W94915	Hs.42419	ESTs	10.8
	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
	450206	AI796450	Hs.201600	ESTs	10.8
65	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 8	10.8
	439492	AF086310	Hs.103159	ESTs	10.8
70	413492	D87470	Hs.75400	KIAA0280 protein	10.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
	417665	AW852858	Hs.22862	ESTs	10.7
75	433285	AW975944	Hs.237396	ESTs	10.7
	419693	AA133749	Hs.301350	FXYD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
80	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7

433923	AI823453	Hs.146625	ESTs	10.7
418196	AI745649	Hs.26549	KIAA1708 protein	10.7
416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	10.7
430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
429350	AI754634	Hs.131987	ESTs	10.7
418601	AA279490	Hs.86368	calmegin	10.6
437267	AW511443	Hs.258110	ESTs	10.6
432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	10.6
414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
418662	AI801098	Hs.151500	ESTs	10.6
449685	AW296669	Hs.66095	ESTs	10.6
441111	AI806867	Hs.126594	ESTs	10.6
436671	AW137159	Hs.146151	ESTs	10.6
447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.6
417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.6
424562	AI420859	Hs.150557	basic transcription element binding prot	10.6
408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
439584	AA838114	Hs.221612	ESTs	10.6
426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
420929	AI694143	Hs.296251	programmed cell death 4	10.6
418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
424433	H04607	Hs.9218	ESTs	10.6
420230	AL034344	Hs.284186	forkhead box C1	10.6
419441	AW023731	Hs.274368	MSTP032 protein	10.6
426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
451900	AB023199	Hs.27207	KIAA0982 protein	10.6
424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
424368	AB037766	Hs.146085	KIAA1345 protein	10.5
402076			C5002020*:gi|1082876|pir||S55467 tropomy	10.5
413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
445041	T64183	Hs.282982	solute carrier	10.5
428927	AA441837	Hs.90250	ESTs	10.5
414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	10.5
407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
452055	AI377431	Hs.141693	hypothetical protein MGC10858	10.5
438913	AI380429	Hs.172445	ESTs	10.5
443684	AI681307	Hs.55098	ESTs	10.5
429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
421040	AA715026	Hs.135280	ESTs	10.5
425277	NM_001241	Hs.155478	cyclin T2	10.5
418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	10.5
440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
419972	AL041465	Hs.182982	golgin-67	10.5
416182	NM_004354	Hs.79069	cyclin G2	10.4
418365	AW014345	Hs.161690	ESTs	10.4
452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	10.4
446716	AA436575	Hs.16602	ESTs	10.4
419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.4
433023	AW864793	Hs.87409	thrombospondin 1	10.4
409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
443228	W24781	Hs.293798	KIAA1710 protein	10.4
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
428728	NM_016625	Hs.191381	hypothetical protein	10.4
423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	10.4
413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
411359	H86088	Hs.22635	ESTs	10.3
420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
412262	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
419875	AA853410	Hs.93557	proenkephalin	10.3
414422	AA147224	Hs.337232	Homeo box A13	10.3
426581	AB040956	Hs.135890	KIAA1523 protein	10.3
424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	10.3
438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	10.3
451593	AF151879	Hs.26706	CGI-121 protein	10.3
435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	10.3
438157	AW137011	Hs.49576	ESTs	10.3

443181	AI039201	Hs.283316	ESTs	10.3
449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	10.2
446553	AB021179	Hs.15299	HMBA-inducible	10.2
418278	AI088489	Hs.83937	hypothetical protein	10.2
419791	AI579909	Hs.105104	ESTs	10.2
418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	10.2
445564	AB028957	Hs.12896	KIAA1034 protein	10.2
435021	AA922192	Hs.54709	ESTs	10.2
457498	AI732230	Hs.191737	ESTs	10.2
425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	10.2
427393	AB029018	Hs.177635	KIAA1095 protein	10.1
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	10.1
437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
448172	N75276	Hs.135904	ESTs	10.1
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
410150	AW382942	Hs.6774	ESTs	10.1
444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	10.1
448148	NM_016578	Hs.20509	HBV pX associated protein-8	10.1
443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
450205	AI219748	Hs.11356	ESTs	10.1
408374	AW025430	Hs.155591	forkhead box F1	10.0
446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
432589	AL135725	Hs.131708	ESTs	10.0
435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
419672	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
444564	AI167877	Hs.143716	ESTs	10.0
426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	10.0
451424	AI862026	Hs.302810	Novel human gene mapping to chomosome 20	10.0
433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	10.0
427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
418884	AA230228	Hs.59197	ESTs	10.0
444821	AA053564	Hs.12040	STE20-like kinase	9.9
451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
453127	AI696671	Hs.294110	ESTs	9.9
435706	W31254	Hs.7045	GL004 protein	9.9
410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	9.9
408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
432887	AI926047	Hs.162859	ESTs	9.9
430291	AV660345	Hs.238126	CGI-49 protein	9.9
440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	9.9
441054	AA913591	Hs.126480	ESTs	9.9
415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
453078	AF053551	Hs.31584	metaxin 2	9.8
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
446720	AI439136	Hs.140546	ESTs	9.8
418475	AI858732	Hs.30443	sentrin/SUMO-specific protease	9.8
417708	N74392	Hs.50495	ESTs	9.8
407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
420568	F09247	Hs.247735	protocadherin alpha 10	9.8
418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
453548	AL079983	Hs.116774	integrin, alpha 1	9.8
427308	D26067	Hs.174905	KIAA0033 protein	9.8
434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	9.8
434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
413174	AA723564	Hs.191343	ESTs	9.8
443250	AI041530	Hs.132107	ESTs	9.8
451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	9.8
422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
427635	BE397988	Hs.179982	tumor protein p53-binding protein	9.8
416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
	404571			NM_015902*:Homo sapiens progestin induce	9.7
5	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439163	AW970600	Hs.303261	ESTs	9.7
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278626	Arg/Abl-interacting protein ArgBP2	9.7
	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
10	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	9.7
	417171	BE613486	Hs.81412	lipin 1	9.7
15	421709	AA159394	Hs.107056	CED-6 protein	9.7
	415156	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
20	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409190	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
25	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523939	Hs.165258	ESTs	9.6
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
	439671	AW162840	Hs.6641	kinesin family member 5C	9.6
30	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
	412766	BE544475	Hs.54347	ESTs	9.6
35	418723	AA504428	Hs.10467	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AI280341	Hs.166571	ESTs	9.6
	424534	D87682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
	447889	AW469180	Hs.170651	ESTs	9.5
40	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	9.5
45	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AI376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
	437444	H46008	Hs.31518	ESTs	9.5
50	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	9.4
	420969	AI636310	Hs.28310	ESTs	9.4
55	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	reticulon 1	9.4
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
60	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10653	ESTs	9.4
	412446	AI768015	Hs.92127	ESTs	9.4
65	441102	AA973905	Hs.331328	intermediate filament protein syncoilin	9.4
	421689	N87820	Hs.106826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
70	441499	AW298235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95665	hypothetical protein	9.4
	420061	AW024937	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.3
75	450580	N40087	Hs.15248	ESTs	9.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
80	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	9.3
5	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
	428465	AW970976	Hs.293653	ESTs	9.3
	422564	AI148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
10	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
	433862	D86960	Hs.3610	KIAA0205 gene product	9.2
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	9.2
	401558			ENSP00000220478*:SECRETOGRANIN III.	9.2
	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
15	437678	AA829860	Hs.122834	ESTs	9.2
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
	431187	AW971146	Hs.293187	ESTs	9.2
20	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	9.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
	448822	BE149845	Hs.289038	hypothetical protein MGC4126	9.1
25	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	9.1
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	9.1
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	9.1
	434361	AF129755	Hs.117772	ESTs	9.1
	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
30	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	9.1
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
35	418821	AA436002	Hs.183161	ESTs	9.1
	427213	AW007211	Hs.16131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
40	447033	AI357412	Hs.157601	ESTs	9.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
45	445674	BE410347	Hs.13063	transcription factor CA150	9.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope [H.sapi	9.0
50	405523			C8001409*:gi|7441226|pir||S31212 collage	9.0
	416662	T25853	Hs.7538	ESTs	9.0
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
55	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319145	Hs.75426	secretogranin II (chromogranin C)	8.9
	414917	C04863	Hs.47191	ESTs	8.9
60	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	8.9
65	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
70	431316	AA502663	Hs.145037	ESTs	8.9
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	AI821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
	453344	BE349075	Hs.44571	ESTs	8.9
75	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	8.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	8.9
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
	433213	AW665130	Hs.137190	ESTs	8.9
80	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417355	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	8.8
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
5	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	8.8
	409643	AW450866	Hs.257359	ESTs	8.8
10	428647	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
	424113	AI743880	Hs.12876	ESTs	8.8
15	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW008798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypotheti	8.8
	424238	AA337401	Hs.137635	ESTs	8.8
20	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	8.8
	429831	AA564489	Hs.137526	ESTs	8.8
25	453468	W00712	Hs.32990	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	8.8
	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
30	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
35	408242	AA251594	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypotheti	8.7
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
40	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein (S. c	8.7
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	8.7
	427723	AI355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	8.7
45	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	klotho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
	452335	AW188944	Hs.61272	ESTs	8.7
50	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
55	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
	425907	AA365752	Hs.155965	ESTs	8.6
60	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
65	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119563	ESTs	8.6
	438160	AA779332	Hs.122671	ESTs	8.6
70	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434851	AA806164	Hs.116502	ESTs	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
75	454058	AI273419	Hs.135146	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
	447894	AW204253	Hs.21912	ESTs	8.5
80	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

434747	AA837085	Hs.220585	ESTs	8.5
415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	8.5
450813	AI739625	Hs.203376	ESTs	8.5
413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	8.5
407891	AA486620	Hs.41135	endomucin-2	8.5
411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
432620	AA777749	Hs.5978	LIM domain only 7	8.5
424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
408170	AW204516	Hs.31835	ESTs	8.5
452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	8.5
417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	8.5
430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
418120	AA213437	Hs.192249	ESTs	8.4
419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	8.4
448474	AI792014	Hs.13809	hypothetical protein FLJ10648	8.4
434384	AA631910	Hs.162849	ESTs	8.4
452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	8.4
411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
421622	AB037748	Hs.106204	KIAA1327 protein	8.4
431160	AW971174	Hs.324330	ESTs	8.4
449567	AI990790	Hs.188614	ESTs	8.4
411088	BE247593	Hs.145053	ESTs	8.4
452186	AA120761	Hs.26307	WW domain binding protein 4 (formin bind	8.3
437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	8.3
438440	AA807228	Hs.225161	ESTs	8.3
431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
422295	AF051151	Hs.114408	toll-like receptor 5	8.3
440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
425242	D13635	Hs.155287	KIAA0010 gene product	8.3
432769	AA620814	Hs.144959	ESTs	8.3
433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
427229	AI799751	Hs.5635	ESTs	8.3
446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
403149			NM_001450:Homo sapiens four and a half L	8.3
436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	8.3
453121	AI968264	Hs.232286	ESTs	8.3
420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434O0921 (f	8.3
426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	8.2
419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	8.2
440080	AW051597	Hs.143707	ESTs	8.2
422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	8.2
432695	D63480	Hs.278634	KIAA0146 protein	8.2
407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	8.2
408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
418051	AW192535	Hs.19479	ESTs	8.2
412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	8.2
417958	AA767382	Hs.193417	ESTs	8.2
452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	8.2
430468	NM_004673	Hs.241519	angiopoietin-like 1	8.2
407802	D84145	Hs.39913	novel RGD-containing protein	8.2
420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
414138	AA135884	Hs.3772	ESTs	8.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	8.2
408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypotheti	8.2
408108	AI580492	Hs.42743	hypothetical protein	8.2
408418	AW963897	Hs.44743	KIAA1435 protein	8.2
430334	AI824719	Hs.328700	ESTs	8.2
422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 59B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

409752	115301_1	AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
418866	179788_1	T65754 AA229857 AA229658
418876	179960_1	AA740616 AA654854 AA229923
419536	185688_1	AA603305 AA244095 AA244183
419544	185760_2	AI909154 AA526337 AA244193 AI909153
423800	232161_1	AA331156 AA331157 AA331155
426413	266650_1	AA377823 AW954494 AI022688
429163	300543_1	AA884766 AW974271 AA592975 AA447312
430848	324621_1	AW021726 AA487752 AA488085
431121	328275_1	AW971157 AA492575 AA492520
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
434415	385931_1	BE177494 AW276909 AA632849
434579	38916_1	T55958 T57205 AF147346
439518	47334_1	W76326 AF086341 W72300
443161	561305_1	AI038316 AI344631 AI261653
447974	745643_1	R76886 AI453674 R77049

TABLE 59C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400860	9757499	Minus	151830-152104,152649-152744
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
402076	8117410	Plus	128316-128627
402812	6010110	Plus	25026-25091,25844-25920
402855	9662953	Minus	59763-59909
403047	3540153	Minus	59793-59968
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403149	9799833	Plus	25034-25185
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404571	7249169	Minus	112450-112648
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	56.6
419526	AI821895	Hs.193481	ESTs	56.2
420154	AI093155	Hs.95420	JM27 protein	44.0
432441	AW292425	Hs.163484	ESTs	41.9
414569	AF109298	Hs.116258	prostate cancer associated protein 1	39.9
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	37.9
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	36.0
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	32.9
425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	30.0
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	AI918950	Hs.123642	EphA3	26.3
	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	26.2
5	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
	401424			NM_001172:Homo sapiens arginase, type II	24.5
10	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AI267700		ESTs	20.2
	407709	AA456135	Hs.23023	ESTs	20.0
15	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
	410929	H47233	Hs.30643	ESTs	18.0
20	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418961	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656*:Homo sapiens transmembrane pr	17.3
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
25	418396	AI765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
	440260	AI972867	Hs.7130	copine IV	16.0
30	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	429220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
35	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AI202703	Hs.152414	ESTs	14.4
	450693	AW450461	Hs.203965	ESTs	14.4
	431548	AI834273	Hs.9711	novel protein	14.4
40	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	14.3
	430187	AI799909	Hs.158989	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	14.2
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
45	450642	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432966	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.159425	ESTs	13.4
	434666	AF151103	Hs.112259	T cell receptor gamma locus	13.1
50	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	12.5
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
55	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	12.3
	428398	AI249368	Hs.98556	ESTs	12.2
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.2
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	12.2
60	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	436032	AA150797	Hs.109276	latexin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
	434792	AA649253	Hs.132458	ESTs	12.0
65	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	11.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
70	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	11.6
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	11.6
75	432435	BE218886	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	11.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	10.5
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
5	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	10.3
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
10	415263	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
15	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
20	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
25	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	9.4
	450325	AI935962	Hs.26289	ESTs	9.4
30	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416795	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
	418848	AI820961	Hs.193465	ESTs	9.2
35	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW628686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
40	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
45	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.7
50	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI085198	Hs.164226	ESTs	8.6
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
55	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
	453006	AI362575	Hs.303171	ESTs	8.4
60	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	8.2
	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
65	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
70	424692	AA429834	Hs.151791	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
75	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
80	453160	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6

451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
443180	R15875	Hs.258576	claudin 12	7.5
454119	BE549773	Hs.40510	uncoupling protein 4	7.5
418693	AI750878	Hs.87409	thrombospondin 1	7.5
426581	AB040956	Hs.135890	KIAA1523 protein	7.5
417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
439569	AW602166	Hs.222399	CEGP1 protein	7.4
416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.4
436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
410252	AW821182	Hs.61418	microfibrillar-associated protein 1	7.3
424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
428218	AA424266	Hs.123642	EphA3	7.3
434158	T86534	Hs.14372	ESTs	7.3
413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.2
420871	AA702972	Hs.65300	ESTs	7.2
418278	AI088489	Hs.83937	hypothetical protein	7.1
456516	BE172704	Hs.222746	KIAA1610 protein	7.1
417511	AL049176	Hs.82223	chordin-like	7.1
411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
414422	AA147224	Hs.249195	Homeo box A13	7.1
407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	7.1
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.0
418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.0
437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
432887	AI926047	Hs.162859	ESTs	6.8
444931	AV652066	Hs.75113	general transcription factor IIIA	6.8
421823	N40850	Hs.28625	ESTs	6.8
426981	AL044675	Hs.173081	KIAA0530 protein	6.8
425170	AU077315	Hs.154970	transcription factor CP2	6.8
411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
439492	AF086310	Hs.103159	ESTs	6.8
449919	AI674685	Hs.200141	ESTs	6.8
452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
431555	AI815470	Hs.260024	Cdc42 effector protein 3	6.7
441111	AI806867	Hs.126594	ESTs	6.7
457498	AI732230	Hs.191737	ESTs	6.7
415293	R49462	Hs.106541	ESTs	6.7
429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
433908	AW298141	Hs.157975	ESTs	6.7
446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	6.7
418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
443745	AB039670	Hs.9728	ALEX1 protein	6.6
427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
447805	AW627932	Hs.302421	gemin4	6.6
440995	T57773	Hs.10263	ESTs	6.6
422173	BE385828	Hs.250619	phorbolin-like protein MDS019	6.6
431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
437052	AA861697	Hs.120591	ESTs	6.6
444030	AW021254	Hs.135055	ESTs	6.6
416836	D54745	Hs.80247	cholecystokinin	6.6
447033	AI357412	Hs.157601	ESTs	6.5
428927	AA441837	Hs.90250	ESTs	6.5
432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	6.5
448779	BE042877	Hs.177135	ESTs	6.4
430598	AK001764	Hs.247112	hypothetical protein FLJ10902	6.4
411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.4
432682	AI376400	Hs.159588	ESTs	6.4
441499	AW298235	Hs.101689	ESTs	6.4
441676	BE564206	Hs.49889	ESTs	6.4
421077	AK000061	Hs.101590	hypothetical protein	6.4
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	6.4
452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	6.3
452277	AL049013	Hs.28783	KIAA1223 protein	6.3

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	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	6.3
	453390	AA862496	Hs.28482	ESTs	6.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
5	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.3
	433610	AA806822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
	412977	AA125910	Hs.191461	ESTs	6.3
10	441217	AI922183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
	425465	L18964	Hs.1904	protein kinase C, iota	6.2
15	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AI800470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
20	427078	AI676062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282906	ESTs	6.1
	437323	AA371145	Hs.194397	leptin receptor	6.1
25	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.260024	ESTs	6.0
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
30	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	6.0
	409047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmegin	6.0
	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
35	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AI766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
	428730	AA625947	Hs.25750	ESTs	6.0
40	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chomosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
	431359	AW993522	Hs.292934	ESTs	5.9
45	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	405523			C8001409*:gi|7441226|pir||S31212 collage	5.9
	448807	AI571940	Hs.7549	ESTs	5.8
50	404642			NM_021965*:Homo sapiens phosphoglucomuta	5.8
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.8
55	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
	414528	AA148950	Hs.188836	ESTs	5.7
60	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	5.7
	420184	AA188408	Hs.95665	hypothetical protein	5.7
65	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AI041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
	448172	N75276	Hs.135904	ESTs	5.7
70	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.6
	418019	R68911	Hs.176275	ESTs	5.6
75	450813	AI739625	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.6
	451684	AF216751	Hs.26813	CDA14	5.6
	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
80	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

428465	AW970976	Hs.293653	ESTs	5.5
431316	AA502663	Hs.145037	ESTs	5.5
434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	5.5
411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	5.5
416239	AL038450	Hs.48948	ESTs	5.4
421470	R27496	Hs.1378	annexin A3	5.4
408177	AI241733	Hs.43871	ESTs	5.4
424084	AI940675	Hs.20914	hypothetical protein FLJ23056	5.4
414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
448072	AI459306	Hs.24908	ESTs	5.4
420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.4
418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.4
428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
447186	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
412677	AW029608	Hs.17384	ESTs	5.3
430412	AW341754	Hs.189305	ESTs	5.3
423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
421433	AI829192	Hs.22380	ESTs	5.3
435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 ferri	5.3
441054	AA913591	Hs.126480	ESTs	5.3
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
433409	AI278802	Hs.25661	ESTs	5.3
441102	AA973905		intermediate filament protein syncoilin	5.3
453387	AI990741	Hs.252809	ESTs	5.3
421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
433923	AI823453	Hs.146625	ESTs	5.3
426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.2
447574	AF162666	Hs.18895	tousled-like kinase 1	5.2
421896	N62293	Hs.45107	ESTs	5.2
410870	U61599	Hs.66731	homeo box B13	5.2
420729	AW964897	Hs.290825	ESTs	5.2
425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	5.2
429467	NM_004477	Hs.203772	FSHD region gene 1	5.2
447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
446553	AB021179	Hs.15299	HMBA-inducible	5.2
453308	AW959731	Hs.323099	ESTs	5.2
452576	AB023177	Hs.29900	KIAA0960 protein	5.2
421437	AW821252	Hs.104336	hypothetical protein	5.2
422295	AF051151	Hs.114408	toll-like receptor 5	5.2
453942	AW190920	Hs.19928	hypothetical protein SP329	5.2
400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
452588	AA889120	Hs.110637	homeo box A10	5.2
448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.1
413991	H44725	Hs.176090	ESTs	5.1
444454	BE018316	Hs.11183	sorting nexin 2	5.1
446795	AI797713	Hs.156471	ESTs	5.1
407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.1
432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	5.1
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	5.1
453293	AA362267	Hs.10653	ESTs	5.1
408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
409643	AW450866	Hs.257359	ESTs	5.1
427723	AI355260	Hs.279789	histone deacetylase 3	5.1
438157	AW137011	Hs.49576	ESTs	5.1
420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
418051	AW192535	Hs.19479	ESTs	5.1
419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
425843	BE313280	Hs.159627	death associated protein 3	5.1
440594	AW445167	Hs.126036	ESTs	5.1
452449	AW058658	Hs.20943	ESTs	5.1
429769	NM_004917	Hs.218366	kallikrein 4 (prostase, enamel matrix, p	5.1
428898	AB033070	Hs.194408	KIAA1244 protein	5.1
415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
433023	AW854793	Hs.87409	thrombospondin 1	5.0
433862	D86960	Hs.3610	KIAA0205 gene product	5.0
451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
418624	AI734080	Hs.104211	ESTs	5.0
430291	AV660345	Hs.238126	CGI-49 protein	5.0
432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

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	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
	427176	AW381569	Hs.40334	ESTs	5.0
5	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
10	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963608	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	4.9
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.9
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
20	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
	430523	AW451385	Hs.161954	ESTs	4.9
25	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
30	418818	AA226899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	4.8
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
35	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
	420210	AI557257	Hs.44811	ESTs	4.8
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	4.8
45	416030	H15261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	4.8
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.7
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
50	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
55	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
60	452260	AA453208		RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	4.7
	418836	AI655499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*:SECRETOGRANIN III,	4.7
	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	4.7
65	443881	R64512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	4.7
	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALUB_HUMAN !	4.6
70	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
75	403046			NM_005656*:Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	4.6
	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
80	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861896	Hs.304505	ESTs	4.6

	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
5	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	4.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW188687	Hs.44748	ESTs	4.6
	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
10	434423	NM_006769	Hs.3844	LIM domain only 4	4.5
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
15	446720	AI439136	Hs.140546	ESTs	4.5
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
	433507	AI817336	Hs.191791	ESTs	4.5
20	426966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.5
	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
25	428715	AW293716	Hs.53126	ESTs	4.5
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459561	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
	414272	AI651603	Hs.46988	ESTs	4.5
30	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	4.5
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
35	401519			C15000476*:gi|12737279|ref|XP_012163.1|	4.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	4.4
40	433517	AW022133	Hs.189838	ESTs	4.4
	429559	AI985345	Hs.26425	ESTs	4.4
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
45	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.4
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
	434384	AA631910	Hs.162849	ESTs	4.4
50	444564	AI167877	Hs.143716	ESTs	4.4
	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	diubiquitin	4.4
	448766	AI473827	Hs.31793	ESTs	4.4
55	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	4.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
	434022	R18374	Hs.117956	ESTs	4.4
60	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	4.4
	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccaride-specific response 5-li	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	4.3
65	448550	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	4.3
70	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
75	435023	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	4.3
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
	420405	AA743396	Hs.189023	ESTs	4.3
80	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26535	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
414312	AA155694	Hs.191060	ESTs	4.3
438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
414680	AA743331		hemoglobin, alpha 2	4.3
423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.3
449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	4.2
431429	AF072813		reticulon 3	4.2
413492	D87470	Hs.75400	KIAA0280 protein	4.2
419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
435846	AA700870	Hs.14304	ESTs	4.2
441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	4.2
450546	AA010200	Hs.175551	ESTs	4.2
414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
416445	AL043004	Hs.79337	KIAA0135 protein	4.2
409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.2
442991	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.2
449685	AW296669	Hs.66095	ESTs	4.2
407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
450377	AB033091	Hs.74313	KIAA1265 protein	4.2
419647	AA348947	Hs.91816	hypothetical protein	4.2
442049	AA310393	Hs.190044	ESTs	4.2
430669	AW969657	Hs.291029	ESTs	4.2
424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
443634	H73972	Hs.134460	ESTs	4.1
426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	4.1
422634	NM_016010	Hs.118821	CGI-62 protein	4.1
445895	D29954	Hs.13421	KIAA0056 protein	4.1
447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	4.1
447752	M73700	Hs.105938	lactotransferrin	4.1
402855			NM_001839*:Homo sapiens calponin 3, acid	4.1
443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	4.1
415827	H17462	Hs.23079	ESTs	4.1
408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
418365	AW014345	Hs.161690	ESTs	4.1
429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.1
421141	AW117261	Hs.125914	ESTs	4.1
430335	D80007	Hs.239499	KIAA0185 protein	4.1
435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
410763	AF279145	Hs.8966	hypothetical protein FLJ21776	4.1
410592	R94088	Hs.43569	ESTs	4.1
423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.1
428634	AA811845	Hs.106290	Kelch motif containing protein	4.1
430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.0
443273	AI042063	Hs.132156	ESTs	4.0
428055	AA420564	Hs.101760	ESTs	4.0
425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
451294	AI457338	Hs.29894	ESTs	4.0
430519	AF129534	Hs.49210	F-box only protein 4	4.0
441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
446354	AW449650	Hs.346335	ESTs	4.0
451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
409706	BE158773	Hs.213207	ESTs	4.0
447082	T85314		thioredoxin-like	4.0
418594	AI732083	Hs.187619	ESTs	4.0
426501	AW043782	Hs.293616	ESTs	4.0
436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	4.0
419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
425920	AL049977	Hs.162209	claudin 8	4.0
416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	4.0
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
433209	AB040907	Hs.278436	KIAA1474 protein	4.0
428801	AW277121	Hs.254881	ESTs	4.0
419629	AB020695	Hs.91662	KIAA0888 protein	4.0
451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
400695			C11002514*:gi|11280151|pir||E82756 beta-	3.9
417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 |H.sa	3.9
429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.9

	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
5	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	AI767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
10	451900	AB023199	Hs.27207	KIAA0982 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.9
	442320	AI287817	Hs.129636	ESTs	3.9
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
15	444636	T96667	Hs.17877	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412576	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
20	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	N40087		ESTs	3.8
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
25	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
	426226	AA769045		gb:oa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
30	437816	AI823445	Hs.280699	ESTs	3.8
	444534	AW271626	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
	443484	AI091458	Hs.134559	ESTs	3.8
35	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.8
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
40	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.8
45	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
50	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R98299	Hs.177502	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
	435655	AW105663	Hs.6947	HSPC069 protein	3.7
55	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
60	436024	AI800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
	448207	AI475490	Hs.170577	ESTs	3.7
65	450628	AW382884	Hs.204715	ESTs	3.7
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KA	3.7
70	408312	AF263613	Hs.44198	intracellular membrane-associated calciu	3.7
	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.7
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	3.7
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
75	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.7
80	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7

	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	3.7
5	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyria)	3.7
	445941	AI267371	Hs.172636	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.6
	412533	AA679863	Hs.69606	ESTs	3.6
10	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	3.6
	442710	AI015631	Hs.23210	ESTs	3.6
	448212	AI475858		gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.6
	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.6
15	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	3.6
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	3.6
20	423482	BE280172	Hs.129226	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.6
	433672	BE281165	Hs.288036	TLS-associated serine-arginine protein 1	3.6
	433887	AW204232	Hs.279522	ESTs	3.6
25	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92736	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
	435703	AW630133	Hs.83313	GK003 protein	3.6
30	445674	BE410347	Hs.13063	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	3.6
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.6
	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
35	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3.6
40	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	3.6
45	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.5
	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
	419241	AA523939	Hs.165258	ESTs	3.5
50	410762	AF226053	Hs.66170	HSKM-B protein	3.5
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.5
	420390	AA330047	Hs.191187	ESTs	3.5
55	416662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.5
	413950	AA249096	Hs.32793	ESTs	3.5
60	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411149	N68715	Hs.269128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
	418334	AA319233	Hs.5521	ESTs	3.5
65	422583	AA410506	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
70	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF086431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbb2-interacting protein ERBIN	3.5
	432589	AL135725	Hs.131708	ESTs	3.5
75	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE439899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
	434839	AI743069	Hs.134736	ESTs	3.5
80	435166	AI391470	Hs.158618	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
5	449909	AA004681	Hs.59432	ESTs	3.5
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
10	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AI215632	Hs.147487	ESTs	3.4
15	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.4
	434966	AA657494		gb:nl66f04.s1 NCI_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902*:Homo sapiens progestin induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheti	3.4
20	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-l	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*:Plasma membrane calcium	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
25	449603	AI655662	Hs.197698	ESTs	3.4
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
30	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.4
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
35	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
40	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
45	443242	BE243910	Hs.9082	nucleoporin p54	3.4
	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
50	423044	AA320829	Hs.97266	protocadherin 18	3.4
	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
55	438825	BE327427	Hs.79953	ESTs	3.4
	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
60	433764	AW753676	Hs.39982	ESTs	3.4
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	421234	AA907153	Hs.190060	ESTs	3.3
65	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
70	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
	421476	AW953805	Hs.21887	ESTs	3.3
75	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*:HSPC213.	3.3
	433404	T32982	Hs.102720	ESTs	3.3
80	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

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	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
	444170	AW613879	Hs.102408	ESTs	3.3
5	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
	444324	AI301330	Hs.143838	ESTs	3.3
10	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (fr	3.3
15	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
	428523	AW974540	Hs.98626	ESTs	3.3
20	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.3
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
25	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfbr1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
	411373	BE326276	Hs.8861	ESTs	3.3
30	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
	420969	AI636310	Hs.28310	ESTs	3.3
35	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	3.3
	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
40	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
	426775	AA384564		ESTs	3.3
45	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
50	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
55	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
60	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chai	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
	408412	AW193033	Hs.124436	ESTs	3.2
65	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
70	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
75	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.2
	452295	BE379936	Hs.28866	programmed cell death 10	3.2
80	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
	433852	AI378329	Hs.126629	ESTs	3.2
5	439735	AI635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
	415715	F30364	Hs.302204	ESTs	3.2
10	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
	408784	AW971350	Hs.63386	ESTs	3.2
15	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.2
	405558			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
20	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
25	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
30	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
	438666	AW014493	Hs.126727	ESTs	3.1
35	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
40	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
	437083	AW082597	Hs.244862	ESTs	3.1
45	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
50	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
55	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
	443331	AI052026	Hs.149995	ESTs	3.1
60	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
	430092	AI821399	Hs.16514	ESTs	3.1
65	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
	438979	AW976218	Hs.32565	ESTs	3.1
70	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
	436308	AI343469	Hs.127685	KIAA1627 protein	3.1
75	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
80	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
412088	AI689496	Hs.108932	ESTs	3.1
434361	AF129755	Hs.88474	ESTs	3.1
400664			NM_002425:Homo sapiens matrix metallopro	3.1
436354	AI879252	Hs.5151	RAN binding protein 7	3.1
449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
415245	N59650	Hs.27252	ESTs	3.1
418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
453716	AA037675	Hs.152675	ESTs	3.1
432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
408705	AA312135	Hs.46967	HSPCO34 protein	3.0
430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
441790	AW294909	Hs.132208	ESTs	3.0
414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
439703	AF086538	Hs.196245	ESTs	3.0
444489	AI151010	Hs.157774	ESTs	3.0
453878	AW964440	Hs.19025	DC32	3.0
440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
433680	AI805366	Hs.199945	ESTs	3.0
426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
426044	AA502490	Hs.170290	ESTs	3.0
431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
435712	AA694607	Hs.176956	ESTs	3.0
407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
421988	AW450481	Hs.161333	ESTs	3.0
432833	N51075	Hs.110028	ESTs	3.0
445210	H09323	Hs.27133	ESTs	3.0
447620	AW290951	Hs.224965	ESTs	3.0
449375	R07114	Hs.271224	ESTs	3.0
428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.0
443967	AW294013	Hs.200942	ESTs	3.0
441224	AU076964	Hs.7753	calumenin	3.0
448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
435688	H72286	Hs.128387	ESTs	3.0
441869	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
415954	AA171850	Hs.42251	ESTs	3.0
419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
420077	AW512260	Hs.87767	ESTs	3.0
443475	AI066470	Hs.132809	ESTs	3.0
447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
438436	AA807168	Hs.271552	ESTs	3.0
427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
443280	AA299688	Hs.24183	ESTs	3.0
448264	AI478933	Hs.188260	ESTs	3.0
428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
453843	D25215	Hs.35804	hect domain and RLD 3	3.0
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
445943	AW898533	Hs.181574	ESTs	3.0
432286	AW327432	Hs.255843	ESTs	3.0
431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
432675	AI791855	Hs.105884	ESTs	3.0
443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.0
447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
423583	AL122055	Hs.129836	KIAA1028 protein	3.0
418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	3.0
417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.0
411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
438986	AF085888	Hs.269307	ESTs	3.0
445921	AW015211	Hs.146181	ESTs	3.0
447124	AW976438	Hs.17428	RBP1-like protein	3.0
452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

TABLE 60B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
417379	167238_1	AA196390 AA507837 AA196468
418304	173658_2	AA215702 AA368006 AA215703 BE066555 BE006876
418647	177521_1	AA226198 AA226513 AA383773
418866	179788_1	T65754 AA229857 AA229658
419536	185688_1	AA603305 AA244095 AA244183
419544	185760_2	AI909154 AA526337 AA244193 AI909153
423412	228001_1	AF109300 AI299378 AI202654
423800	232161_1	AA331156 AA331157 AA331155
426226	262918_1	AA769045 AA372590 AW963633
426413	266650_1	AA377823 AW954494 AI022688
426503	268283_1	AA380153 AA380233 AW963529
426775	271683_1	AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
429163	300543_1	AA884766 AW974271 AA592975 AA447312
429220	301384_1	AW207206 AW341473 AA448195 AI951341
429258	301917_1	AA448765 C04967 C03045 AA658293
430935	325772_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
430968	326269_1	AW972830 AA527647 AA489820 AA570362
431429	33313_1	AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA056148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T35956 BE618035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308 AA187561 AA311680
432093	341283_1	H28383 AW972670 H28359 AA525808
432125	341776_1	AW972667 AA526539 AI057032 AW167842
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432340	345248_1	AA534222 AA632632 T81234
432363	345469_1	AA534489 AW970240 AW970323
432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
432810	354375_1	AA863400 AI991439 AW016017 AW014704 AI367512 H17550 AA744752 R46187 AW471324 AI126670 AA626033 AI276287 AI094253 AI286003 AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI539156 AA565542
434579	38916_1	T55958 T57205 AF147346
434966	396504_1	AA657494 AI582663 AI581639
435023	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
437866	44433_2	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581805 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
438147	45074_1	AW250553 L07876 Z36843 R30693 AI190097 AW965317
439092	468554_1	AA830149 AW978407 M85983 AW503637
439518	47334_1	W76326 AF086341 W72300
439904	479942_1	AW892676 AA853877 D44747
440840	50357_2	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877
441102	509604_1	AA973905 AI299888 AA917019 H63235 T90771
442562	54500_2	BE379584 R34211 BE544768 AW973709 AI653056 AI653173 AI266043 AI656750 H74180 AI492830 AI376090 AI472184 D59940 AW170056 AI082443 AW021142 AI167921 AI348677 AI278577 AW130886 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA554902 D62102 AI0007
443161	561305_1	AI038316 AI344631 AI261653
445808	65133_1	AV655234 AW966332 AA340239
447082	707248_1	T85314 AI360684 T85528 T91254
448212	755099_1	AI475858 AW969013
449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
452260	9074_1	AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228 BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI659875 AW272338 AI423136 AI089270 AI160904 AA664354 BE1
452598	92338_2	AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AL138076 BE180510 AI926721 AI399955 AA749139 AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI816834 N25206 AA828301 AI084565 AI302816 AA026905 AA77255
452815	93255_1	AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
453802	981589_1	AL134757 AW079131
455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034

457728 393853_1 AW974811 AA651634 AA650072

TABLE 60C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal adult body tissue
R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*:HSPC213.	3.0	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	9.4	7.3
425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1	6.1
437147	AL049964	Hs.8358	hypothetical protein FLJ20366	2.6	6.0

432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9	5.9
427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-l	3.3	5.9
431548	AI834273	Hs.9711	novel protein	15.7	5.8
417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
422538	NM_006441	Hs.118131	5,10-methenyltetrahydrofolate synthetase	5.7	5.7
414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5	5.5
414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
451684	AF216751	Hs.26813	CDA14	3.9	5.4
421470	R27496	Hs.1378	annexin A3	5.3	5.3
426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
437571	AA760894	Hs.153023	ESTs	5.2	5.2
447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
444917	R68651	Hs.144997	ESTs	5.1	5.1
417318	AW953937	Hs.240845	ESTs	4.6	5.1
434170	AA626509	Hs.122329	ESTs	5.1	5.0
432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
421823	N40850	Hs.28625	ESTs	5.0	5.0
451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
439024	R96696	Hs.35598	ESTs	5.4	4.8
407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7	4.7
437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
451952	AL120173	Hs.301663	ESTs	4.7	4.7
431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	9.1	4.7
452242	R50956	Hs.159993	gycosyltransferase	4.7	4.7
401519			C15000476*:gi|12737279|ref|XP_012163.1|	4.6	4.6
414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
429467	NM_004477	Hs.203772	FSHD region gene 1	2.1	4.6
408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
425907	AA365752	Hs.155965	ESTs	2.2	4.6
427078	AI676062	Hs.111902	ESTs	4.8	4.5
419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
443250	AI041530	Hs.132107	ESTs	8.1	4.4
423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
428826	AL048842	Hs.194019	attractin	2.0	4.3
447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
429900	AA460421	Hs.30875	ESTs	4.2	4.2
439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
420544	AA677577	Hs.96732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
443622	AI911527	Hs.11805	ESTs	2.2	4.1
410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
421129	BE439899	Hs.89271	ESTs	4.1	4.1
428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
433887	AW204232	Hs.279522	ESTs	4.1	4.1
436556	AI364997	Hs.7572	ESTs	4.1	4.1
400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
443646	AI085198	Hs.164226	ESTs	4.1	4.1
430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
433409	AI278802	Hs.25661	ESTs	4.0	4.0
447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9	3.9
444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9	3.9
431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9	3.9
423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
410330	AW023630	Hs.159425	ESTs	6.2	3.8

422975	AA347720	Hs.122669	KIAA0264 protein	2.2	3.8
425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
418821	AA436002	Hs.183161	ESTs	2.8	3.8
422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
453160	AI263307	Hs.239884	H2B histone family, member L	9.2	3.8
424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7	3.7
452259	AA317439	Hs.28707	signal sequence receptor, gamma (transla	3.7	3.7
448807	AI571940	Hs.7549	ESTs	3.6	3.7
439209	AF087993	Hs.91954	ESTs	2.1	3.6
420077	AW512260	Hs.87767	ESTs	4.4	3.6
451009	AA013140	Hs.115707	ESTs	4.1	3.6
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
452561	AI692181	Hs.49169	KIAA1634 protein	3.2	3.6
447033	AI357412	Hs.157601	ESTs	7.7	3.6
427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
414680	AA743331		hemoglobin, alpha 2	3.5	3.5
417380	T06809	Hs.332086	ESTs	3.5	3.5
425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5	3.5
426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.2	3.5
417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
432101	AI918950	Hs.123642	EphA3	16.5	3.5
429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
418293	AI224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.1	3.4
440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
400277			Eos Control	2.4	3.3
432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
443912	R37257	Hs.184780	ESTs	3.3	3.3
414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.4	3.3
424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
444489	AI151010	Hs.157774	ESTs	3.2	3.2
453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
453078	AF053551	Hs.31584	metaxin 2	2.1	3.1
439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	10.6	3.1
413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	2.1	3.1
445840	AI277811	Hs.146291	ESTs	3.1	3.1
423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
420154	AI093155	Hs.95420	JM27 protein	27.4	3.1
453293	AA382267	Hs.10653	ESTs	3.7	3.1
457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	2.4	3.0
419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
433285	AW975944	Hs.237396	ESTs	7.7	3.0
450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
445921	AW015211	Hs.146181	ESTs	4.3	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
450580	N40087		ESTs	3.0	3.0
447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
420407	AA814732	Hs.145010	lipopolysaccaride-specific response 5-li	5.1	2.9
422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	2.9	2.9
	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	2.9	2.9
5	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
	451796	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (f	2.9	2.9
10	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
15	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
	433865	N29862	Hs.44104	ESTs	2.8	2.8
20	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
25	444668	AA654650	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abl-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
30	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyria)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
35	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
40	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
45	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	8.1	2.7
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
50	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
55	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
60	414312	AA155694	Hs.191060	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
65	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
	431474	AL133990	Hs.190642	ESTs	9.3	2.5
70	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
75	403047			NM_005656*:Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
	436401	AI087958	Hs.29088	ESTs	2.5	2.5
80	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

446791	AI632278	Hs.195922	ESTs	2.5	2.5
418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
419791	AI579909	Hs.105104	ESTs	2.7	2.5
447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.0	2.5
425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
447702	AI420256	Hs.161271	ESTs	2.1	2.4
412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	2.4	2.4
421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
429128	AA446869	Hs.119316	ESTs	2.0	2.4
429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	2.4	2.4
435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
447713	AI420733	Hs.207083	ESTs	2.4	2.4
456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
432378	AI493046	Hs.146133	ESTs	5.2	2.4
443180	R15875	Hs.258576	claudin 12	10.1	2.4
445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
450693	AW450461	Hs.203965	ESTs	2.3	2.3
452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
414869	AA157291	Hs.21479	ubinuclein 1	2.5	2.3
407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfbr1)	4.1	2.3
421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
431147	AI767751	Hs.20300	ESTs	5.8	2.3
442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
446091	AW022192	Hs.200197	ESTs	4.0	2.3
431563	AI027643	Hs.120912	ESTs	2.2	2.3
439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
413049	NM_002151	Hs.623	hepsin (transmembrane protease, serine 1	3.5	2.3
405685			C2002829:gi|4507689|ref|NP_003298.1| tra	2.3	2.3
407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
450378	AW249181	Hs.19954	ESTs, Weakly similar to T19373 hypotheti	2.3	2.3
429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
431542	H63010	Hs.5740	ESTs	7.0	2.2
401558			ENSP00000220478*:SECRETOGRANIN III.	2.2	2.2
418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
422295	AF051151	Hs.114408	toll-like receptor 5	2.2	2.2
432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
450325	AI935962	Hs.26289	ESTs	11.9	2.2
422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
408833	AW612232	Hs.254835	ESTs	3.0	2.2

422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
433444	AW975324	Hs.129816	ESTs	11.7	2.2
446354	AW449650	Hs.346335	ESTs	2.6	2.2
438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
424036	AA770688		H2A histone family, member L	3.8	2.2
440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
404641			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
406068			C2002008:gi|7303957|gb|AAF59000.1| (AE00	3.1	2.1
415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
452959	AI933416	Hs.189674	ESTs	2.1	2.1
427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
418727	AA227609	Hs.94834	ESTs	2.1	2.1
440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.5	2.1
434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
438520	AA706319	Hs.98416	ESTs	2.7	2.1
414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
450861	AI523898	Hs.17617	ESTs	2.4	2.1
419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
407182	AA312551	Hs.230157	ESTs	2.1	2.1
421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
432833	N51075	Hs.110028	ESTs	2.1	2.1
425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
413627	BE182082	Hs.246973	ESTs	3.3	2.0
414133	AW022188	Hs.41167	ESTs	2.3	2.0
411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
450244	AA007534	Hs.125062	ESTs	3.1	2.0
422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
409219	AA393383	Hs.133331	ESTs	2.1	2.0
419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
434128	W93170	Hs.284164	protein x 0004	2.7	2.0
434503	T96231	Hs.17762	ESTs	2.0	2.0
443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
448172	N75276	Hs.135904	ESTs	6.0	2.0
452039	AI922988	Hs.172510	ESTs	2.0	2.0
400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
451369	AA017321	Hs.269691	ESTs	2.1	2.0
434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
446783	AW138343	Hs.141867	ESTs	4.4	2.0
437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
410076	T05387	Hs.7991	ESTs	2.9	2.0
421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 61B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
416882	162718_1	AI633044 AW016212 AW241143 AA759058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
419544	185760_2	AI909154 AA526337 AA244193 AI909153
419733	187589_1	AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
424036	23460_1	AA770688 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI385781 AI188567 AI290658 C15404
426413	266650_1	AA377823 AW954494 AI022688
429258	301917_1	AA448765 C04967 C03045 AA658293
431676	336411_1	AI685464 AW971336 AA513587 AA525142
432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
438869	46651_1	AF075009 R63109 R63068
439516	47334_1	W76326 AF086341 W72300
442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
445808	65133_1	AV655234 AW966332 AA340239
449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T613
450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
453802	981589_1	AL134757 AW079131

TABLE 61C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402802	3287156	Minus	53242-53432
403047	3540153	Minus	59793-59968
404641	9796810	Minus	32247-32362
405685	4508129	Minus	37956-38097
406068	9114084	Plus	382-543

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
420729	AW964897	Hs.290825	ESTs	15.8
412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	12.6
401197			ENSP00000229263*:HSPC213.	12.6
426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
443271	BE568568	Hs.195704	ESTs	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
5	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
10	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
15	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
	425174	D87450	Hs.154978	KIAA0261 protein	8.6
20	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
	434217	AW014795	Hs.23349	ESTs	8.3
25	417363	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
30	443837	AI984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
35	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
40	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
45	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
50	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
	426759	AI590401	Hs.21213	ESTs	6.8
55	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
60	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
65	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
70	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
	411373	BE326276	Hs.8861	ESTs	6.3
75	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AI745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
80	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9

	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-l	5.9
	431548	AI834273	Hs.9711	novel protein	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
5	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	5.8
10	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methenyltetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	sialyltransferase 6 (N-acetyllacosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
15	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
20	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	5.5
25	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
30	451684	AF216751	Hs.26813	CDA14	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449907	AA004825	Hs.103281	ESTs	5.4
	419159	AW974945	Hs.268049	hypothetical protein	5.3
35	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
	403851			C5002154*:gi|7299015|gb|AAF54217.1| (AE0	5.3
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
40	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2+dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
	422746	NM_004484	Hs.119651	glypican 3	5.2
45	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
50	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
	414212	AA136569	Hs.10848	KIAA0187 gene product	5.1
55	451593	AF151879	Hs.26706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
	434170	AA626509	Hs.122329	ESTs	5.0
60	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
65	433560	AI925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
70	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
75	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
80	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
451952	AL120173	Hs.301663	ESTs	4.7
416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
451831	NM_001674	Hs.460	activating transcription factor 3	4.7
414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
427176	AW381569	Hs.40334	ESTs	4.7
441390	AI692560	Hs.131175	ESTs	4.7
447382	AW027790	Hs.182261	ESTs	4.7
431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	4.7
422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
452242	R50956	Hs.159993	glycosyltransferase	4.7
401519			C15000476*:gi|12737279|ref|XP_012163.1|	4.6
414342	AA742181	Hs.75912	KIAA0257 protein	4.6
426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
414341	D80004	Hs.75909	KIAA0182 protein	4.6
408380	AF123050	Hs.44532	diubiquitin	4.6
431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
425907	AA365752	Hs.155965	ESTs	4.6
419111	AA234172	Hs.137418	ESTs	4.6
425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
427078	AI676062	Hs.111902	ESTs	4.5
419326	W94915	Hs.42419	ESTs	4.5
419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
408705	AA312135	Hs.46967	HSPCO34 protein	4.5
429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
449673	AA002064	Hs.18920	ESTs	4.5
438440	AA807228	Hs.225161	ESTs	4.5
427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
456974	M12529	Hs.169401	apolipoprotein E	4.4
416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
443123	AA094536	Hs.272808	putative transcription regulation nuclea	4.4
436420	AA443966	Hs.31595	ESTs	4.4
443250	AI041530	Hs.132107	ESTs	4.4
411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	4.4
423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	4.4
430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
436446	AW016809	Hs.119021	ESTs	4.3
450704	H85157	Hs.40696	ESTs	4.3
438666	AW014493	Hs.126727	ESTs	4.3
417308	H60720	Hs.81892	KIAA0101 gene product	4.3
428826	AL048842	Hs.194019	attractin	4.3
444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
447858	AW080339	Hs.80426	ESTs	4.3
418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	4.3
432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	4.3
425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
417986	AA481003	Hs.97128	ESTs	4.3
438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
410853	H04588	Hs.30469	ESTs	4.3
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	4.2
408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
429900	AA460421	Hs.30875	ESTs	4.2
437672	AW748265	Hs.5741	flavohemoprotein b5?	4.2
439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	4.2
450661	AW952160	Hs.146550	ESTs	4.2
443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
456804	AI421645	Hs.139851	caveolin 2	4.2
414291	AI289619	Hs.13040	G protein-coupled receptor 86	4.2
420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
443622	AI911527	Hs.11805	ESTs	4.1

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436576	AI458213	Hs.77542	ESTs	4.1
443958	BE241880	Hs.10029	cathepsin C	4.1
410037	AB020725	Hs.58009	KIAA0918 protein	4.1
411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
421129	BE439899	Hs.89271	ESTs	4.1
421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
431475	AI567669	Hs.40342	putative nuclear protein	4.1
446468	AI765890	Hs.16341	MAWD binding protein	4.1
448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
404390			Target Exon	4.1
408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
433887	AW204232	Hs.279522	ESTs	4.1
436556	AI364997	Hs.7572	ESTs	4.1
430157	BE348706	Hs.278543	ESTs	4.1
451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
400301	X03635	Hs.1657	estrogen receptor 1	4.1
443646	AI085198	Hs.164226	ESTs	4.1
451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	4.1
430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
413275	W94748	Hs.48821	ESTs	4.0
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0
432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
433409	AI278802	Hs.25661	ESTs	4.0
452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	4.0
417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
415710	J04543	Hs.78637	annexin A7	4.0
457794	AA689292	Hs.246850	ESTs	4.0
451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
424401	H67220	Hs.169681	death effector domain-containing	4.0
435905	AW997484	Hs.5003	KIAA0456 protein	4.0
442731	AI868167	Hs.131044	ESTs	4.0
418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
439394	AA149250	Hs.56105	ESTs	3.9
442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
436758	AW977167	Hs.155272	ESTs	3.9
451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
405934			Target Exon	3.9
439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9
447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	3.9
428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
412978	AI431708	Hs.820	homeo box C6	3.9
414962	AF273304	Hs.235376	XPMC2 protein	3.9
447482	AB033059	Hs.18705	KIAA1233 protein	3.9
449590	AA694070	Hs.268835	ESTs	3.9
450203	AF097994	Hs.301528	L-kynurenine/alpha-amino adipate aminotra	3.9
450899	T77447	Hs.177864	ESTs	3.9
423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
452588	AA889120	Hs.110637	homeo box A10	3.8
422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
450506	NM_004460		fibroblast activation protein, alpha	3.8
407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	3.8
410330	AW023630	Hs.159425	ESTs	3.8
444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
422975	AA347720	Hs.122669	KIAA0264 protein	3.8
403100			C2001027*:gi|7296271|gb|AAF51562.1| (AE0	3.8
422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
424806	AA382523	Hs.105689	MSTP031 protein	3.8
425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
443441	AW291196	Hs.92195	ESTs	3.8
432529	AI989507	Hs.162245	ESTs	3.8
432908	AI861896	Hs.304505	ESTs	3.8
424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
424855	AW204725	Hs.25560	ESTs	3.8
414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
421828	AW891965	Hs.279789	histone deacetylase 3	3.8

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451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
418821	AA436002	Hs.183161	ESTs	3.8
422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
453160	AI263307	Hs.239884	H2B histone family, member L	3.8
416072	AL110370	Hs.79000	growth associated protein 43	3.7
424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
452259	AA317439	Hs.28707	signal sequence receptor, gamma (transio	3.7
417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
448807	AI571940	Hs.7549	ESTs	3.7
413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
408089	H59799	Hs.42644	thioredoxin-like	3.7
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
439209	AF087993	Hs.91954	ESTs	3.6
434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
456619	AV647917	Hs.107153	inhibitor of growth family, member 1-lik	3.6
458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
411213	AA676939	Hs.69285	neuropilin 1	3.6
414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
452260	AA453208		RAB9, member RAS oncogene family	3.6
439506	AI361238	Hs.41136	ESTs	3.6
420077	AW512260	Hs.87767	ESTs	3.6
451009	AA013140	Hs.115707	ESTs	3.6
436473	AI193122	Hs.132275	ESTs	3.6
413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
452561	AI692181	Hs.49169	KIAA1634 protein	3.6
433269	AI343543	Hs.126890	ESTs	3.6
445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
447033	AI357412	Hs.157601	ESTs	3.6
414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
401807			C7001350:gi|6578126|gb|AAF17706.1|AF0496	3.5
413979	BE218090	Hs.279453	ESTs	3.5
414680	AA743331		hemoglobin, alpha 2	3.5
417380	T06809	Hs.332086	ESTs	3.5
425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5
445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.5
417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
446416	AV658299	Hs.163959	ESTs	3.5
449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
432101	AI918950	Hs.123642	EphA3	3.5
453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
415528	R17236		gb:yg12c04.r1 Soares infant brain 1NIB H	3.5
435513	AW404075	Hs.42785	DC11 protein	3.5
440643	M78878	Hs.7314	KIAA0614 protein	3.5
409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
439132	H72803	Hs.38363	ESTs	3.5
451173	AI765082	Hs.48317	ESTs	3.5
422673	N59027		gb:yv59d11.r1 Soares fetal liver spleen	3.4
401597	AA172106		Rag C protein	3.4
401744			Target Exon	3.4
432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
450628	AW382884	Hs.204715	ESTs	3.4
432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
435411	AW444619	Hs.138211	ESTs	3.4
434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
437158	AW090198		KIAA1150 protein	3.4
416375	H95567	Hs.124700	ESTs	3.4
419441	AW023731	Hs.274368	MSTP032 protein	3.4

	432741	AI732358	Hs.185118	ESTs, Moderately similar to A37413 calbi	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
	428466	AF151063	Hs.184456	hypothetical protein	3.4
5	447397	BE247676	Hs.18442	E-1 enzyme	3.4
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
10	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.4
15	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cet	3.4
	403389			C3001393*:gi|3327090|dbj|BAA31613.1| (AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
	410494	M36564	Hs.64016	protein S (alpha)	3.3
20	426997	BE620738	Hs.173125	peptidylprotyl isomerase F (cyclophilin	3.3
	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
	417295	AW993524	Hs.43148	ESTs	3.3
25	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
30	425836	AW955696	Hs.90960	ESTs	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
	436499	AJ276678	Hs.283102	HEF like Protein	3.3
35	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	3.3
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
40	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	integrin, alpha 1	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
45	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	410366	AI267589	Hs.302689	hypothetical protein	3.2
50	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
55	444451	AV650179	Hs.282431	ESTs	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
60	406247			Target Exon	3.2
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
65	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
	417386	AL037228	Hs.82043	D123 gene product	3.2
70	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
75	453864	AW021407	Hs.21068	hypothetical protein	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
80	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
	452413	AW082633	Hs.212715	ESTs	3.1
5	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
	441124	T97717	Hs.119563	ESTs	3.1
10	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0260 protein	3.1
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
15	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177664	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
	445840	AI277811	Hs.146291	ESTs	3.1
20	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
25	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
	403423			Target Exon	3.1
30	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1
35	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
	422481	AL050163	Hs.117339	DNAX-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
40	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
45	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
50	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
55	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
60	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
	421786	AI188653	Hs.21351	ESTs	3.0
65	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
70	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
	428130	AW444985	Hs.77603	ESTs	3.0
75	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R06054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
	445921	AW015211	Hs.146181	ESTs	3.0
80	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI674468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148 AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282766 AA137264 AW236107 AW769
414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA706749 AA644620 AA652769 AA242975 AA151074 T19890
415528	1539409_1	R17236 R52580 F11642
416128	157163_1	AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
422673	219674_1	N59027 AA314694 N53937 R08100
426448	267323_1	R06054 AA378789 AW956453
430935	325772_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
430968	326269_1	AW972830 AA527647 AA489820 AA570362
431304	331286_1	BE157283 BE157287 AA502438
431676	336411_1	AI685464 AW971336 AA513587 AA525142
432125	341776_1	AW972667 AA526539 AI057032 AW167842
432363	345469_1	AA534489 AW970240 AW970323
437158	43392_5	AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766 AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
437866	44433_2	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
439047	468139_1	AW979177 AA846994 AA829672
439518	47334_1	W76326 AF086341 W72300
450506	836_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772 AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
452260	9074_1	AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228 BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI
453024	944876_28	AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352 AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
455473	1292917_1	AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793 AW984789 AW984823 AW948021 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
456719	222707_1	Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8119067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39624-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75th percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75th percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of normal prostate tissue to prostate tumor tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	AI738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	AI791314		gb:ae46g12.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AI459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	AI280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936:gi|3746443|gb|AAC63969.1| (AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	AI523646	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel,su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1NIB H	4.6
441040	AW449782	Hs.178803	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*:Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.2

436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
400164			Eos Control	4.1
435519	AI218950	Hs.125461	hypothetical protein FLJ11539	4.1
425094	AI955956	Hs.21417	ESTs	4.1
415928	R46799	Hs.23966	ESTs	4.1
415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
426663	AI028767	Hs.262603	ESTs	4.1
453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
404260			Target Exon	4.0
453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	4.0
415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
402817	H24185		hypothetical protein	4.0
449233	BE048401	Hs.196511	ESTs	3.9
435457	AA682421	Hs.59125	ESTs	3.9
444105	AW189097	Hs.166597	ESTs	3.9
430610	AI821455	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
409679	BE250521		ras homolog gene family, member A	3.8
415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	3.8
459707	AA631362	Hs.120866	gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens	3.8
406917	X65964		gb:H.sapiens nestin gene.	3.8
455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
443313	AI796730	Hs.55513	ESTs	3.8
452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
400499			C10001858:gi|6679124|ref|NP_032759.1| ne	3.7
411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
427318	AF186081	Hs.175783	zinc transporter	3.7
417620	R02530	Hs.191198	ESTs	3.7
404660			C9000841*:gi|12654691|gb|AAH01185.1|AAH0	3.7
409144	AW341187	Hs.279714	ESTs	3.7
436524	AA922236	Hs.221037	ESTs	3.7
459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
418833	AW974899	Hs.292776	ESTs	3.7
424887	AA348112	Hs.259461	ESTs	3.7
404984			Target Exon	3.7
454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
426736	AA431615	Hs.130722	ESTs	3.7
434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
438040	AI222422	Hs.121846	ESTs	3.6
443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
442097	AW015799	Hs.128474	ESTs	3.6
435186	AL119470	Hs.145631	ESTs	3.6
429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
400749			NM_003105*:Homo sapiens sortilin-related	3.6
450295	AI766732	Hs.210628	ESTs	3.5
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
434378	AA631739	Hs.335440	EST	3.5
421342	AA504749		gb:aa63f08.r1 NCI_CGAP_GCB1 Homo sapiens	3.5
406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
429043	AI824977	Hs.145319	ESTs	3.5
438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
405258			Target Exon	3.4
440207	AI371978	Hs.128326	ESTs	3.4
445045	AI652676	Hs.147256	ESTs	3.4
406177			Target Exon	3.4
438535	L09078		gb:Homo sapiens mRNA fragment	3.4
405735			ENSP00000252164*:KIAA1578 protein (Fragm	3.4
445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
444286	AI625304	Hs.190312	ESTs	3.4
442027	AI652926	Hs.128395	ESTs	3.4
447889	AW469180	Hs.346398	ESTs	3.4
405152			Target Exon	3.4
402460			C1001261*:gi|2695979|emb|CAA70854.1| (Y0	3.4
448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
450588	AA010319	Hs.60389	ESTs	3.4
447600	AI420990		ESTs	3.4
406085			Target Exon	3.3
417959	AW977642	Hs.291742	ESTs	3.3
418672	L44264	Hs.12915	ESTs	3.3
446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
410140	AL134435	Hs.247837	neurexin 3	3.3
458539	AI733837	Hs.145661	ESTs	3.3
422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
428561	AW973652	Hs.283105	ESTs	3.2

	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
5	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
	418092	R45154	Hs.338439	ESTs	3.2
10	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	titin-cap (telethonin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
15	451686	AA059246	Hs.110293	ESTs	3.1
	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
20	401278			Target Exon	3.1
	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Brn52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW293237	Hs.202037	ESTs	3.1
25	445316	AI219833	Hs.166767	ESTs	3.1
	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
30	421894	AI418464	Hs.190836	ESTs	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658*:HYPOTHETICAL 133.5 kDa	3.0
35	420543	AA278221	Hs.173344	ESTs	3.0
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD002 protein	3.0
40	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
45	435713	AA699313	Hs.114071	ESTs	3.0
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI636539	Hs.224296	ESTs	3.0
50	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
55	435534	AA830927	Hs.117306	ESTs	2.9
	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp761I071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
60	441543	AI733014	Hs.269715	ESTs	2.9
	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
65	453698	AW003512	Hs.232770	arachidonate lipoxygenase 3	2.9
	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
70	400461			Target Exon	2.9
	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien	2.8
75	407142	AA412535		gb:zt99b10.s1 Soares_testis_NHT Homo sap	2.8
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
80	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
401656			Target Exon	2.8
407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
435754	AA700752	Hs.117341	ESTs	2.8
433565	AA599763	Hs.112520	ESTs	2.8
451004	AA044967		gb:zf53d09.r1 Soares retina N2b4HR Homo	2.8
425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
405770			NM_002362:Homo sapiens melanoma antigen,	2.8
456227	T84239	Hs.189788	ESTs	2.8
454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
419494	W01060	Hs.34382	ESTs	2.8
427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
428079	AA421020	Hs.208919	ESTs	2.7
406337			C14000021:gi|7242973|dbj|BAA92547.1| (AB	2.7
401884			Target Exon	2.7
406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
428986	AA442884	Hs.201201	ESTs	2.7
450044	R66444	Hs.51891	ESTs	2.7
403630			C3001708*:gi|4758028|ref|NP_004360.1| co	2.7
445514	AI241280	Hs.148906	ESTs	2.7
446362	AW612481	Hs.104105	ESTs	2.7
432492	AW275110	Hs.271106	ESTs	2.7
430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
434316	AW411330	Hs.118796	annexin A6	2.7
413155	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
433329	AF015041	Hs.199291	numb (Drosophila) homolog-like	2.7
446523	NM_003063	Hs.334629	sarcolipin	2.7
449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
453626	AL138129		gb:DKFZp547F152_r1 547 (synonym: hfbr1)	2.7
405678			CX001454:gi|8393794|ref|NP_058681.1| myo	2.7
432789	D26361	Hs.3104	KIAA0042 gene product	2.7
455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
436255	F01143	Hs.284284	zinc finger 1111	2.7
415984	R19046	Hs.5010	gb:yg21f11.r1 Soares infant brain 1NIB H	2.7
402844			C1000116*:gi|9951913|ref|NP_062832.1| pr	2.7
456666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
414620	AA150120	Hs.244621	ribosomal protein S14	2.7
404979			Target Exon	2.7
412318	AW936911	Hs.326729	hypothetical protein MGC11082	2.7
424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
412542	AW961516	Hs.95097	ESTs	2.7
441975	AW173248	Hs.344285	EST	2.7
457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
457861	AW450205	Hs.305890	BCL2-like 1	2.7
439204	AF087987	Hs.42696	EST	2.7
415642	U19878	Hs.336224	transmembrane protein with EGF-like and	2.7
446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
443359	AI792583	Hs.135354	ESTs	2.7
447336	AW139383	Hs.245437	ESTs	2.7
449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
436030	R02287	Hs.121052	ESTs	2.7
449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
436092	AI345995	Hs.127383	ESTs	2.6
415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
412908	AA121913	Hs.293896	pregnancy-associated plasma protein-E	2.6
409583	AW440117	Hs.256879	ESTs	2.6
410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
435383	R61083		wee1 (S. pombe) homolog	2.6
426629	AI203933	Hs.97142	ESTs	2.6
415831	H15145	Hs.30509	ESTs	2.6
412281	AI810054	Hs.14119	ESTs	2.6
434898	AW500458	Hs.29956	KIAA0460 protein	2.6
422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
447518	T80061		gb:yd22f06.s1 Soares fetal liver spleen	2.6
458546	AI215667	Hs.175044	ESTs	2.6
438648	AA813125	Hs.146335	ESTs	2.6
450399	AW511049	Hs.202007	ESTs	2.6
420833	R47948	Hs.188732	ESTs	2.6
453903	AW299606	Hs.232777	ESTs	2.6
443650	AI698330	Hs.151444	ESTs	2.6
427419	NM_000200	Hs.177888	histatin 3	2.6
423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
451577	N69101	Hs.40730	ESTs	2.6
441358	AW173212	Hs.129041	ESTs	2.6
402706			Target Exon	2.6
436054	AI076262	Hs.119813	ESTs	2.6
402749			Target Exon	2.6
442472	AW806859		gb:MR0-ST0020-081199-004-c03 ST0020 Homo	2.6
445762	AI734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
441420	AA932872		gb:oo57d07.s1 NCI_CGAP_Lu5 Homo sapiens	2.6
405564			Target Exon	2.6

406003			Target Exon	2.6
459584	AI910884	Hs.346429	ESTs	2.6
441597	AW135032	Hs.203625	ESTs	2.6
411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
420509	M83554	Hs.1314	tumor necrosis factor receptor superfami	2.6
445060	AA830811	Hs.282908	ESTs	2.6
436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
401716			C16000902:gi|403440|gb|AAA73168.1| (M817	2.6
416628	W03955		gb:za62d04.r1 Soares fetal liver spleen	2.6
443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypotheti	2.6
440702	AA904178	Hs.148233	ESTs	2.6
456310	AA225522		gb:nc25c06.r1 NCI_CGAP_Pr1 Homo sapiens	2.6
451255	AA020857	Hs.90744	ESTs	2.6
455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
445326	AI220072	Hs.344672	ESTs	2.6
408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.6
445874	BE326671	Hs.170058	ESTs	2.6
441063	AA913819	Hs.188025	ESTs	2.6
455505	AW970640	Hs.309071	ESTs	2.6
453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
444130	AI125263	Hs.170410	ESTs	2.5
422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.5
451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
400427	AB044934	Hs.287388	histamine H4 receptor	2.5
410443	BE062906	Hs.28338	KIAA1546 protein	2.5
455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
429909	AW977090	Hs.184860	CGI-203 protein	2.5
441191	AI693930	Hs.148816	ESTs	2.5
413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
448215	N34740	Hs.6658	ESTs	2.5
419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
447610	AW296286	Hs.255534	ESTs	2.5
450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	2.5
414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	2.5
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
434152	AI792665	Hs.291190	ESTs	2.5
412671	AW977734	Hs.37931	gb:EST389963 MAGE resequences, MAGO Homo	2.5
456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.5
404678			Target Exon	2.5
408520	AA225063	Hs.161614	ESTs	2.5
411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
429906	AL080137	Hs.193743	ESTs	2.5
433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
438353	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408229	1048462_1	AW176091 H24234
408432	1058667_1	AW195262 R27868 AW811262
409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
411356	1240273_1	H45377 H21137 AW838640
411426	1245515_1	BE141714 AW845993 AW845989
411829	1260309_1	AW865749 BE179419 BE179492
411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
413489	1373392_1	BE144228 BE144291
415054	151827_1	AI733907 AA159708 AI732614
415098	1522174_1	D59687 D59694 D59656 D59589
415131	1523680_1	D61119 D81508 D81734
415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
415981	1564242_1	R35694 H12035 R53312
416628	1604848_1	W03955 H82332 H69247 H72486
416935	163179_1	AA190712 AA190665 AA252564
419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
419896	1888682_1	Z99362 Z99363
420778	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

421342	201427_1	AA504749 AA287498
421813	207654_1	BE048255 AA313083 AA298419
422731	220507_1	AL138411 AL138412 AA315860
423741	231582_1	AA330362 AW962525 H87796
423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859620 AA367436 AW516957 BE614519 AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW468227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599 C02215 AI6525
423871	232749_1	AA331906 AA332484
426481	267878_1	AW963941 AW963944 AA379825 AA379564
428132	287430_1	AA421765 AA456076 AI290275 AA455579
431847	338402_1	AI791314 AI791434 AA516511
434407	385744_1	AW815333 AW815409 AA632563
435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
436190	41555_1	AK001059 AA633055
438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
441420	516748_1	AA932872 W28068 W28643 T96110
442472	543371_1	AW806859 AW806852 AF049582
445797	650943_1	AI253414 AI366014 R34822
447518	724787_1	T80061 AI382804
447600	728288_1	AI420990 AI399725 AI401757
448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
449923	81926_1	BE258051 R45758 AA004732 BE255126
450724	844585_1	R55428 AI820704 AI732283 R54983
451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
452351	91233_1	AA025647 R45716 AW753786
453412	966264_1	AJ003290 AJ003288 AW276947
453491	969172_-1	AL040177
453752	979899_1	AL120800 BE378580
453826	982669_1	AL138129 AL138179 BE064231
454445	1204468_1	AW749432 AW749434 R47332
454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
455048	1250599_1	AW852749 AW852755 AW852620
455210	1260650_1	AW866599 AW866294 AW866468 AW866467
455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072256 BE072211 BE072242
455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
455887	1380836_1	BE154173 BE154098 BE154096
456075	1476756_1	N73442 R98100 BE410380
456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
456401	1844649_2	W28146 W28187

TABLE 63C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400461	9929654	Plus	32727-32846,32929-33051
400499	9796071	Minus	148495-148806
400749	7331445	Minus	9162-9293
400831	8576271	Minus	56502-57407
401278	9799936	Plus	98428-98573
401411	7799787	Minus	144144-144329
401656	9100664	Minus	1-382
401716	6715703	Plus	174722-174911
401884	8140731	Minus	89182-90053
401896	8569194	Plus	115129-115294
401917	9502466	Plus	25054-25229
402422	9796344	Minus	32843-33008
402460	9796884	Minus	108901-109254,110246-110581,113613-113960
402490	9797648	Plus	149982-150929
402706	8894426	Minus	148640-148805
402749	9212740	Minus	68787-68882,76602-76768
402797	3421043	Minus	15758-15930
402817	6822166	Minus	48611-49012
402844	9369286	Plus	54958-55313
403451	9838240	Plus	77382-78300
403612	8469060	Minus	94723-94859
403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
403649	8705159	Minus	27141-27247
404260	9366879	Plus	51396-51513
404267	9581792	Minus	12209-12313,18241-18397
404606	9212936	Minus	22310-23269
404660	9797068	Plus	168215-168916
404678	9797204	Plus	115196-115448
404979	4160139	Minus	87762-88217
404984	6939882	Plus	87221-87505
405001	6015406	Minus	104646-104819
405150	9929758	Plus	126475-126773

405152	9965561	Minus	137662-137969
405258	7329310	Plus	129930-130076
405422	7243869	Minus	101938-102079,102261-102443,102896-103202
405564	2114222	Minus	16766-17344
405678	4079670	Plus	151821-152027
405735	9931101	Minus	29854-29976
405770	2735037	Plus	61057-62075
406003	8247800	Plus	42079-42516
406085	9123888	Plus	18665-18843
406177	7279760	Minus	18930-19148
406337	9213455	Plus	90117-90337
406398	9256276	Minus	118691-118959
406600	8248616	Minus	36296-36610

Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of BPH tissue to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
420154	AI093155	Hs.95420	JM27 protein	49.6
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	47.2
419526	AI821895	Hs.193481	ESTs	43.6
432441	AW292425	Hs.163484	ESTs	42.7
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	30.2
407202	N58172	Hs.109370	ESTs	26.1
432101	AI918950	Hs.123642	EphA3	25.8
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	25.5
425075	AA506324	Hs.1852	acid phosphatase, prostate	24.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	24.4
410929	H47233	Hs.30643	ESTs	21.1
400287	S39329	Hs.181350	kallikrein 2, prostatic	20.3
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	19.8
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	18.6
415989	AI267700		ESTs	17.8
428336	AA503115	Hs.183752	microseminoprotein, beta-	17.3
450693	AW450461	Hs.203965	ESTs	16.7
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	16.7
407168	R45175	Hs.117183	ESTs	15.5
408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	15.5
454119	BE549773	Hs.40510	uncoupling protein 4	14.5
428819	AL135623	Hs.193914	KIAA0575 gene product	14.5
400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	14.4
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	14.3
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	14.2
433444	AW975324	Hs.129816	ESTs	13.8
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	13.5
428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	12.9
401424			NM_001172:Homo sapiens arginase, type II	12.7
432435	BE218886	Hs.282070	ESTs	12.5
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	12.3
446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	12.0
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_UI4 Homo sapiens	11.8
452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.7
432473	AI202703	Hs.152414	ESTs	11.3
410330	AW023630	Hs.159425	ESTs	11.2
431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	11.2
452792	AB037765	Hs.30652	KIAA1344 protein	11.2
418648	AI820961	Hs.193465	ESTs	10.9
400292	AA250737	Hs.72472	BMP-R1B	10.9
433647	AA603367	Hs.222294	ESTs	10.8
453160	AI263307	Hs.239884	H2B histone family, member L	10.8
409262	AK000631	Hs.52256	hypothetical protein FLJ20624	10.6
431474	AL133990	Hs.190642	CEGP1 protein	10.3
429220	AW207206		ESTs	10.3
428134	AA421773	Hs.161008	ESTs	10.2
408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	10.1
456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	9.8
434792	AA649253	Hs.132458	ESTs	9.7
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	9.5
428398	AI249368	Hs.98558	ESTs	9.4

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
	429918	AW873986	Hs.119383	ESTs	9.1
5	440260	AI972867	Hs.7130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
10	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
	450642	R39773	Hs.7130	copine IV	8.7
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
	446336	AW815036	Hs.151251	ESTs	8.4
20	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
25	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
	433923	AI823453	Hs.146625	ESTs	7.7
30	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
35	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
40	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
45	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799909	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
50	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
	449821	AI671141	Hs.211122	ESTs	6.8
55	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
60	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
	450164	AI239923	Hs.63931	ESTs	6.5
65	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
	440911	AA909536	Hs.143562	ESTs	6.4
70	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
	431359	AW993522	Hs.292934	ESTs	6.2
75	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
	439569	AW602166	Hs.222399	CEGP1 protein	6.1
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
80	446004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0

436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.0
432527	AW975028	Hs.102754	ESTs	5.9
447156	AW274731	Hs.157920	ESTs	5.9
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
438138	R98299	Hs.177502	ESTs	5.9
440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
434973	AW449285	Hs.313636	EST	5.8
408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
434485	AI623511	Hs.118567	ESTs	5.8
429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
432966	AA650114	Hs.325198	ESTs	5.7
448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	5.7
425810	AI923627	Hs.31903	ESTs	5.6
414312	AA155694	Hs.191060	ESTs	5.6
404571			NM_015902*:Homo sapiens progestin induce	5.6
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
439092	AA630149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
427078	AI676062	Hs.111902	ESTs	5.6
422805	AA436989	Hs.121017	H2A histone family, member A	5.6
417511	AL049176	Hs.82223	chordin-like	5.6
449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	5.6
433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
441676	BE564206	Hs.49889	ESTs	5.5
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
432682	AI376400	Hs.159588	ESTs	5.5
435021	AA922192	Hs.54709	ESTs	5.5
454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.5
426581	AB040956	Hs.135890	KIAA1523 protein	5.5
439079	AF085937	Hs.38348	ESTs	5.5
443635	AI080230	Hs.134214	ESTs	5.5
400080			Eos Control	5.5
410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
450325	AI935962	Hs.26289	ESTs	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
435072	AW592176	Hs.116932	ESTs	5.4
428647	AA830050	Hs.124344	ESTs	5.4
441111	AI806867	Hs.126594	ESTs	5.4
433087	AI720686	Hs.152520	ESTs	5.3
450244	AA007534	Hs.125062	ESTs	5.3
400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.3
415539	AI733881	Hs.72472	BMP-R1B	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
423101	M83941	Hs.123642	EphA3	5.3
445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
450813	AI739625	Hs.203376	ESTs	5.3
409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2
415890	H08225	Hs.268712	ESTs	5.2
454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
441054	AA913591	Hs.126480	ESTs	5.2
408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
448072	AI459306	Hs.24908	ESTs	5.2
419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.2
421040	AA715026	Hs.135280	ESTs	5.2
446495	D60923	Hs.153460	ESTs	5.2
415263	AA948033	Hs.130853	ESTs	5.2
426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
436338	W92147	Hs.118394	ESTs	5.2
445238	AA883971	Hs.187506	ESTs	5.1
450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
450582	AI339732		G-rich RNA sequence binding factor 1	5.1
438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
440995	T57773	Hs.10263	ESTs	5.0
412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.0
5	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	5.0
	403696			C4001100*:gi|5852342|gb|AAD54015.1| (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
10	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
	414422	AA147224	Hs.249195	Homeo box A13	4.9
15	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
	420851	AA261062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
	435136	R27299	Hs.10172	ESTs	4.8
20	438132	AA907076	Hs.122060	ESTs	4.8
	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
	420871	AA702972	Hs.65300	ESTs	4.8
25	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA466591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	4.7
	452843	AI796769	Hs.206320	ESTs	4.7
30	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
35	443361	AI792628	Hs.133273	ESTs	4.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
	450330	AW500775	Hs.24617	hypothetical protein FLJ20136	4.6
	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
40	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	447805	AW627932	Hs.302421	gemin4	4.6
45	438875	AA827640	Hs.189059	ESTs	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
50	418836	AI655499	Hs.161712	ESTs	4.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
55	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
60	431060	AF039307	Hs.249171	homeo box A11	4.5
	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
	418019	R68911	Hs.176275	ESTs	4.4
65	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
70	445210	H09323	Hs.27133	ESTs	4.4
	416706	AA314676	Hs.268945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
75	444030	AW021254	Hs.135055	ESTs	4.4
	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376*:PRED65 protein (Fragmen	4.4
	435265	AW272603	Hs.266134	ESTs	4.4
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
80	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	4.3

	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
5	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001664:gi|12698061|dbj|BAB21849.1| (AB	4.3
10	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
15	420905	AA521307	Hs.186651	ESTs	4.2
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
20	450597	AI701635	Hs.207077	ESTs	4.2
	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
25	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
30	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
35	436714	AA728964	Hs.293399	ESTs	4.1
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	430523	AW451385	Hs.161954	ESTs	4.1
40	445206	AI350199	Hs.269990	ESTs	4.1
	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449907	AA004825	Hs.103281	ESTs	4.1
	430467	D87742	Hs.241552	KIAA0268 protein	4.1
45	448152	AI741053	Hs.170770	ESTs	4.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
	400746			Target Exon	4.1
50	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
55	442338	AI761976	Hs.156080	ESTs	4.0
	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
	418259	AA215404		ESTs	4.0
60	418818	AA226899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
65	421312	AA824627	Hs.291670	ESTs	4.0
	448131	AI675054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partia	4.0
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
70	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
75	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
80	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	3.9
420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
429066	AA868555	Hs.178222	ESTs	3.9
435878	R08330	Hs.20152	ESTs	3.9
446862	AV660697	Hs.282700	ESTs	3.9
447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
401403			Target Exon	3.9
448779	BE042877	Hs.177135	ESTs	3.9
420533	AI809510	Hs.118971	ESTs	3.9
411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
419629	AB020695	Hs.91662	KIAA0888 protein	3.9
423453	AW450737	Hs.128791	CGI-09 protein	3.9
434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
419038	AW134924	Hs.190325	ESTs	3.9
421129	BE439899	Hs.89271	ESTs	3.9
424332	AA338919	Hs.101615	ESTs	3.9
441766	R53790	Hs.23294	hypothetical protein FLJ14393	3.9
447033	AI357412	Hs.157601	ESTs	3.9
439306	BE220199		WD40 protein Ciao1	3.8
410352	AW969725	Hs.150444	KIAA0373 gene product	3.8
407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	3.8
410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.8
439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
440450	AI333129	Hs.156147	ESTs	3.8
458611	AI268407	Hs.211458	DC-specific transmembrane protein	3.8
419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	3.8
447280	BE617907	Hs.97635	ESTs	3.8
438379	N23018	Hs.171391	C-terminal binding protein 2	3.8
416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
423044	AA320829	Hs.97266	protocadherin 18	3.8
424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.8
433507	AI817336	Hs.191791	ESTs	3.8
437718	AI927288	Hs.196779	ESTs	3.8
419831	AW448930	Hs.5415	ESTs	3.8
424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
426981	AL044675	Hs.173081	KIAA0530 protein	3.8
431447	AA505138	Hs.291341	ESTs	3.8
435932	W03928	Hs.114524	ESTs	3.8
442447	AA999723	Hs.129607	ESTs	3.8
403242			Target Exon	3.8
433908	AW298141	Hs.157975	ESTs	3.8
452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	3.7
412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
418759	AA227879	Hs.187621	ESTs	3.7
422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.7
452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
423096	AA732684	Hs.278428	progestin induced protein	3.7
454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
428055	AA420564	Hs.101760	ESTs	3.7
447785	AL041765	Hs.340375	ESTs	3.7
451746	M86178	Hs.311258	ESTs	3.7
453293	AA382267	Hs.10653	ESTs	3.7
436671	AW137159	Hs.146151	ESTs	3.7
407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
408418	AW963897	Hs.44743	KIAA1435 protein	3.7
420092	AA814043	Hs.88045	ESTs	3.7
446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	3.7
441865	AA384726	Hs.5722	hypothetical protein FLJ23316	3.7
419875	AA853410	Hs.93557	proenkephalin	3.7
431231	AA653552	Hs.116532	ESTs	3.7
418348	AI537167	Hs.96322	hypothetical protein FLJ23560	3.7
419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
439075	AF085933	Hs.292620	ESTs	3.7
440947	AA910403		ESTs	3.7
404561			trichorhinophalangeal syndrome I gene (T	3.6
430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	3.6
444794	AI419991	Hs.145225	ESTs	3.6
426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
431316	AA502663	Hs.145037	ESTs	3.6
414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
450630	AA010429	Hs.191939	ESTs	3.6
411067	AI681006	Hs.71721	ESTs	3.6
436326	BE085236		aldo-keto reductase family 1, member B1	3.6
410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
5	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
10	425465	L18964	Hs.1904	protein kinase C, iota	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517*:gi|4758712|ref|NP_004659.1| a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
15	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
	427304	AA761526	Hs.163853	ESTs	3.5
20	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
25	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
30	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
35	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
40	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769*:BG153O3.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	3.4
45	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
50	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
55	419964	AA811657	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
	431421	AW969118	Hs.106144	ESTs, Weakly similar to unnamed protein	3.4
60	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
65	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
70	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50126	Hs.173400	ESTs	3.3
	427615	BE410107	Hs.179817	CGI-82 protein	3.3
75	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
80	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
436854	AA749167	Hs.173911	ESTs	3.3
430865	AI073424	Hs.5232	HSPC125 protein	3.3
447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
423645	AI215632	Hs.147487	ESTs	3.3
429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
418051	AW192535	Hs.19479	ESTs	3.3
418719	AW975590	Hs.161707	ESTs	3.3
437714	AA766346	Hs.293242	ESTs	3.3
455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
445707	AI248720	Hs.114390	ESTs	3.3
411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
423412	AF109300		prostate cancer associated protein 5	3.3
436962	AW377314	Hs.5364	DKFZP564I052 protein	3.3
415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
433213	AW665130	Hs.137190	ESTs	3.3
453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
428043	T92248	Hs.2240	uteroglobin	3.2
407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.2
423595	R82826	Hs.220702	ESTs	3.2
407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
418986	AI123555	Hs.81796	ESTs	3.2
438118	AW753311	Hs.346690	ESTs	3.2
447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.2
425657	T89839	Hs.119471	ESTs	3.2
459646	AW863968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
451025	AW028689	Hs.301985	ESTs	3.2
401416			C14000338*:gi|7459502|pir||S74665 outer	3.2
421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
436995	AI160015	Hs.118112	ESTs	3.2
428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
422352	AA766296	Hs.99200	ESTs	3.2
429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
447597	AI886036	Hs.213675	ESTs	3.2
437866	AA156781		metallothionein 1E (functional)	3.2
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
410870	U81599	Hs.66731	homeo box B13	3.2
438899	AF085833	Hs.135624	ESTs	3.2
415862	R51034	Hs.144513	ESTs	3.2
420969	AI636310	Hs.28310	ESTs	3.2
415467	R60891	Hs.260274	ESTs	3.2
412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
417380	T06809	Hs.332086	ESTs	3.2
418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
419088	AI538323	Hs.52620	integrin, beta 8	3.2
422165	AL041199	Hs.1481	histidine decarboxylase	3.2
448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
452862	AW378065	Hs.8687	ESTs	3.2
405548			Target Exon	3.1
439584	AA838114	Hs.221612	ESTs	3.1
419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
434512	AW139932	Hs.188941	ESTs	3.1
452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
416836	D54745	Hs.80247	cholecystokinin	3.1
432589	AL135725	Hs.131708	ESTs	3.1
420512	AA262886	Hs.143817	ESTs	3.1
417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
423855	AA331761	Hs.254859	ESTs	3.1
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	3.1
427773	AA412290	Hs.98124	ESTs	3.1
441817	AW969706	Hs.293332	ESTs	3.1
456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
421823	N40850	Hs.28625	ESTs	3.1
416812	H91010	Hs.44940	ESTs	3.1
445784	AI253155	Hs.146065	ESTs	3.1
434384	AA631910	Hs.162849	ESTs	3.1
416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
5	420179	N74530	Hs.21168	ESTs	3.1
	433610	AA806822	Hs.112547	ESTs	3.1
	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
10	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	3.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	Homo sapiens cDNA: FLJ22437 fis, clone H	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
15	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	3.1
20	433852	AI378329	Hs.126629	ESTs	3.0
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50956	Hs.159993	gycosyltransferase	3.0
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	3.0
	405264			NM_030813*:Homo sapiens suppressor of po	3.0
25	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.0
	434497	AI821803	Hs.136580	ESTs	3.0
	420355	AW968263	Hs.123126	ESTs	3.0
	403481			Target Exon	3.0
30	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	426174	AA547959	Hs.115838	ESTs	3.0
35	430459	BE178539	Hs.278634	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	Hs.263478	ESTs	3.0
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
40	414441	AA234759	Hs.132950	ESTs	3.0
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450963	AI864668	Hs.48832	ESTs	3.0
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.0
45	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
	420407	AA814732	Hs.145010	lipopolysaccaride-specific response 5-li	3.0
50	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	437323	AA371145	Hs.194397	leptin receptor	3.0
55	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.0
60	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	428634	AA811845	Hs.106290	Kelch motif containing protein	3.0
	431869	AA521136	Hs.190176	ESTs	3.0
65	435008	AF150262	Hs.162898	ESTs	3.0
	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retroviru	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

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TABLE 64B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410790	1221131_1	AW803357 AW803423 AW812233 R06814
410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
411436	1245660_1	AW846433 AW846159 AW846377 AW846528

	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
5	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416009	1566379_1	Z43062 R13213 H14422
	416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
10			AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
	418259	173388_1	AA215404 AI990909 BE464132 AW271459 N74332 AI262061
	418866	179788_1	T65754 AA229857 AA229658
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
	419536	185688_1	AA603305 AA244095 AA244183
15	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420352	192979_1	BE256835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	423412	228001_1	AF109300 AI299378 AI202654
	424200	236595_1	AA337221 AA336756 AW966196
	426413	266650_1	AA377823 AW954494 AI022688
20	426503	268283_1	AA380153 AA380233 AW963529
	426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
			AI092404 AI085630 AA731340
25	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	429220	301384_1	AW207206 AW341473 AA448195 AI951341
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
	432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	432765	353907_1	AJ003429 AJ003367 AA564825
30	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434763	392847_1	AA648618 AW974389 H51771
	436295	41733_1	N73895 AJ001872
	436326	41795_2	BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281
35			AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706 AW270601 AW873282
	437866	44433_2	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
	439092	468554_1	AA830149 AW978407 M85983 AW503637
40	439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
	440840	50357_2	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
45	445432	63943_1	AV653771 BE089370
	448044	747196_1	AI458682 H24240 R14537 R18426 AW867082
	449343	80517_2	AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053 AW889353 AA521308 AA001203 W92828 AI207798 AA746555 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467 H00789 R76925 AW1828
50	449570	81018_1	AA001793 AA001871
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
	450317	831956_1	AI692689 R14223 R18395
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
55			AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150663 AW687764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495600 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
60	453682	977454_1	T79703 T96307 AL079725
	454037	996287_1	AW998716 AW022148 N68020
	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
65	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176515 BE176555 BE176489 BE176610 BE176362
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
70	457374	328758_1	AA493662 AW897396 BE154814
	458912	823104_1	AI911066 AI933734 AI680888 AJ003599

75 TABLE 64C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
80 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position

400533	6981826	Minus	277132-277595	
400746	7329328	Minus	147703-147896	
401132	8705350	Minus	85679-85795	
401403	7710966	Plus	146180-146294	
401416	7452889	Minus	121456-121626	
401424	8176894	Plus	24223-24428	
403242	7637817	Minus	11297-12511	
403481	9965004	Plus	93496-93633	
403510	7652047	Plus	61866-62027	
403667	6850483	Minus	1344-1442,1545-1697	
403696	3135242	Minus	143467-143634	
404003	8655948	Plus	198349-199096	
404561	9795980	Minus	69039-70100	
404571	7249169	Minus	112450-112648	
404592	9943965	Minus	39067-39225	
404848	8248647	Minus	23955-24034,25143-25264	
405264	7329374	Plus	28556-28684	
405348	2914717	Minus	43310-43462	
405510	7630909	Minus	101028-101174	
405548	1532158	Plus	11552-11686	

Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85th percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of BPH tissue to prostate tumor tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
428134	AA421773	Hs.161008	ESTs	9.4
446336	AW815036	Hs.151251	ESTs	9.3
456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	8.9
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
400533			ENSP00000209376*:PRED65 protein (Fragmen	8.7
418310	AA814100	Hs.86693	ESTs	8.7
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	8.1
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
400080			Eos Control	7.4
459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	7.4
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
418387	R18085		gb:yg16b12.r1 Soares infant brain 1NIB H	7.2
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	6.9
404967			Target Exon	6.9
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	6.9
454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	6.9
423789	AK002084	Hs.132851	hypothetical protein FLJ11222	6.8
412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	6.8
400440	X83957	Hs.83870	nebulin	6.6
454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	6.6
400086			Eos Control	6.4
440911	AA909536	Hs.143562	ESTs	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
419015	T79262	Hs.14463	ESTs	6.3
453789	AA628517	Hs.118502	ESTs	6.2
424940	AA985308	Hs.283902	ESTs	6.1
403667			Target Exon	6.1
429014	AI800518	Hs.118158	ESTs	6.0
417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte	6.0
419999	AI760942	Hs.191754	ESTs	6.0
405348			C7001664:gi|12698061|dbj|BAB21849.1| (AB	6.0
404003			Target Exon	5.9
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
432319	AW510770	Hs.128386	ESTs	5.7
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	5.6
439079	AF085937	Hs.36348	ESTs	5.5
422081	AW136820	Hs.196011	ESTs	5.5
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	5.5
423529	T87318	Hs.120411	ESTs	5.5

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	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
5	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
10	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
15	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
20	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
25	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
30	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
35	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
40	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
45	405549			C7001976*:gi|4758712|ref|NP_004659.1| al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
	444800	AW119071	Hs.153287	ESTs	4.5
50	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	414441	AA234759	Hs.132950	ESTs	4.5
55	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE069128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	418059	AA211586		gb:zn56d05.s1 Stratagene muscle 937209 H	4.4
60	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
65	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
	441620	R59595	Hs.26675	ESTs	4.2
70	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
75	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmi	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	430124	AW204994	Hs.253450	ESTs	4.2
80	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
5	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
10	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
15	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	454806	AW872430	Hs.273743	ESTs	3.9
20	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	407834	AW084991	Hs.26100	ESTs	3.9
25	400398	AF137396	Hs.283879	ubiquilin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482*:gi|9790241|ref|NP_062628.1| S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
30	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
	402145			Target Exon	3.8
35	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	434381	AA631834		gb:np77h05.s1 NCI_CGAP_Pr2 Homo sapiens	3.8
40	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
50	449264	AI637649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
55	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
	448135	AI470874	Hs.343799	ESTs	3.7
60	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
65	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
70	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
75	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	429073	AA446167	Hs.47385	ESTs	3.6
80	419002	T78525	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
	451193	N29850	Hs.44098	ESTs	3.6
5	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
10	401132			C12000517*:gi|4758712|ref|NP_004659.1| a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
15	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
	403510			Target Exon	3.5
20	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
	434497	AI821803	Hs.136580	ESTs	3.4
25	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG153O3.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
30	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
35	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI339732		G-rich RNA sequence binding factor 1	3.4
	437662	AA765387	Hs.145095	ESTs	3.4
40	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
45	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
50	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	453328	AW292635	Hs.346145	ESTs	3.3
55	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA059050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	3.3
60	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	452011	AW628911	Hs.211429	ESTs	3.3
65	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypotheti	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
70	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*:gi|129092|sp|P23270|OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
75	435786	H09175	Hs.26085	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
80	426629	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

451399	AL042110	Hs.326728	ESTs	3.1
450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
416812	H91010	Hs.44940	ESTs	3.1
452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
434512	AW139932	Hs.188941	ESTs	3.1
458251	AL040927	Hs.210422	ESTs	3.1
439950	AW937417	Hs.293561	ESTs	3.1
429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
403805			Target Exon	3.1
422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
429350	AI754634	Hs.131987	ESTs	3.1
430454	AW469011	Hs.105635	ESTs	3.1
441817	AW969706	Hs.293332	ESTs	3.1
427773	AA412290	Hs.98124	ESTs	3.1
415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
445758	R60715	Hs.25804	ESTs	3.1
403291			Target Exon	3.1
436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
418037	AI990212	Hs.86447	ESTs	3.1
438142	T90309	Hs.269651	ESTs	3.1
416423	H54375	Hs.268921	ESTs	3.1
448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
420721	AA927802	Hs.159471	ZAP3 protein	3.1
436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
441492	AI149998	Hs.146346	ESTs	3.1
410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
435628	W88732	Hs.36107	ESTs	3.0
444326	AI939357	Hs.270710	ESTs	3.0
413774	AA131782	Hs.182314	ESTs	3.0
434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
416642	T96118	Hs.226313	ESTs	3.0
439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
433796	AA810867	Hs.186997	ESTs	3.0
427813	D29833	Hs.2207	salivary proline-rich protein	3.0
405733			NM_021140*:Homo sapiens ubiquitously tra	3.0
426743	AA383833	Hs.245022	ESTs	3.0
449913	AA004696	Hs.333016	ESTs	3.0
454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	3.0
410929	H47233	Hs.30643	ESTs	3.0
458187	D56919	Hs.265848	myomegalin	3.0
429430	AI381837	Hs.155335	ESTs	3.0
451391	AA017410	Hs.40568	ESTs	3.0
414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

TABLE 65B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263 AW810325 AW810443 AW8
409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
410559	1208283_1	AW754192 W00554 AW857797 AW754203 AW754197 AW754193
410790	1221131_1	AW803357 AW803423 AW812233 R06814
410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
411436	1245660_1	AW846433 AW846159 AW846377 AW846528
411518	1248692_1	AW850246 AW850251 AW850302
411552	1249255_1	AW851255 AW851432 AW850955
412701	1322288_1	AW984757 AW984797 AW984734 AW984745
412988	1342150_1	BE046680 BE046738 BE044958
413081	1348563_1	BE064415 BE064430 BE064448
413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
416009	1566379_1	Z43062 R13213 H14422
416422	1593811_1	H60457 H68709 H73528 H54335 R87154
418059	171879_1	AA211586 F35799 AA211641 F29720 AW937387 AW937408
418387	174731_1	R18085 AA219028 R17712 Z44345
418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043

	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H03961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
5	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
	432765	353907_1	AJ003429 AJ003367 AA564825
10	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
	436295	41733_1	N73895 AJ001872
15	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
	450317	831956_1	AI692689 R14223 R18395
20	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
25	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
	454860	1237732_1	AW835767 AW835537 BE160187
30	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
35	455490	1297826_1	AW953477 Z41970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
	455772	1363114_1	W28799 BE086078
40	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

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TABLE 65C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
401459	9212270	Minus	182001-183323
402145	8018280	Plus	113086-114800
402454	7534025	Minus	14826-15803
402703	8705069	Minus	15335-15500
403242	7637817	Minus	11297-12511
403291	7230870	Plus	95177-95435
403305	8099945	Plus	114632-114805
403333	8568833	Minus	124794-124941
403371	9087278	Plus	105655-106050
403433	9719611	Minus	72225-72437
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
403667	6850483	Minus	1344-1442,1545-1697
403805	8140491	Minus	51483-51742,53429-53511
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
405510	7630909	Minus	101028-101174
405549	1552494	Plus	10878-11048
405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85th percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of BPH tissue to prostate tumor and normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI990741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PRED65 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3

423101	M83941	Hs.123642	EphA3	5.3
437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
415890	H08225	Hs.268712	ESTs	5.2
454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
446495	D60923	Hs.153460	ESTs	5.2
422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
436338	W92147	Hs.118394	ESTs	5.2
416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.1
445238	AA883971	Hs.187506	ESTs	5.1
450562	AI339732		G-rich RNA sequence binding factor 1	5.1
420533	AI809510	Hs.118971	ESTs	5.1
438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
440354	AA889386	Hs.125468	ESTs	5.0
452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
408829	NM_006042	Hs.46384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
448041	AW292769	Hs.206228	ESTs	5.0
457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
450497	H64159	Hs.15328	ESTs	4.8
438132	AA907076	Hs.122060	ESTs	4.8
414818	BE541217	Hs.23606	ESTs	4.8
429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
433523	H29882		ESTs	4.8
450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
443635	AI080230	Hs.134214	ESTs	4.8
430172	AA468591	Hs.161889	ESTs	4.8
452843	AI796769	Hs.208320	ESTs	4.7
427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
405348			C7001664:gi|12698061|dbj|BAB21849.1| (AB	4.6
419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
447058	AI939456	Hs.160870	ESTs	4.6
428218	AA424266	Hs.123642	EphA3	4.6
430697	AA484207	Hs.211867	ESTs	4.5
433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
449821	AI671141	Hs.211122	ESTs	4.5
420905	AA521307	Hs.186651	ESTs	4.5
439752	T78968	Hs.14411	ESTs	4.5
452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
423352	AA324808	Hs.193576	ESTs	4.4
438042	AW296971	Hs.180610	ESTs	4.4
452978	AA029994	Hs.61523	ESTs	4.4
420154	AI093155	Hs.95420	JM27 protein	4.4
428249	AA130914	Hs.183291	zinc finger protein 268	4.4
442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
433597	AA708205	Hs.100343	ESTs	4.3
416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
459045	N69101	Hs.40730	ESTs	4.3
409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	4.2
427908	AA417272	Hs.24122	ESTs	4.2
432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
420355	AW968263	Hs.123126	ESTs	4.2
427521	AW973352	Hs.290585	ESTs	4.2
458912	AI911066		ESTs	4.2
410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
415245	N59650	Hs.27252	ESTs	4.1
434360	AW015415	Hs.127780	ESTs	4.1
442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
450597	AI701635	Hs.207077	ESTs	4.1
424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
445206	AI350199	Hs.269990	ESTs	4.1
438431	AW207860	Hs.293116	ESTs	4.1
448152	AI741053	Hs.170770	ESTs	4.1
438875	AA827640	Hs.189059	ESTs	4.1
400746			Target Exon	4.1
413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
404967			Target Exon	4.0
427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	4.0
	435136	R27299	Hs.10172	ESTs	4.0
5	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
10	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
15	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
20	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	440450	AI333129	Hs.156147	ESTs	3.8
25	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
30	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
35	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
	432101	AI918950	Hs.123642	EphA3	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
40	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	436345	AA873008	Hs.121572	ESTs	3.7
45	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.7
50	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
55	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
60	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
65	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
70	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
75	401132			C12000517*:gi|4758712|ref|NP_004659.1| a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	449938	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153267	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
5	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
	436714	AA728964	Hs.293399	ESTs	3.4
10	404848			ENSP00000240769*:BG153O3.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	AOP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	3.4
15	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
20	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
25	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	433628	AI821784	Hs.188578	ESTs	3.4
30	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
35	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	448108	AW300021	Hs.170685	ESTs	3.3
40	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
45	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
50	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
55	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein Ciao1	3.2
	420608	BE546277	Hs.103104	ESTs	3.2
60	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
65	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
70	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
	434408	AI031771	Hs.132586	ESTs	3.2
75	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
80	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321			Target Exon	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
5	433444	AW975324	Hs.129816	ESTs	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
	415861	Z43123	Hs.144513	ESTs	3.1
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.1
	432527	AW975028	Hs.102754	ESTs	3.1
10	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	417958	AA767382	Hs.193417	ESTs	3.1
	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
15	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
20	405548			Target Exon	3.1
	423595	R62826	Hs.220702	ESTs	3.1
	412533	AA679863	Hs.69606	ESTs	3.1
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.1
	405264			NM_030813*:Homo sapiens suppressor of po	3.1
25	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
	435021	AA922192	Hs.54709	ESTs	3.0
30	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.0
	450580	N40087		ESTs	3.0
	432319	AW510770	Hs.128386	ESTs	3.0
	453713	R20640	Hs.79133	cadherin 8, type 2	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
35	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	404995			ENSP00000251890*:Monocytic leukemia zinc	3.0
40	444794	AI419991	Hs.145225	ESTs	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	420133	AA426117	Hs.155543	ESTs	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
45	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	419622	AA452054	Hs.119338	ESTs	3.0
	449745	AI668593		gb:yl38a05.x5 Soares breast 3NbHBst Homo	3.0
50	428412	AA428240	Hs.126083	ESTs	3.0
	428200	AI039624	Hs.98388	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	431869	AA521136	Hs.190176	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
55	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 66B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410790	1221131_1	AW803357 AW803423 AW812233 R06814
410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
411436	1245660_1	AW846433 AW846159 AW846377 AW846528
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
412988	1342150_1	BE046680 BE046738 BE044958
413081	1348563_1	BE064415 BE064430 BE064448
413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
416009	1566379_1	Z43062 R13213 H14422
418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
420111	190755_1	AA255652 AA280911 AW967920 AA262684
420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
424200	236595_1	AA337221 AA336756 AW966196
424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912

	428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
	432765	353907_1	AJ003429 AJ003367 AA564825
5	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434763	392847_1	AA648618 AW974389 H51771
	436295	41733_1	N73895 AJ001872
	439092	468554_1	AA830149 AW978407 M85983 AW503637
	439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
10	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	448044	747196_1	AI458682 H24240 R14537 R18426 AW867082
	449570	81018_1	AA001793 AA001871
15	449745	814534_1	AI668593 AI820774 R86205 H39971 H22177 H26241
	450317	831956_1	AI692689 R14223 R18395
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
20	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
	454037	996287_1	AW998716 AW022148 N68020
25	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454665	1226599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
	454860	1237732_1	AW835767 AW835537 BE160187
30	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854536 AW854418 AW854412
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
35	457374	328758_1	AA493662 AW897396 BE154814
	458912	823104_1	AI911066 AI933734 AI680888 AJ003599

40 TABLE 66C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
45 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
50 401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
55 403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
60 404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
65 405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

70 TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult 75 tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
80 UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
432441	AW292425	Hs.163484	ESTs	56.0
446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
419526	AI821895	Hs.193481	ESTs	35.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
400292	AA250737	Hs.72472	BMP-R1B	28.8
400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
415539	AI733881	Hs.72472	BMP-R1B	27.0
428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
407168	R45175	Hs.117183	ESTs	24.5
400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
403047			NM_005656*:Homo sapiens transmembrane pr	23.4
444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
407709	AA456135	Hs.23023	ESTs	21.5
401424			NM_001172:Homo sapiens arginase, type II	20.6
448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
415989	AI267700		ESTs	17.9
437052	AA861697	Hs.120591	ESTs	17.8
451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
431548	AI834273	Hs.9711	novel protein	16.6
425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	16.5
413597	AW302885	Hs.117183	ESTs	16.1
411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
407122	H20276	Hs.31742	ESTs	15.1
427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
426501	AW043782	Hs.293616	ESTs	13.9
428898	AB033070	Hs.194408	KIAA1244 protein	13.7
418961	AW967646	Hs.23023	ESTs	13.3
448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	13.2
418848	AI820961	Hs.193465	ESTs	13.1
428398	AI249368	Hs.98558	ESTs	13.0
429220	AW207206		ESTs	12.7
401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
419078	M93119	Hs.89584	insulinoma-associated 1	12.3
450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
429918	AW873986	Hs.119383	ESTs	11.3
427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
412446	AI768015		ESTs	11.1
433404	T32982		ESTs	10.9
420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
418278	AI088489	Hs.63937	hypothetical protein	10.3
430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	10.1
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	9.8
437718	AI927288	Hs.196779	ESTs	9.8
440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
453160	AI263307		H2B histone family, member L	9.7
432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
450325	AI935962	Hs.91973	ESTs	9.6
434170	AA626509	Hs.122329	ESTs	9.6
428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

447033	AI357412	Hs.157601	ESTs	9.5
401747			Homo sapiens keratin 17 (KRT17)	9.3
434423	NM_006769	Hs.3844	LIM domain only 4	9.3
411887	AW182924	Hs.128790	ESTs	9.2
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
415263	AA948033	Hs.130853	ESTs	9.2
432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
421896	N62293	Hs.45107	ESTs	9.1
432101	AI918950	Hs.123642	EphA3	9.1
451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
420218	AW958037		ribosomal protein L4	8.8
434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	8.5
400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.5
416182	NM_004354	Hs.79069	cyclin G2	8.5
431542	H63010	Hs.5740	ESTs	8.4
447397	BE247676	Hs.18442	E-1 enzyme	8.3
432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	8.1
456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
451684	AF216751	Hs.26813	CDA14	8.1
437124	AA554458		KIAA0666 protein	8.0
416239	AL038450	Hs.48948	ESTs	8.0
432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
428728	NM_016625	Hs.191381	hypothetical protein	7.9
418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.8
442049	AA310393	Hs.190044	ESTs	7.8
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
443180	R15875	Hs.258576	claudin 12	7.5
433285	AW975944	Hs.237396	ESTs	7.5
410870	U81599	Hs.66731	homeo box B13	7.4
418836	AI655499	Hs.161712	ESTs	7.4
444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
432586	AA568548		ESTs	7.3
431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.3
422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
426108	AA622037	Hs.166468	programmed cell death 5	7.1
433323	AA805132	Hs.159142	ESTs	7.1
423349	AF010258	Hs.127428	homeo box A9	7.0
416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
418601	AA279490	Hs.86368	calmegin	6.8
429769	NM_004917	Hs.218366	kallikrein 4 (prostase, enamel matrix, p	6.8
436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
425465	L18964	Hs.1904	protein kinase C, iota	6.6
450377	AB033091		KIAA1265 protein	6.6
451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.5
426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
440774	AI420611	Hs.153934	ESTs	6.5
413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
451027	AW519204	Hs.40808	ESTs	6.4
436063	AK000028		ribosomal protein S24	6.3
440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
448045	AJ297436	Hs.20166	prostate stem cell antigen	6.0
428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
433517	AW022133	Hs.189838	ESTs	6.0
424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	5.8
5	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	5.7
10	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	5.4
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	5.4
20	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-B protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
25	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
30	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
35	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptojanin 2	5.0
	403046			NM_005656*:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
40	450164	AI239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
45	433852	AI378329	Hs.126629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
50	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
55	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	4.7
	431724	AA514535	Hs.283704	ESTs	4.7
60	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
65	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
70	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.5
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
75	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
80	451752	AB032997		KIAA1171 protein	4.3
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
440300	N39760	Hs.8659	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
427308	D26067	Hs.174905	KIAA0033 protein	4.3
435706	W31254	Hs.7045	GL004 protein	4.3
416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	4.2
410076	T05387	Hs.7991	ESTs	4.2
410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
442501	AA315267	Hs.23128	ESTs	4.2
436761	AI817776	Hs.236557	ESTs	4.2
420380	AA640891	Hs.102406	ESTs	4.2
436556	AI364997	Hs.7572	ESTs	4.2
458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
446416	AV658299	Hs.163959	ESTs	4.2
417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
421305	BE397354	Hs.324830	diptheria toxin resistance protein requi	4.1
429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
407894	AJ276313	Hs.41143	phosphoinositide-specific phospholipase	4.1
414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
408418	AW963897	Hs.44743	KIAA1435 protein	4.1
430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.1
447574	AF162666	Hs.18895	tousled-like kinase 1	4.0
447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
444108	R55784	Hs.140942	ESTs	4.0
422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	4.0
418821	AA436002	Hs.183161	ESTs	4.0
438825	BE327427	Hs.79953	ESTs	4.0
433233	AB040927	Hs.301804	KIAA1494 protein	4.0
415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
407819	R42185		ESTs	4.0
450402	BE218027	Hs.89969	ESTs	4.0
432527	AW975028	Hs.102754	ESTs	4.0
419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
432435	BE218886	Hs.282070	ESTs	3.9
450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
436420	AA443966	Hs.31595	ESTs	3.9
430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
411031	W37943	Hs.34892	KIAA1323 protein	3.9
429259	AA420450	Hs.292911	Plakophilin	3.9
407813	AL120247	Hs.40109	KIAA0872 protein	3.9
417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
417958	AA767382	Hs.193417	ESTs	3.9
427176	AW381569	Hs.40334	ESTs	3.9
448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
432675	AI791855		ESTs	3.8
419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.8
427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
413950	AA249096	Hs.32793	ESTs	3.8
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
447620	AW290951		ESTs	3.8
430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.7
418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
453469	AB014533	Hs.33010	KIAA0633 protein	3.7
408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	3.7
422072	AB016255	Hs.111138	KIAA0712 gene product	3.7
420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
420522	AW957137	Hs.98541	hypothetical protein	3.6
408833	AW612232	Hs.254835	ESTs	3.6
426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6

	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
	422424	AI186431	Hs.296638	prostate differentiation factor	3.6
5	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
	412520	AA442324	Hs.795	H2A histone family, member O	3.6
10	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
15	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
	428055	AA420564	Hs.101760	ESTs	3.5
20	416827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
25	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
	443884	N20617	Hs.194397	leptin receptor	3.4
30	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
35	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.3
40	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
45	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
50	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
55	409960	BE261944		hexokinase 1	3.3
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
	419972	AL041465	Hs.182982	golgin-67	3.3
60	445707	AI248720	Hs.114390	ESTs	3.3
	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
65	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.2
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476*:gi|12737279|ref|XP_012163.1|	3.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.2
75	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
80	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
5	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
	414222	AL135173		sorbitol dehydrogenase	3.1
10	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
15	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
	445943	AW898533	Hs.181574	ESTs	3.1
20	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
	423453	AW450737	Hs.128791	CGI-09 protein	3.1
25	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
	436278	BE396290	Hs.5097	synaptogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
30	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
	434293	NM_004445	Hs.3796	EphB6	3.1
35	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278962	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
40	448807	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
45	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
55	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.0
60	429966	BE081342	Hs.283037	HSPC039 protein	3.0
	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.0
65	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
	415172	AF079529	Hs.78106	phosphodiesterase 8B	2.9
70	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
	439609	AW971945	Hs.293236	ESTs	2.9
75	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
80	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
5	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.9
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
15	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
20	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
	418166	AI754416		Cdc42 effector protein 3	2.8
25	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
	425320	U29344	Hs.83190	fatty acid synthase	2.8
30	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
35	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
	450546	AA010200	Hs.175551	ESTs	2.7
40	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
45	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
50	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
55	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.26777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	2.7
	438157	AW137011	Hs.49576	ESTs	2.7
60	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
	453390	AA862496	Hs.28482	ESTs	2.7
65	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
70	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
	409650	T08490	Hs.288969	HSCARG protein	2.7
75	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
80	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	niban protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
5	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*:HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		tumican	2.6
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
10	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
	408157	AA047685	Hs.62946	ESTs	2.6
15	420805	L10333	Hs.99947	reticulon 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
20	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
25	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
30	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
35	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.6
40	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
	451040	AA324743	Hs.40808	ESTs	2.6
45	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
50	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
55	436165	AI373544	Hs.331328	intermediate filament protein syncoilin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
	431108	AA991508	Hs.105317	ESTs	2.5
60	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
	421091	W22821		ribosomal protein L26	2.5
65	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.5
	431615	AW295859	Hs.235860	ESTs	2.5
70	433037	NM_014158	Hs.279938	HSPC067 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
	450628	AW382884	Hs.204715	ESTs	2.5
75	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
80	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubinuclein 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.5
407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
414556	AW975063	Hs.343443	ribosomal protein L36	2.5
446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
435126	AI393666	Hs.42315	p10-binding protein	2.5
421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.5
443837	AI984625	Hs.9884	spindle pole body protein	2.5
421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
435021	AA922192	Hs.73962	ESTs	2.5
435750	AB029012	Hs.4990	KIAA1089 protein	2.5
435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.5
407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
425976	C75094	Hs.334514	NG22 protein	2.5
449458	At805078	Hs.208261	ESTs	2.5
428013	AF151020	Hs.181444	hypothetical protein	2.5
424369	R87622	Hs.26714	KIAA1831 protein	2.5
431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
452779	AA418775	Hs.47234	ESTs	2.5
433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.5
438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.5
427515	T79526	Hs.179516	integral type I protein	2.5
418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259
412446	63467_1	BC021735 AI569212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422
432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
438869	52134_1	AF075009 R63109 R63068
450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939596 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164
436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901 BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333
432363	1234917_1	AW970240 AA534489 AW970323

	422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 D81142 C15616 AL538697 Z25032 Z43784 R13362 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
	417379	1610005_1	AA196390 AA507837 AA196468
	407819	7392_2	AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
	419733	7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826
	432675	1237917_1	AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610
	447620	687223_1	AI973051 AI400921 AI796154 AW241817 AW290951
	409151	4123_1	NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
	409960	39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296866 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257
	433891	647290_1	AW182329 AA613792 T05304 AW858385
	414922	1563_2	BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695677 AL562079 AI700926 AI470561 BF063058 AW196387 AU132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW664827
	414222	18695_1	BC021085 AL527872 AL526296 AL557087 BI255090 AU143499 AL560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AL564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463926 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI420449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AW143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857926 BF372568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106
	426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
	434194	62680_1	AF119847 AA437261 AA436987 AI132965
	432908	452541_1	AF150424 AI861896 AA570057 AV738855
	412652	18858_2	AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
	437179	12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422
	418166	18858_1	AK055915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376692 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732
	431416	120918_1	AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974
	447881	44623_1	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
	407192	2200202_1	AA602964 AA609200
	434747	117643_1	AW976537 AI033582 AA837085 AA745261 AA648395
	410297	2990_1	BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954386
	424339	50559_1	NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF805256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528652 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833

	445636	8561_5	BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
	419175	35068_1	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H60618 BE221942 R52609 AI915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
	441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322
	406789	0_0	AI041403 Z49148
	421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AL567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896
	400263	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868869 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859,56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833,5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AI821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
	400292	AA250737	Hs.72472	BMP-R1B	31.4
5	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	30.3
	407168	R45175	Hs.117183	ESTs	29.6
10	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	AI733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
15	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
	407709	AA456135	Hs.23023	ESTs	24.7
20	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI267700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
	437052	AA861697	Hs.120591	ESTs	22.6
25	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	20.8
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
30	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.7
35	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW967646	Hs.23023	ESTs	17.3
	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
40	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98558	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	15.2
45	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	14.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
50	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820961	Hs.193465	ESTs	14.3
	429918	AW873986	Hs.119383	ESTs	14.2
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
	418278	AI088489	Hs.83937	hypothetical protein	14.1
55	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
	412446	AI768015		ESTs	12.7
60	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
65	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
70	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
	416182	NM_004354	Hs.79069	cyclin G2	11.3
75	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
	450325	AI935962	Hs.91973	ESTs	11.1
80	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21716 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
	434170	AA626509	Hs.122329	ESTs	10.6
5	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
10	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
15	410889	X91662	Hs.56744	twist (Drosophila) homolog (acrocephalos	9.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
	443180	R15875	Hs.258576	claudin 12	9.5
20	406964	M21305		FGENES predicted novel secreted protein	9.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
	451684	AF216751	Hs.26813	CDA14	9.5
25	440594	AW445167	Hs.126036	ESTs	9.4
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
	437124	AA554458		KIAA0666 protein	9.2
30	426728	NM_016625	Hs.191381	hypothetical protein	9.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
35	418836	AI655499	Hs.161712	ESTs	8.8
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	8.7
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	8.7
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
	416239	AL038450	Hs.48948	ESTs	8.5
45	436962	AW377314	Hs.5364	DKFZP564I052 protein	8.4
	450164	AI239923	Hs.63931	ESTs	8.4
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AI420611	Hs.153934	ESTs	8.3
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
50	410870	U81599	Hs.66731	homeo box B13	8.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	8.2
55	423349	AF010258	Hs.127428	homeo box A9	8.1
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
60	416653	AA768553	Hs.193145	metallothionein 1E (functional)	7.9
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (prostase, enamel matrix, p	7.7
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
65	433323	AA805132	Hs.159142	ESTs	7.7
	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
	420092	AA814043	Hs.88045	ESTs	7.6
70	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	7.6
	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
75	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AI648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
80	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AI623511	Hs.118567	ESTs	7.2

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	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
5	436063	AK000028		ribosomal protein S24	7.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
10	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
15	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
20	409648	AW451449	Hs.57749	ESTs	6.4
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
25	404632			NM_022490:Homo sapiens hypothetical prot	6.3
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410762	AF226053	Hs.66170	HSKM-B protein	6.3
30	436032	AA150797	Hs.109276	latexin protein	6.3
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
35	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
40	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
45	419647	AA348947	Hs.91816	hypothetical protein	6.0
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446416	AV658299	Hs.163959	ESTs	5.9
50	407819	R42185		ESTs	5.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
55	410240	AL157424	Hs.61289	synaptojanin 2	5.8
	421305	BE397354	Hs.324830	diptheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
60	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GL004 protein	5.6
65	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
70	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	5.5
	403046			NM_005656*:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	germin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
75	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
80	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
	417318	AW953937	Hs.240845	ESTs	5.3
5	429467	NM_004477	Hs.203772	FSHD region gene 1	5.3
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
10	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
	450832	AW970602	Hs.105421	ESTs	5.1
15	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
20	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
25	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
30	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
35	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
	442501	AA315267	Hs.23128	ESTs	4.8
40	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
45	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.7
	447574	AF162666	Hs.18895	tousled-like kinase 1	4.7
50	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.7
55	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.7
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
60	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
	420380	AA640891	Hs.102406	ESTs	4.7
65	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
70	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.5
75	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
80	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
5	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
	417958	AA767382	Hs.193417	ESTs	4.4
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
15	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
20	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
25	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
	432675	AI791855		ESTs	4.2
30	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AI248720	Hs.114390	ESTs	4.2
	410297	AA148710		lumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
35	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
40	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AI355260	Hs.279789	histone deacetylase 3	4.2
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
45	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	4.1
50	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	4.1
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
55	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
60	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	4.0
65	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
	418827	BE327311	Hs.47166	HT021	4.0
70	446791	AI632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	leptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476*:gi|12737279|ref|XP_012163.1|	4.0
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
75	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
80	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubinuclein 1	3.9
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
5	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
10	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421867	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AI249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
15	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
20	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AI186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
25	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
30	411190	AA306342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
	432426	AW973152	Hs.31050	ESTs	3.7
35	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AI861896		ESTs	3.7
	432800	BE391046	Hs.278962	AIM-1 protein	3.7
40	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	AI806583	Hs.125291	ESTs	3.7
	401197			ENSP00000229263*:HSPC213.	3.7
45	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
	420805	L10333	Hs.99947	reticulon 1	3.7
50	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.7
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
55	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
60	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
65	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
70	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
75	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*:Homo sapiens mitogen-activate	3.6
	418559	AA225048	Hs.104207	ESTs	3.6
80	438523	H66220	Hs.278177	ESTs	3.6
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

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	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	3.5
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
5	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
10	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
15	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
20	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300296	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
	439609	AW971945	Hs.293236	ESTs	3.5
25	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
30	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
35	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
40	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
45	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
50	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
	452295	BE379936	Hs.28866	programmed cell death 10	3.4
55	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
60	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
65	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
	442064	AI422867	Hs.88594	ESTs	3.3
70	431663	NM_016569	Hs.267182	TBX3-iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.3
75	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.3
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
80	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase I	3.2

	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.2
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	3.2
5	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	3.2
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	3.2
	422173	BE385828	Hs.250619	phorbolin-like protein MDS019	3.2
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
10	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371:Homo sapiens hydroxysteroid (1	3.2
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
15	438714	AA814859	Hs.160074	ESTs	3.2
	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
20	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
	437179	AA393508		serologically defined colon cancer antig	3.2
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
	450546	AA010200	Hs.175551	ESTs	3.2
25	409995	AW960597	Hs.129206	ESTs	3.2
	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638:Homo sapiens hypothetical prot	3.2
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
30	414341	D80004	Hs.75909	KIAA0182 protein	3.1
	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
	423551	AA327598	Hs.89633	ESTs	3.1
35	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AI187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.1
40	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
	421254	AK001724	Hs.102950	coat protein gamma-cop	3.1
	424339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
	425320	U29344	Hs.83190	fatty acid synthase	3.1
45	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
50	433036	AA574091	Hs.105964	ESTs	3.1
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
55	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437296	AA350994	Hs.20281	KIAA1700	3.1
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
	448913	AA194422	Hs.22564	myosin VI	3.1
60	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
	437546	AW074836	Hs.173984	T-box 1	3.0
65	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
70	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
75	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
	434974	AA778711		eukaryotic translation initiation factor	3.0
80	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
5	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
10	445596	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.0
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
15	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
20	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.26777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
25	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
30	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
35	428801	AW277121	Hs.254881	ESTs	2.9
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
	418222	AI675881	Hs.86538	ESTs	2.9
40	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
45	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
50	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AI200281	Hs.123910	ESTs, Highly similar to B34087 hypotheti	2.9
	437050	AA766420		ESTs	2.9
	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
55	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	niban protein	2.9
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
	436823	AW749865		ESTs, Weakly similar to I38022 hypotheti	2.8
60	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
	400860			Target Exon	2.8
65	436165	AI373544	Hs.331328	intermediate filament protein syncoilin	2.8
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
70	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40608	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
	418196	AI745649	Hs.26549	KIAA1708 protein	2.8
75	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
80	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
5	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor , S. cerev	2.8
	419286	AA236005	Hs.128764	ESTs	2.8
10	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
	440080	AW051597		ESTs	2.8
15	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.8
20	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10600	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
25	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
	432651	AW973744	Hs.293100	ESTs	2.8
30	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
35	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
	410339	AI916499	Hs.298258	ESTs	2.7
40	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
	410099	AA081630		KIAA0036 gene product	2.7
45	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gb:nt78f05.x5 NCI_CGAP_Pr3 Homo sapiens	2.7
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
50	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.7
	400263			Eos Control	2.7
55	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000061	Hs.101590	hypothetical protein	2.7
	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
60	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
65	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	intron of:trichorhinophalangeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
	427515	T79526	Hs.179516	integral type I protein	2.7
70	447673	AI823987	Hs.182285	ESTs	2.7
	411960	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
	441551	AA318224	Hs.296141	ESTs	2.7
75	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
80	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
5	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	456082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
10	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
15	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
20	404913			NM_024408*:Homo sapiens Notch (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	2.6
25	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
30	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.6
35	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
40	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	2.6
	412774	AA120865	Hs.23136	ESTs	2.6
45	445922	AI337316	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
	417327	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.6
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
50	408743	AL110246	Hs.47367	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
55	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
60	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283476	Hs.263478	ESTs	2.6
	440191	AI990417		tubulin, beta 5	2.6
65	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	2.6
70	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
	458946	AA009716	Hs.42311	ESTs	2.6
75	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	2.6
	442336	AW340958	Hs.7572	ESTs	2.6
80	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
5	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
10	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
15	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
	414528	AA148950	Hs.188836	ESTs	2.5
20	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
25	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62620	chromosome 6 open reading frame 1	2.5
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamidine syntha	2.5
30	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.5
	449500	AW956345	Hs.12926	ESTs	2.5
35	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
40	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.5
	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
45	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
	418039	R06659	Hs.193172	ESTs, Weakly similar to I38022 hypotheti	2.5
50	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
55	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W05656	Hs.169755	ESTs	2.5
	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
60	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
65	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
	421026	AL047332	Hs.101067	GCN5 (general control of amino-acid synt	2.5
70	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259

449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422
438869	52134_1	AF075009 R63109 R63068
428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164
436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
407819	7392_2	AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
409151	4123_1	NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 D81142 C15616 AL538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901 BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333
432363	1234917_1	AW970240 AA534489 AW970323
417379	1610005_1	AA196390 AA507837 AA196468
414922	1563_2	BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695677 AL562079 AI700926 AI470561 BF063058 AW196387 AU132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW664827
419733	7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826
432675	1237917_1	AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610
410297	2990_1	BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954386
447620	687223_1	AI973051 AI400921 AI796154 AW241817 AW290951
407192	2200202_1	AA602964 AA609200
434194	62680_1	AF119847 AA437261 AA436987 AI132965
448663	16112_4	BE966763 AA659765 AI961656 AI520918 AA761743 AA281477 N66431 BE463652 AA281329 AW272944 AA058687 BM145087 AA045516 AW341820 AA112515 AA258766 AI886639 AA714133 AA768245 AA035533 AI630459 T20165 AW971268 BE966269 AA522722
429163	1238297_1	AW974271 AA592975 AA447312 AA884766

426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
432908	452541_1	AF150424 AI861896 AA570057 AV738855
433891	647290_1	AW182329 AA613792 T05304 AW858385
409960	39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257
414222	18695_1	BC021085 AL527872 AL526296 AL557087 BI255090 AU143499 AL560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AL564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI420449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857926 BF372568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106
412652	18858_2	AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
418166	18858_1	AK055915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376692 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R36484 AA249043 AA249732
434747	117643_1	AW976537 AI033582 AA837085 AA745261 AA648395
437179	12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422
448044	1111791_1	AW867082 AI458682 H24240 R18426 R14537
424339	50559_1	NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF805256 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833
418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
411089	5597_6	BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680
431416	120918_1	AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974
434974	77302_1	AL079283 BF792538 AA744861 AI871888 AI478580 AI720775 AI888937 AI808966 BE463436 BF725510 AW675767 BF589111 BE855951 AW197232 AW272173 AI480335 BF589044 AA443540 AI420128 AI056029 AI650755 AW274589 AW183510 AI440198 AI271801 AW080345 AW189506 AW008293 AA884731 AA579802 AI968645 AI620822 AI222117 AA677146 AI346296 BI792788 AA446615 AI183488 AA897113 AW271851 AW241299 W90134 AA482921 AI049496 AA492010 AA846639 AA983603 AA969293 AI890036 BI254992 AA463513 AA476659 AW673442 AL557763 AA868312 H28886 AA778711 AA081838 AI989340 AL557762 N99654 Z28545 N28874 AA442388 AW887818 AW663156 BG252539 BG501262 BG714174 BG499052 AA058524 BE881198 C75278 R59648 AI829311 AA037656 AW026747 N64518 AW103253 BF529731 AW241677 AW194855 AA917531 R96578 H94036 AA856665 T10342 AW439112 AI090044 AA661591 N71704 AI474928 AU152235 D53426 N21634 R59590 R51072 R96601 H06171 AA084440 H84172 AW118714 C04928 W90092 AA039267 AA136445 R52391 T66024 BG778916 AA428153 N41394 AA283639 R96600 H94122 BF743684 AA147009 T65867 Z19487 BF697478
431155	1235742_1	AW971213 AA493925 AA493567 AA876839 AA934462
409927	2333801_1	T69981 T69924 AA078476
447881	44623_1	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
433009	2142268_1	AA761668 AA573621 R09670 R92814
412719	1634_2	BI918715 BF594193 AI073494 AI363077 AI656655 AA121979 BF983131 AA491795 BG152545 AI350401 BF939121 AI479401 BI493099 BF057693 AI970550 BF111919 BF448282 BI493100 AW043768 AW006202 AI564010 BF433292 AI458202 AI954746 BE220962 AI375411 AI361048 AA115853 AI364474 AI669815 AA133407 AI928647 AW016610 AA133334 AA504948 AI291629 AI161208 AA837042 AI867138 AA987255 AI830219 AU150404 AI680674 AW969901
437050	1240141_1	AW976442 AA743319 AA766420
436823	MH1660_153	BG180003 AW975741 AW749865 AA731828 AA731829
457733	119160_1	AW974812 AI821822 AI821820 AI821075 AI821073 AA651643 AA651662
453912	32562_3	BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849 AW614893 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW388482 AW388420 BF374777 W01360 N94710 H87967
440080	517737_1	AW051597 AI733052 AI167287 AI732999 AI566918 AI476787 AI791542 AA887204 AW025394 AA863338 AI240285 AI791393
419175	35068_1	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618

			AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
	421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AL567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896
	441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322
	406789	0_0	AI041403 Z49148
	410099	16732_1	AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL563737 BG029709 W52882 AI439658 BE551237 AA283724 BF109530 AI457096 AI805992 BE467736 AA693467 AI697593 AI887863 AI167419 AW901980 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 AI418634 T31586 AA436630 AI366472 AA706191 AI422304 AI204899 AI041169 AA211402 AW827081 AA788593 T32736 AI767935 AA747914 T03534 AW959843 AL119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60090 N79906 D52685 T07735 BE702069 BE702172 T08671 BE767121 BE767117 BE767113
	432745	112643_1	AA658826 AI821926 AI791191 AA635129 AA564492
	400263	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BF772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
	411605	10026_3	BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09685 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA699780 T57386 BF903022 R09933 AA678298
	445636	8561_5	BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
	420223	191648_1	N27807 AA256634 BE276324
	423476	32437_1	AF263306 BF951698 T66089 F11783 F11794 H29379 R19493 H18042 AL133995 AW134660 AI299437 AA057405 AA917450 AI002692 T09262 R43839 H29290 T65008 N78357
	441054	2641490_1	AI221207 AI659856 AA913591 AI220302
	429925	33135_1	NM_000786 U23942 BI601050 BG771947 BG773455 BI561558 BI460206 BG714348 BM126447 AU129411 AU129401 AL119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 AI217668 AA399409 BE182318 BM128040 AI693998 AW615411 AW070426 AI124550 AW778736 AA477781 AW263013 AI459619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 BI916393 BM470755 BI333211 AA095636 BI256415 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H47580 R48858 T91611 H42019 BI869421 BG502073 BG425943 W37290 W31363 BE004451 BF208311 BI048717 N78122 AA226597 AI525334
	434976	121716_1	AI963821 AA657925 AA935436 AW975068
	440191	MH790_2	BC000222 AL136871 NM_032261 BC009497 BM461705 BG470749 BG826905 BG285127 BI253235 BE397026 BG704967 AW961225 BM352817 BI227161 BG820180 AA454463 AA255685 N31549 AA326504 BC019924 BG257230 BI092368 BI869896 BG251883 BF034444 BG286577 BE260391 AA599912 BF686779 AI755222 AA452272 AW241170 AU156565 F28259 T16319 AA362506 N64153 BM016416 BM458963 BG739972 AV729565 BE268285 BE867433 BM011110 BG285856 AI922439 BE270975 AL119339 BF956085 AI565178 AL554305 AL573240 AL572917 AI129627 AL546640 BE392285 AI092843 AI371057 BE302410 AI608753 AW674261 AI750057 AI052649 N47822 AL516249 AI589903 BG258439 AI123662 AI126014 AA778101 AA243218 AW498837 AA748311 AI754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 AI061112 AI783806 AL569622 AA070466 BF229936 N58159 H80288 N32598 H80293 H80279 AL581253 AW571884 AI361698 AW073321 AA876464 H95640 T34421 AA331419 N99897 H80274 BI262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA362527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 BI085686 AA564566 AI221630 D52045 C14510 AA029390 W60153 H98743 AI682641 H28485 AA723093 AI081730 AA641309 AA687083 BI224818 AW204722 AI309186 AI215122 AI200785 BE467373 BM352502 AI304400 AI193071 AI742483 AW003408 AI400201 AI656740 AW665173 AI215120 AI147599 AI803429 AI076110 AI754349 AW205103 AI262491 AI808243 AI281007 AI051273 AI004801 AW768918 AW103289 AI474637 AI264446 AI699509 BE704420 AA989278 AA918256 AA830956 AA989425 AA911929 AA262598 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94863 N69544 AA181762 D20132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 AI813809 AA933607 AA129695 AA548261 AA714393 AA775006 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51696 D55942 D52740 AI000118 AL516304 AL534259 N54940 AL579194 AI669399 AI342925 BE939201 AA633000 BI222963 AI619676 AW190306 BF035010 AW087897 AI864969 T57243 R48211 AA113880 R26594 C14457 C14444 BI195459 BE896346 BE270780 AL568073 BG389833 BE891549 BI223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304
	440409	588375_1	AI380443 AI240179 AA977516 AA884643 AW079380 AW294316 AI913755 AI864320 AI685770 H25135 AI972654 AI538592
	444610	2145292_1	AI174783 R12271 R83569
	446091	515091_1	AI274757 AI559500 AW022192
	431843	445334_1	AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656
	400262	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BF772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 68C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859,56369-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719705	Plus	176341-176452
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833,5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
406214	7342036	Plus	86320-86523
403532	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104,152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigeneID	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624:Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (	2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW996651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
436729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970*:CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
407061	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
	453789	AA628517	Hs.118502	ESTs	1.41
5	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.46
	420174	AI824144	Hs.199749	ESTs	1.75
	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
10	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmi	1.64
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
15	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
	438142	T90309	Hs.269651	ESTs	1.45
20	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
25	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
	417805	U38545	Hs.82587	phospholipase D1, phophatidylcholine-spe	1.35
30	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
35	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gb:yb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AI821409	Hs.304471	EST	1.45
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.14
40	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
	406506			Target Exon	1.97
45	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.36
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	1.41
	450152	AI138635	Hs.22968	intron of VEGFR	1.70
50	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptojanin 2	1.61
	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
55	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
	412564	X83703		cardiac ankyrin repeat protein	1.51
60	414786	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiopoietin-2	1.91
	406627	T64904	Hs.163780	ESTs	1.76
	405025			Bone morphogenetic protein 6	1.69
	422648	D86983	Hs.118893	Melanoma associated gene	2.33
65	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfami	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.65
70	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.69
75	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
80	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	1.74
444409	AI792140	Hs.49265	ESTs	1.88
421340	F07783	Hs.1369	decay accelerating factor for complement	1.74
445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
444009	AI380792	Hs.135104	ESTs	1.90
409220	BE243323	Hs.51233	tumor necrosis factor receptor superfami	2.16
416940	N75620	Hs.43157	ESTs	2.03
418922	AW956580	Hs.42699	ESTs	2.09
431548	AI834273	Hs.9711	novel protein	1.81
434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
434558	AW264102	Hs.39168	ESTs	1.93
438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
428438	NM_001955	Hs.2271	endothelin 1	2.46
453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
439410	AA632012	Hs.188746	ESTs	1.93
453467	AI535997	Hs.30089	ESTs	2.39
420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
417933	X02308	Hs.82962	thymidylate synthetase	1.70
436420	AA443966	Hs.31595	ESTs	1.97
414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	1.80
442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
413745	AW247252	Hs.75514	nucleoside phosphorylase	1.99
405121			mitogen-activated protein kinase 8 inter	2.99
425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
421937	AI878857	Hs.109706	hematological and neurological expressed	1.65
408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
408243	Y00787	Hs.624	interleukin 8	2.09
418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
407891	AA486620	Hs.41135	endomucin-2	2.34
407891	AA486620	Hs.41135	endomucin-2	2.34
436032	AA150797	Hs.109276	latexin protein	2.24
439382	BE247684	Hs.103070	ESTs	2.07
419172	AW338625	Hs.22120	ESTs;similar to TRANSMEMBRANE 4 SUPERF	2.00
442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.33
447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
432128	AA127221	Hs.296502	ESTs	2.27
417426	NM_002291	Hs.82124	laminin, beta 1	2.11
434217	AW014795	Hs.23349	ESTs	2.03
439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
449722	BE280074	Hs.23960	cyclin B1	1.76
413794	AF234532	Hs.61638	myosin X	2.01
422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
406964	M21305		gb:Human alpha satellite and satellite 3	3.08
448231	AI701916	Hs.202509	ESTs	2.27
408989	AW361666	Hs.49500	KIAA0746 protein	1.43
429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
417308	H60720	Hs.81892	KIAA0101 gene product	1.86
407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
400666			NM_002425:Homo sapiens matrix metallopro	2.59
431728	NM_007351	Hs.268107	multimerin	2.72
440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	2.25
413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
444330	AI597655	Hs.49265	ESTs	3.08
422424	AI186431	Hs.296638	prostate differentiation factor	2.96
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession

	453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745642 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI025328 AI298436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805
	436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222533 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
	442506	29197_1	NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882
	436772	1239464_1	AA156151 Z25109 C05177 AW975688 AA731063 N67084
	434596	14701_1	AF147374 T59538 T59589 T59598 T59542
	412564	18571_1	X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048
	442006	1239046_1	AW975183 AA973583 AI365103 AI699495 AI301767

TABLE 69C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402463	9796896	Minus	8818-8952
400494	9714719	Plus	169845-170272
401234	9929642	Plus	120173-120337
406506	7711374	Minus	6843-8077
405025	7107727	Plus	105267-105343,106184-106294,106387-10653
405121	8102330	Minus	35816-36004,36587-36684
400666	8118496	Plus	17982-18115,20297-20456

TABLE 70A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of the mean of the vessel AI's to the mean of the HUVEC AI's

Pkey	ExAccn	UnigeneID	Unigene Title	R1
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	0.99
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.06
412636	NM_004415		desmoplakin (DPI, DPII)	1.25
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.36
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.50
417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.55
414572	AU077174	Hs.288181	cathepsin H	1.64
415314	N88802	Hs.5422	glycoprotein M6B	1.70
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	1.75
406973	M34996	Hs.198253	major histocompatibility complex, class	1.88
456974	M12529	Hs.169401	apolipoprotein E	1.90
430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.91
406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of m	1.97
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	1.99

	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
5	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	AI193115	Hs.16611	tumor protein D52-like 1	2.27
	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
10	427451	AI690916	Hs.178137	transducer of ERBB2, 1	2.31
	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	2.38
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	2.39
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
15	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
20	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	2.51
	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
25	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
	425751	T19239	Hs.1940	crystallin, alpha B	2.63
30	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
35	425869	AA524547	Hs.160318	FXYD domain-containing ion transport reg	2.73
	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
40	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plakophilin 4	2.94
	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
45	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425622	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
50	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	3.06
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
	414840	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	3.14
55	424651	AI493206		ESTs	3.17
	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
60	423961	D13666	Hs.136348	periostin(OSF-2os)	3.24
	447384	AI377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.25
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
65	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
70	410614	AI091195	Hs.65029	growth arrest-specific 1	3.35
	451529	AI917901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
75	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
	407938	AA905097	Hs.85050	phospholamban	3.48
80	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	integrin, alpha 8	3.52
	404277			NM_019111*:Homo sapiens major histocompa	3.54

	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
5	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
10	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.86
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	3.89
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
15	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
20	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
25	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78065	complement component 7	4.37
	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
30	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
35	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
40	414290	AI568801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
45	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
	426406	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
50	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hevin)	9.91

TABLE 70B
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL503116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW760435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406

			BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487
	454042	30254_1	AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570
	440820	3091_1	AW964381 BG007409 BM314056 AA465642 T30661 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 AI267360 N64249 W67500 F07962 AA322394 BI489987 BE644965 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BM141766 AI742325 AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383 AI694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280
	424651	46029_5	BG435302 BM083687 AA904035 AA488889 W76175 AA761874 H28767 AA910081 AA837086 AI521825 BG986378 AI478562 AA743152 AA746092 H88863 BG986375 AA635644 AI493206 AA669979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495

TABLE 70C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source.The 7 digit numbers in this column are Genbank Identifier (GI) numbers."Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404277	1834458	Minus	91665-91946

TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 75th percentile of ewing sarcoma to 85th percentile of body map

Pkey	ExAccn	UnigeneID	Unigene Title	R1
104659	AW969769	Hs.105201	ESTs	70.3
101447	M21305		gb:Human alpha satellite and satellite 3	64.7
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
115861	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	46.6
110278	AF061573	Hs.19492	protocadherin 8	46.1
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
116752	AL008583	Hs.91622	neuronal pentraxin receptor	40.9
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9
110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	35.5
121362	AF050147	Hs.97932	chondromodulin I precursor	34.7
131291	NM_004350	Hs.170019	runt-related transcription factor 3	33.0
101063	D54745	Hs.80247	cholecystokinin	31.7
121619	AA526339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	28.7
122651	AW975398	Hs.293836	ESTs	26.0
100299	D49493	Hs.2171	growth differentiation factor 10	26.5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2
123619	AA602964		gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	26.1
124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	23.1
116301	AW969706	Hs.293332	ESTs	22.6
121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	22.3
106533	AL134708	Hs.145998	ESTs	22.3
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	21.3
131313	R96290	Hs.75874	ribosomal protein L44	20.8
116790	AW161357		microtubule-associated protein tau	18.7
105316	AI671245	Hs.24835	hypothetical protein FLJ14594	18.2
102123	NM_001809	Hs.1594	centromere protein A (17kD)	17.8
126218	AL049801	Hs.13649	Novel human gene mapping to chomosome 13	17.8
119791	AA554907	Hs.58291	ESTs	16.7
113003	AW292315	Hs.7215	ESTs	16.3
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
126799	AW753865	Hs.74376	olfactomedin related ER localized protei	16.3
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	15.5
107160	AA314490	Hs.27669	KIAA1563 protein	14.8
115313	AA808001	Hs.184411	albumin	14.6
123308	C14187	Hs.103538	ESTs	14.2

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	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
	110288	H40665	Hs.31564	ESTs	13.8
5	106498	AI221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;calsyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
10	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
15	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
	104968	AI249502	Hs.29669	ESTs	11.1
20	123532	AA608733		gb:ae56f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	10.6
25	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
	110730	N67655	Hs.26411	ESTs	10.3
30	119186	AI979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
35	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
40	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
45	121910	AI204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
	111109	AI940675	Hs.20914	hypothetical protein FLJ23056	9.0
50	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-lin	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AI085153	Hs.143764	ESTs, Weakly similar to unknown [H.sapie	8.8
	113903	AI368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
55	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
60	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AI347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
	106575	AW970602	Hs.105421	ESTs	8.2
65	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AI918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
	107098	AI823593	Hs.27688	ESTs	8.0
70	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
	133063	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.8
75	105730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp761I1912 (f	7.8
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP586D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (	7.6
	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	7.6
	131170	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	7.5
5	104548	R39398	Hs.91559	ESTs	7.5
	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
10	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	7.1
15	128478	AA708205	Hs.100343	ESTs	7.1
	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc08a07.r1 NCI_CGAP_Pr1 Homo sapiens	7.0
20	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
	118013	AI674126	Hs.94031	ESTs	6.9
25	120147	AI917116		hemoglobin, beta	6.8
	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
30	127742	AW293496	Hs.180138	ESTs	6.7
	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
35	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
40	118499	N67274	Hs.50141	EST	6.4
	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
45	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
50	132256	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
55	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530I15	6.0
60	104689	AA420450	Hs.292911	Plakophilin	6.0
	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:yj32h01.s1 Soares placenta Nb2HP Homo	5.9
65	115522	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.8
	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86538	ESTs	5.8
70	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
75	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
80	107230	AI034467	Hs.34650	ESTs	5.7
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
5	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
	106668	R49390	Hs.254129	KIAA1678	5.4
10	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
	131185	BE280074	Hs.23960	cyclin B1	5.4
15	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
20	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	5.3
25	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	5.2
	120830	AI568170	Hs.96886	ESTs	5.2
30	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
	116680	AW902848	Hs.273829	ESTs	5.2
35	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
40	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
	125321	T86652	Hs.176294	ESTs	5.1
45	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	116814	H50834	Hs.77899	gb:yp86a10.s1 Soares fetal liver spleen	5.0
	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	5.0
50	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
55	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
60	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	126769	AA083456		gb:zn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
	130262	D63216	Hs.153684	frizzled-related protein	4.8
65	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.8
70	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
75	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
	123778	AW352149	Hs.102314	ESTs	4.7
80	126521	AI475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

	113974	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
5	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
10	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
15	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
	106489	AA452054	Hs.119338	ESTs	4.5
20	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123595	AA421130	Hs.112640	EST	4.5
	125447	AI582222	Hs.128686	ESTs	4.5
25	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AI031650		ESTs	4.4
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
30	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
35	115167	AA749209	Hs.43728	hypothetical protein	4.3
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
40	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
45	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
50	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
	106073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
55	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
	106012	AI240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130832	AW838006	Hs.20082	zinc finger protein 3 (A8-51)	4.2
	125960	AI754693	Hs.145968	ESTs	4.2
60	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
65	101266	L36645	Hs.73964	EphA4	4.2
	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothetic	4.1
70	129001	AA443323	Hs.107812	BPOZ protein	4.1
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
75	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
	129948	AI537162	Hs.263988	ESTs	4.1
80	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW068276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.283316	ESTs	4.1

	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retroviru	4.0
	127153	AI732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
5	124105	H11484	Hs.79133	ESTs	4.0
	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.0
10	126965	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.0
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
15	111387	AI244489	Hs.285724	ESTs	4.0
	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
20	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_	4.0
	126522	W31912	Hs.21168	gb:zc76d03.s1 Pancreatic Islet Homo sapi	4.0
25	131965	W79283	Hs.35962	ESTs	3.9
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
	105808	AI133161	Hs.286131	CGI-101 protein	3.9
30	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
	118967	AI668670	Hs.216756	ESTs	3.9
35	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
40	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	3.9
	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
45	112921	R91095	Hs.4276	KIAA1701 protein	3.9
	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
	105476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
50	122682	AA984531	Hs.159293	ESTs	3.8
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
	129785	H19006	Hs.184780	ESTs	3.8
55	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.8
	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
60	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
	103319	X83492	Hs.82359	tumor necrosis factor receptor superfami	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA296874	Hs.77494	deoxyguanosine kinase	3.8
	127262	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.7
65	126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	3.7
	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
	116203	AW137166	Hs.87306	ESTs	3.7
70	123377	AW969183	Hs.271297	ESTs	3.7
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
75	131163	AA099524	Hs.23754	ESTs	3.7
	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
	110834	AW273860	Hs.5759	ESTs	3.7
80	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
5	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	AI300699	Hs.111334	PRO0470 protein	3.6
	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
10	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.6
15	125174	W51835	Hs.231082	EST	3.6
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X16866	Hs.333497	cytochrome P450, subfamily IID (debrisoq	3.6
	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
20	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
	126600	AA699949	Hs.191385	ESTs	3.6
25	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
30	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
35	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	3.5
40	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1NIB H	3.5
	117265	AA451966		RAB9-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
	109482	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
45	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
50	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
55	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
60	105395	AI580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	106367	AA504747	Hs.136102	KIAA0853 protein	3.5
	103392	X94563		gb:H.sapiens dbifacbp gene exon 1 & 2.	3.5
65	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
70	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
	109734	AI927212	Hs.3734	ESTs	3.4
75	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
	108687	BE544475	Hs.54347	ESTs	3.4
80	113115	AI141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
5	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
10	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
15	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
20	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal olfact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
25	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Soares infant brain 1NIB H	3.3
	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
30	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
35	105463	AA825974	Hs.32646	hypothetical protein FLJ21901	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	3.3
	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
40	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
45	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
50	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
	121292	AA401807		gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_	3.3
55	123284	AA488988	Hs.293796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
	114988	AA251089		gb:zs04f05.s1 NCI_CGAP_GCB1 Homo sapiens	3.3
60	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
	111520	AI985369	Hs.301134	ESTs	3.3
65	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
70	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
	129284	AA318224	Hs.296141	ESTs	3.3
75	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
80	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
5	133761	AF041430	Hs.75922	brain protein I3	3.2
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
10	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
15	109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
20	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
	129056	AI769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN !!!!	3.2
25	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA926960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
	132305	AI806090	Hs.44344	hypothetical protein FLJ20534	3.2
30	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
	126153	H85692	Hs.40730	ESTs	3.2
35	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
40	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
	134964	AI803516	Hs.272891	hippocalcin-like protein 4	3.1
45	105551	AW005822	Hs.25292	ribonuclease HI, large subunit	3.1
	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group I, m	3.1
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
50	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
	129179	AW969025	Hs.109154	ESTs	3.1
55	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AI652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
	134937	AI251449	Hs.171939	ESTs	3.1
60	125756	BE174587	Hs.269721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
	117121	H95044	Hs.321386	EST	3.1
65	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AI914699	Hs.13297	ESTs	3.1
	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
70	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
75	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
	123485	AI308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
80	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LIM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hn88a05.x1 NCI_CGAP_Kid11 Homo sapien	3.1

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	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
5	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
10	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
15	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
	106057	BE614474	Hs.289074	F-box only protein 22	3.0
20	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128660	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
25	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133966	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
30	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
	129928	AI338993	Hs.134535	ESTs	3.0
35	118922	AW206193		hypothetical protein DKFZp761B2423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	3.0
	122219	AA436002	Hs.183161	ESTs	3.0
	132195	BE018717	Hs.42124	ESTs	3.0
40	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
	128902	AA036637	Hs.107052	ESTs	3.0
45	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
50	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	106735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
55	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 5	3.0
	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
60	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
65	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	126887	H20832		gb:ym48d03.s1 Soares infant brain 1NIB H	3.0
	117960	AA310417	Hs.47044	ESTs	3.0
70	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109968	H09232	Hs.26484	HIRA-interacting protein 3	3.0
	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

75

TABLE 71B

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession

108451	13766_27	AA079195 AA084955 AA126308 AA084956
107908	46987_1	AF087999 N29296 AI928858 AA846757 N20229 AA026894 D80634 AW388923 AW388802 AW388957 AW571771 AW388839 AI686662 AW389079 AA602099 AW134567 AW517843 AI682674 AI474874 AA374167
123619	371681_1	AA602964 AA609200
131495	142008_1	AA812434 AI831542 AA766261 AI769894 N63376 AA214392 AA135833 AW605017 AA135965 AW450072 H04812 AA446459 AW439151 AA426273 AI061423 AA598549 Z40087 AI753216 AA743075 AA854268 AA458920 AA843893 AI566516 AI864957 AI566634 AW971760 AA211796 AA430089
101445	1650_-5	M21259
100944	25682_2	L07518 AW815215
117265	10421_1	AA451966 NM_016370 AB036693 AL139228 R58124 AI634847 AL119333 W07356 AI334284 H29050 AI192685 AA652438 AW172843 W19794 N21460 AI743862 AW130622 AA991348 AI204553 AA992664 N80848 AA699329 AI824676 R26624 R49653
117297	647718_1	AW779829 N22494 AI248120
108859	137143_1	AL121500 AW291763 AI732432 AA129708 AA133309 AI733750 AI225224
125165	1852047_1	W45350 W45406
116790	19864_1	AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671 AA476718 AW772454 AI807703 R44253 AA976667 AI985186 AI650254 H38942 R84829 AA018724 AA001000 H85934 AA019126 H85609 AA017000 AA339355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477 AI857475 AW249771 AW162661 H38943 AA018628 R85885 AI984613 AI934765 AI796172 AW157488 AI929191 R85523 D51221 D53851 H85610 AI749674 F21582 AA323145 AA019127 AA687444 T06745 AI699293 H29532 AA214029 AA223656 NM_016834 X14474 R19697 H09695 R17455 R13812 R19056 AI681231 AI590200 R37671 AA861828 AI990023 AI935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AI890696 AA308884 AA507078 R41274 AI365507 T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045
103038	15024_1	AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 AI459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA962596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211 AW059601 AW886710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
126086	1606216_1	H75681 H70975
126098	1629789_1	M79088 N88221
125464	168460_1	N71807 AA203399
126127	1205826_1	N95428 W24040 AW751366 H81987
125558	1703083_1	R59305 R19748
126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
118644	81501_1	AA443241 R23784 R67255 R00047 AI457612 R63254 R28645 R27616 H01310 R78329 R76046 R76055 AA369734 N57914 H94864 AI953638 R31669 AW769278 R82398 AA131925 R21776 R79031 AI129553 N70340 AI276116 AA709381 N63734 AI342605 AA327133 AI805980 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732 R78932 AA368675 R16780 R26523 H40161 W93671 R99823 R77956 H61601 R98785 R09738 H78317 H53537 H81056 T53780 H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 AI702300 R30775 H68996 AI014957 AA369082 AF075351 AI110886 AI742050 AW954245 AI768458 C19062 AI393674 C18911 C18029 AA708613 AI168432 R67389 AI168453 H00188 R21233 H03055 R53822 AA367558 R75872 W04151 AI220869 AI090290 AA368730 R94434 H81153 H70950 AA367783 H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070 R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615 H60972 R98784 W86323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957062 R82759 C19002 H01715
127262	231725_1	AA828125 AA834883 AA330555
127315	37938_1	AF116622 AI114507 AA640834 AA377999
103898	187213_-3	AA248884
126769	119008_1	AA083456 AA127026 AA084934 AA120972 AA085317
120147	386607_2	AI917116 AA633698 AI580389 Z39483
128080	1540039_1	F12310 T66402 H07020
104590	44964_1	AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
127496	340470_1	AI031650 AA860882 AI458212 AA524453
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
126887	1572189_1	H20832 Z40184
128132	177108_1	AA225632 AI820970 AI820952 AA226472 AI732140 AI732059 AA226307 AA225500
126967	169750_1	AA205976 AA205930
120325	166688_1	AA195651 AW235123
112511	17406_2	AW970420 AW973132 AA811736 AW301029 BE207945 AW449936 AI376801 AA039581 AI424444 AA810925 AA749267 BE205843 AI360184 BE205945 AI761796 AI185049 R94606 AI343947 AI565814 AI341735 AI749190 AW269588 AI393145 AI620080 AW003752 AI750035 AI624837 AI797658 AA679066 N87192 AI937537 AW003753 R72610 R72274 AA757401 AA553744 AA460166 AA535727 AW304422 R68273 AW027615 C01651 AI090327 AI538258 AW003744 AA938372 AW051486 AA505513 BE466452 AA931719 AI174548 AW182752 T84462 R11149 AI767627 BE218556 BE217986 BE222697 AI762382 BE299599 AA987212 AI767136 AI268928 AA090761 AA329290 AI700593 AA460766 BE222710 BE550651 R11148 AI979278 AW235819 AW874095 AW196492

106012	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
127705	966283_2	AJ003322 AJ003324
127728	3398_5	AW404061 R09654 T67160 N50566 N53259
129012	22280_4	R81936 D78695 D78806 D78780 C17009 AA004406 AA122102 R70625 AA148932 H59583 H81146 H80378 H49863 H21182 H46534 H51478 H20702 H46515 H40200 H50046 H23647 H50439 H18383 H21846 H23849 H40182 R21924 H01290 H01283 H42464 W31947 W39660 AA046219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 AI492481 AA088608 R69918 R36334 H80281 N58483 AI075154 AI086754 AA595787 H81051 H01187 AI057251 T96992 H59584 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 R92416 H89486 R36617 R65795 AI088338 AI373324 H66992 R96235 AI494132 R16678 AA088178 AA705356 AA962143 AA148933 R09231 AI160937 R70525 T46980 AI200046 H02301 AA367587 R35968 T97106 D78703 N78072 D78668 D63268 R28197 AA085579 R63766 R92415 W00998 R80766 R67875 R27583 R09343 H13646 R27682 T89007
106498	245223_1	AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 AI193667 AI341984 N92658 T32870 R52664 N50428 AW089291 AI934175 AI423737 D60665
120934	177521_1	AA226198 AA226513 AA383773
115197	42406_1	R18656 AW968014 AA262288 AW968002 X93079 AJ002788 R51324 AI381600 D80031 AW500520 AW593740 F09382 AA810597 AA262174 AA810595 AA810596
129706	81501_1	AA443241 R23784 R67255 R00047 AI457612 R63254 R28645 R27616 H01310 R78329 R76046 R76055 AA369734 N57914 H94864 AI953638 R31669 AW769278 R82398 AA131925 R21776 R79031 AI129553 N70340 AI276116 AA709381 N63734 AI342605 AA327133 AI805980 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732 R78932 AA368675 R16780 R26523 H40161 W93671 R99823 R77956 H61601 R98785 R09738 H78317 H53537 H81056 T53780 H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 AI702300 R30775 H68996 AI014957 AA369082 AF075351 AI110886 AI742050 AW954245 AI768458 C19062 AI393674 C18911 C18029 AA708613 AI168432 R67389 AI168453 H00188 R21233 H03055 R53822 AA367558 R75872 W04151 AI220869 AI090290 AA368730 R94434 H81153 H70950 AA367783 H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070 R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615 H60972 R98784 W86323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957062 R82759 C19002 H01715
131019	223488_3	W28614 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI828466 AW572486 N52583 N89687 AW075567 AI571047 AI887479 AI559469 AI685802 AA805256 AI458777 AA974369 AI866929 AI886032 AI823925 AI823566 AW198135 AI287510 AI565910 AA765775 AI866019 AI263697 AI355825 R42668 AA894603 AW105585 AI824555 AW339175 D20479
131170	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
123470	8785_29	AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630166 AL041326 AA780690 L40517 U21556 AI093182 AW062487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389484 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 AI673095 AA599106 AW601545 AI538739 AI538730 AI521786 AW366369 AW021010 AA362576 AI289927 AA382592
123532	genbank_AA608733	AA608733
125032	genbank_T74884	T74884
123808	genbank_AA620552	AA620552
102398	entrez_U42359	U42359
118129	genbank_N57493	N57493
109841	genbank_H01052	H01052
118922	220560_1	AW206193 AW137594 AI953685 AI919143 AI424371 AW007698 AW025681 AI954289 R40438 AW070364 AI679653 AI679081 AI623213 AI652310 AI631411 AI565384 AI566734 AA149597 AI538172 AI040831 AI770021 AI914287 AA279311 W73001 AI493117 AI693374 AI802007 AI990645 N29752 R94559 AA806475 AA806828 R90998 R94558 AW300112 W24097 AW003016 N91920
113119	genbank_T47910	T47910
104799	genbank_AA029703	AA029703
113560	genbank_T91015	T91015
129794	39565_1	AF093097 AI869509 T27070 AA326718 AA024743 W23922 AA479593 AI765668 W23908 U92986 AA081632 N50578 AA065245 AW365046 AW365014 AA961091 AA150231 H53426 AA234651 N50522 T79343 T87399 N91858 H41179 AW009453 AA024744 T27069 AI346379 H88431 AA152289 R45373 AA477432 AI745607 AI807602 H41152 AA065244 AI242569 AI091032 AI251849 F03857 H88369 AI174488 AI002695 H53427 T87293 N91869 W35270 AA453723 AA453705 AW071829 AI393866 AW071807 W23592 AI342074 D31158 AA833756 AI991896 AA447791 AI864125 AW377239 AA295365 AI687970 R34076 F07607 AA521310 AW499865 R94584 R21283
124250	314220_1	AA350256 H68126
101447	entrez_M21305	M21305
117357	genbank_N24829	N24829
103392	entrez_X94563	X94563
135029	H58818_at	H58818
105225	genbank_AA211777	AA211777
121292	genbank_AA401807	AA401807
105909	82840_1	AA195191 AA190578 AI632307 AA195227 AA743633 AI823408 AI832203 AI653114 AA205307 AW021913 AI687980 AI674198 AI675563 AI417935 AA707350 AA135157 AI434721 AI151036 AI038305 R52643 AA780141 AW207645 D19691 AI474370 AA401739 N22905 N70378
100237	entrez_D30715	D30715
114988	genbank_AA251089	AA251089
123423	genbank_AA598484	AA598484

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 73.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title

Seq ID No: Seq ID number correlation for those sequences in Table 73

Pkey*	ExAccn	UnigeneID	Unigene Title	Seq ID No
103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	Seq ID No B1 & B2
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	Seq ID No B3 & B4
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	Seq ID No B5 & B6
447761	AF061573	Hs.19492	protocadherin 8	Seq ID No B7 & B8
428183	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	Seq ID No B9 & B10
439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	Seq ID No B11 & B12
121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	Seq ID No B13, B14, & B15
104659	AW969769	Hs.105201	ESTs	Seq ID No B16
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	Seq ID No B17 & B18
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	Seq ID No B19 & B20
100299	D49493	Hs.2171	growth differentiation factor 10	Seq ID No B21 & B22
116301	AW969706	Hs.293332	ESTs	Seq ID No B23 & B24
106533	AL134708	Hs.145998	ESTs	Seq ID No B25-B27
131313	R96290	Hs.75874	ribosomal protein L44	Seq ID No B28 & B29
105316	AI671245	Hs.24835	hypothetical protein FLJ14594	Seq ID No B30 & B31
113003	AW292315	Hs.7215	ESTs	Seq ID No B32
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	Seq ID No B33 & B34
102745	AW753865	Hs.74376	olfactomedin related ER localized protei	Seq ID No B35-B40
123308	C14187	Hs.157208	ESTs	Seq ID No B41 & B42
120147	AI917116		hemoglobin, beta	Seq ID No B43
123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	Seq ID No B44 & B45
119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	Seq ID No B46 & B47
105301	AW352357	Hs.7457	MAGE1 protein	Seq ID No B48 & B49
128478	AA708205	Hs.100343	ESTs	Seq ID No B50-B53
106111	AW875398	Hs.6451	PRO0659 protein	Seq ID No B54 & B55
131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	Seq ID No B56 & B57
120830	AI568170	Hs.96886	ESTs	Seq ID No B58 & B59
127664	AA806164	Hs.116502	ESTs	Seq ID No B60
102725	AB026187	Hs.159156	protocadherin 11	Seq ID No B61 & B62
132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	Seq ID No B63 & B64
130637	AA356764	Hs.17109	integral membrane protein 2A	Seq ID No B65 & B66
117602	N35020	Hs.44685	C3HC4-like zinc finger protein	Seq ID No B67 & B68
128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	Seq ID No B69 & B70
129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	Seq ID No B71 & B72
125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	Seq ID No B73 & B74
414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	Seq ID No B75 & B76
420462	AF050147	Hs.97932	chondromodulin I precursor	Seq ID No B77 & B78
410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No B79 & B80
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	Seq ID No B81 & B82
416836	D54745	Hs.80247	cholecystokinin	Seq ID No B83 & B84

Table 72B
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
131307	3138_1	NM_000025 X72861 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134
131313	93372_1	R96290 H02411 C18327 AA367588 AA367557 H89632 C17954 AA568860 AI752983 AA699451 H04260 AI126118 AW193364 N94503 AA029995 T40536 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226 AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R65618 H73711 R58545 D79189 AW265710 R77664 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156623 AA368336 H63662
116301	52669_2	AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW968997 AA040053 AI807206 AW663917 AA454645 AA489238 BE241958 AA743491
103080	17092_1	AU077231 AA852219 M74092 X59798 M64349 NM_001758 AA226806 M73554 BE409154 AA160096 BE384352 AA160820 BE382880 BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077 W05266 AI824103 AI499061 AA642944 AI042556 AA906539 W60380 AI571777 AL135581 AA112340 N75459 AA592929 AI085348 AI278890 AA126942 AI023701 AI873252 AA156319 AI190622 W60289 AI274886 R81309 AA100801 AA227161 AI568929 AA160603 AI074344 AI344561 AI150778 AA852218 AA158286 N20142 AA622148 AA864225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI659596 AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE080779 AI918938 BE168117 BE087369 AW995539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H66084 AI146884 BE075154 AW992247 AI186525 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H99284 AA227101 AA631077 AA148042 AI740837 BE082728 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141 BE164704 H98049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329 BE541980 N42086 AA102307 AA113772 BE276181 H20622 W44436 W67604 W46412 AW771113 AI700578 AA502628 AA133137 BE274186 BE396090 BE613371 BE612645 W46650 W95203 W92651 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW169156 H24970 AW298822 AW080962 AI073747 W24123 AA577596 H21715 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W48631 AA908347 AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AA151696 T92084 AI689037 AI624162 W49709 AW514883 AA100676 AI366087 AA069474 AA525859 AW771076 AA029402 AA994114 AI351505 AW770816 AI333594 AI289794 AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI055890 AI660881 AI366117 AA403090 AI272818 AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079968 AI752231 AA076431 AA113245 AI168564 AA918965 AI066484 AI123599 AI921518 W94586 AA535600 AA064665 AA705388 AA064623 AA962503 AI924926 AW131206 AW275281 AI280632 T29597 W48728 AW954336 W38317 W94768 AI084717 W46567 AI245645 AW302501 N72201 AW510563 AW079132 AA207064 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526 AA487486 R92970 AA934071 AI080448 AA063257 C05786 N99099 R42969 AA887065 AA662686 AA533833 AA662304 H51748 BE539444 AI362164 AI814595 BE537043 AI168307 BE408935 AA453606 R89428 AA936527 AA936890 AW369618 AW264602 R18074 AI474189 AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086652 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692

132520	45737_1	AA257992 AA317029 AA362097 D17042 H48100 AW838107 AW838106 AW838110 AW838231 AW610241 AW838442 AA045061 AW384991 BE000988 AA131806 BE180577 AW838269 AL039831 AI754380 C06051 AA131737 AW838239 AI767465 AI480134 AA610312 AW838190 AA379252 AW838282 AA484027 AI423413 AI685064 BE328307 AI241857 AW838281 AW838284 AI671267 AI814928 AA828367 AI476306 AI270180 AA622362 AI076497 AI635919 AI444994 AI194028 AI669159 AI928131 AA448853 AI350143 AW079289 AW467807 AA480442 AA522935 BE180570 AW380087 AW380109 AI081015 AI690818 AI589485 AI698510 AA642019 AA714366 AI580430 AA985527 AI740475 C21398 AA257993 AI302393 AI689018 AW770194 AW753750 AI079164 BE550338 AA559851 T16108 AI864822 AI932827 AA045095 AA045062 AI954225 AA768569 AA709308 AW958363
117602	10565_-4	N35020
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102745	13186_1	AW753865 F07644 F11280 F06355 F08136 U79299 F07459 F08750 F12419 F12842 F06488 F08585 F13403 F05921 F05512 F11683 F05416 F12841 F12810 F05418 F12850 R24551 F06276 H11803 H10237 H11542 H22894 R59563 H19351 H18722 F11237 F08507 H23123 R61595 F07796 F06201 F12289 F07107 T78113 F08734 F13344 F05760 F11784 F08780 F05835 R20588 F07739 F11497 R17410 H17414 R20440 T66090 R25292 T66236 T78766 T79908 R25286 R60071 C14761 AW905192 AA331914 AW965291 H09000 F05212 F08313 F05825 H06399 H15135 H11378 R66424 R61541 AA235405 AI205041 R59564 H23124 H18638 R37359 AI571275 R41780 T66174 T66159 R54102 W07657 H10794 R52337 R42890 H14354 R40952 T17391 H12068 R56797 R51000 R60011 R37617 R39434 H29286 T16403 H09129 R49114 H15161 H11729 R39160 H10468 H24454 H11432 R54433 H08768 H24042 H09511 H17281 H15292 R37849 AI991965 R52815 R42850 T17390 T16438 T17388 T16285 R48963 R50782 R44247 R46729 R59558 R40696 R43575 R44420 T17403 R37754 R46637 R51039 R40513 T23785 F10433 T16350 H10191 R43688 T23543 H08591 R44351 R37575 R49508 F04379 F04056 F05067 F02010 F09158 F10036 F08900 F02559 F09914 F09434 F05034 H17415 F02644 H10650 F10451 H14589 F10444 T16440 R44517 R46643 F03993 F10443 F02170 F09343 F10414 F04794 F11122 F04997 F03894 AW005932 F02767 F10941 F01777 R45260 F03386 R45261 T65009 F10990 F08942 F01673 H23253 F04533 F02082 F01669 F03689 H09568 R40763 H06400 R50958 N80570 AI082296 AI198226 T23763 AA814486 AW015823 AI886272 H06514 AA515969 F10049 AI984267 AI886279 AA558516 F02071 AI783843 AI804884 F01468 AA730438 AF035301 R38389 R41440 R59468 R14437 T89036 R43560 H10821 R52850 R56722 R14559 T09299 H10467 R25829 F13546 R56796 R51151 D82657 T32952 T66257 H06569 F12430 T74326 H08489 R34430 R13083 H23364 R21134 T77098 AW957157 H24150 H11403 R52336 F12830 T77173 T74281 T77663 T74736 H10649 H12067 R20092 T74735 R54530 R17552 R59557 R54529 H17280 T75171 H14694 T74975 H15291 R18574 R54157 R13446 H15221 R35120 R35031 R21277 R19632 R35820 R50899 R13923 R36771 R26485 R33061 R20100 H24426 H09184 H15958 R19253 H15196 H09510 R36032 R19691 H14402 H14885 T17068
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120147	386607_2	AI917116 AA633698 AI580389 Z39483
113003	420161_1	AW292315 AI090408 AW517041 AI928695 AI092060 AA716741 N98235 T23629
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104691	41308_1	U29690 AF272890 AA708166 AA010748 R23839 H59572 R23383 AI625747 AA011176 AW665324 H02674 H59573 AA757931 H12502 R66851 AA702310 AA748431 AA749352 C01127 AI003679 T96352
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127664	394361_1	AA806164 AA678564 AW978234 AW023951 AA651859 AI699785 AA913686 AW974569 AI681287
106111	4671_1	AW875398 AI064861 NM_014138 AF090943 BE071887 BE547232 BE622599 AI345700 AA284315 AA147700 AW376340 BE220170 BE348475 AA025037 AA057284 AA025038 T16193 AW130196 AW594516 AI989991 AI139091 AW675747 AA830435 AI924977 AI670778 AI051887 AA912574 AW130213 AI828335 AI570587 AI332760 AI313115 AA804653 AA477920 AA147645 AI916912 AW768839 AA715098 AA292723 AA732421 T33122 AI631560 AI698686 AI185386 R43829 AA421638 AA961400 C00503 AA604025 AA554026 AA553885 BE172244 R24040
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105782	246361_1	H09748 R61554 AA350215 R40551
120830	244476_1	AI568170 AA731212 AW294848 AW466878 AA568908 AI281804 AI923633 AA347885 AI718854 AA714940
128797	20410_1	NM_002975 AF020044 AB009244 BE620464 AA541683 AW000991 AW089850 AW664612 AI636676 AI627854 AI885823 AI864548 AI554122 AI499682 AI570905 AI376008 AI871364 AI074230 AI383719 AA905016 AA977446 AA844732 T78922 AW244007 AI924747 AI968230 AI824575 AI699224 AI569490 AW379856 AW292314 AI016874 AW292037
106533	305354_1	AL134708 AW206610 AW665919 AW594227 AI917093 AI498361 AA635141 AA453786 D54178 D53224 AI804341 D53111 M78885 AL134707 AA453903 AI278054 AI334339 AI380496 AW235939 D60373 D60993 D81246
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129703	64196_1	BE388665 AA740614 AI394542 AA484451 AW070675 AA877654 AI360981 AI475799 BE349560 AL037351 N29437 AI246453 AW083444 AA844441 AI150871 AI440477 AI889061 AA682422 AA680053 AA740212 AI858728 AA490589 AW243692 AI249450 AI304448 AA534421 AI500317 AI273337 AW027729 AI979132 C06120 AI660916 AW591923 AI803174 AI559264 BE250500 AW675522 AA883284 T71033 AI346838 AI066754 AI197913 AA931979 AA427599 AI304730 AI285159 AI273325 AI038450 AI033760 N74972 AA136517 AI304446 AI262652 AA401348 AW514617 AI361795 AW514389 N30307 N93439 AA190775 BE349902 AI342114 AI186831 AA039628 H74242 AI914825 AI955761 AI343851 AA693856 T71096 AI498539 AA778995 AA084278 AI274678 AI022673 AW339621 AA704929 AW089735 AA041252 AA161337 AI185333 AW189397 AI160990 AI082392 AI935848 AI144404 AI141633 AA447987 AA464241 AI342103 AW026118 AA834025 AW664459 AA603777 AA630752 AA115450 N49944 AW166071 AW769795 AA991877 AA873609 AW083441 H99130 AA910538 AA486199 AW083358 AA151767 AI161193 N54945 AA180193 AI423477 AI188387 AI608747 N58900 AI038449 AA136852 AA565913 AA180502 H61741 AA701125 AI127678 AA278541 R76523 AA666187 H85083 F24755 R77729 AA135137 BE250395 R76239 AW794625 AW794404 H61957 AA308197 AW996031 AA345524 N52726 AA354360 AA179785 N57375 R16447 AA160645 W21481
100299	2801_1	D49493 NM_004962 D49492 AA948479 AA993843 AA017558 AA992567 AA912897 AI185363 AA018254 N93253 AA297544 T19187 R53287 AA069337 AA297489 N62906 AW023929 AA018253 AA017615 W25110 R52085 R52633 W16549 H88916 H89134 AA069338
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123308	322009_1	C14187 AA496211 D80456 AA484051 D80455 AA528446
101104	26442_2	AW862258 L07615
130637	7040_1	AA356764 NM_004867 AF038953 W16828 R50284 AI929589 R01594 AA010474 W37917 N64212 N78175 R57511 AA329322 W77834 AA169869 AA285240 AA356670 T93146 AA325779 AA357064 AA328151 AA306939 AA306801 N31260 AA306202 AA312530 BE242703 AA354371 N42259 AL021786 H50965 H38038 AI655965 AI566732 AI953952 AW972835 AI077300 AI948482 AI760966 AA648335 W72197 N32815 AA768073 AW338181 AW001742 AI819896 AI015666 N58011 AA677584 AI183750 AW105514 W37875 AW301679 AA775257

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		AA730357 AI128690 AA630149 AW241515 AI147003 AI183499 N90923 AI968582 AA354145 AI147297 BE550502 AI085777 AI709087 AA773947 AA469192 AI199289 AI127085 H89232 N30719 AI028165 AW029469 AI709314 AA780834 AA778057 H89125 AI654762 T93061 N59622 AI360625 AA719982 AI248242 AA233925 AW262512 AW438666 AA010378 AA484010 AW438790 N22875 AA483718 AI185407 AA736720 AA664587 AA648672 AA503406 AA508123 AA503140 H46638 N75812 AA730938 D60546 AA483039 AA507705 AA480448 AI768654 AA658955 AA730803 AA330312 AW021127 BE172031 AW961052 AA339070 AA648172 BE172892 AA174175 AA492012 AA491590 AW118733 AA484130 AA730783 AA730510 D62577 D62828 AI469294 AI801343 N53447 AA740226 AI831983 AA516146 D79799 AI758212 AA484040 H38039 AI038772 AI039410 AA528387 AA730576 AA527231 AA748111 D62946 U38439 AA721708 H22130 AA559229 H51620 AA283355 AA730970 R01595 N72450 AA469123 AA579389 AA480477 AA283306 AA347822 AA328013
410102	117657_1	AW248508 AI278454 AI369343 AW291235 AI343946 AI347189 AA970152 AI279668 AI971894 AA664359 AI191039 AA084598 AA081641
410268	11897_1	AA316181 BE439545 AC005053 AF186249 AW386101 AC004969 AA730199 AA032221 AI686139 AI167942 AA809228 AI184070 AI394674 AW969977 AA032279 AW079284 AA513174 AA888312 AI453179 AA483363 AA528432 AA579511
414761	14860_1	AU077228 U61145 AL044256 AA206185 AL044975 NM_004456 X95653 AW890905 AA332806 AW965453 BE299226 U52965 BE275009 AA428252 AA769212 AA312778 AA810901 AA461315 AI969286 AI953668 AW296248 AI291422 AA704747 Z44716 BE541235 AW608806 AA588583 AW403788 AW408386 AA053521 T87571 AA581163 BE183241 T97906 R89149 AI808196 BE618521 AI970278 AI652680 AW130143 AI970272 AW197254 BE550449 AI628403 AA010143 AW005107 AA251815 AA805836 N53459 AA055309 AA643678 AI345616 AI345618 AI635728 AI871286 AI018437 AI262514 H75287 AI033155 AI203388 AA205802 AI475265 AW594186 AI696059 AI333312 AW264710 AA876764 AA864892 AA173156 AI292066 T79837 W93995 AA506427 AA815135 AI376342 AA010144 AI310421 AI223350 AA970576 N33926 T89364 AI090913 N55098 AA101673 AA626665 AA251840 N68857 AI890053 H05930 AI474199 AI436166 AA628810 N64452 AI205538 AA055310 BE244495 AI365179 T99536 AI203088 Z40549 AW139858 AA599627 R91847 AA483681 AW068982 H51746 AA091201 H13030 AA459732 T99430 AI051764 R45991
416836	16233_1	D54745 AU077189 NM_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571 H19813 AI745597 AI769202 AI205982 AW205841 R64324 AI201975 H46993 C18067 R71189 N29729 AI799838 AI091209 H87455 R82443 AW970995 AW072136 N40841 H13148 AI219052 N30191 T28007 AI817428 AA503602
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428183	287965_1	AW969726 AA424028 AI266636 AI271571 AA423988 AI266634 AA702780 AA452037 AI424866 AA742931 AA483361
439221	46993_1	AA737106 N35765 N35779 AF086045 N30152 AW374028 AI478237 AA923562 AI382236 AA846668 AI627389 AI371709 H98083 H95983 H26576 H95984 AA745021 AA639180 H26575
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Table 73: Sequences

Seq ID NO: B1 DNA sequence
Nucleic Acid Accession #: NM_053056.1
Coding sequence: 210..1097

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TCGGCGCAGT AGCAGCGAGC AGCAGAGTCC GCACGCTCCG GCGAGGGGCA GAAGAGCGCG   120
AGGGAGCGCG GGGCAGCAGA AGCGAGAGCC GAGCGCGGAC CCAGCCAGGA CCCACAGCCC   180
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AAACCATCCG CCGCGCGTAC CCCGATGCCA ACCTCCTCAA CGACCGGGTG CTGCGGGCCA   300
TGCTGAAGGC GGAGGAGACC TGCGCGCCCT CGGTGTCCTA CTTCAAATGT GTGCAGAAGG   360
AGGTCCTGCC GTCCATGCGG AAGATCGTCG CCACCTGGAT GCTGGAGGTC TGCGAGGAAC   420
AGAAGTGCGA GGAGGAGGTC TTCCCGCTGG CCATGAACTA CCTGGACCGC TTCCTGTCGC   480
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CTAAGATGAA GGAGACCATC CCCCTGACGG CCGAGAAGCT GTGCATCTAC ACCGACAACT   600
CCATCCGCCC CGAGCAGCTG CTGCAAATGG AGCTGCTCCT GGTGAACAAG CTCAAGTGGA   660
ACCTGGCCGC AATGACCCCG CACGATTTCA TTGAACACTT CCTCTCCAAA ATGCCAGAGG   720
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CAGATGTGAA GTTCATTTCC AATCCGCCCT CCATGGTGGC AGCGGGGAGC GTGGTGGCCG   840
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CCGAGGAGGA GGAAGAGGAG GAGGAGGAGG TGGACCTGGC TTGCACACCC ACCGACGTGC  1080
GGGACGTGGA CATCTGAGGG CGCCAGGCAG GCGGGCGCCA CCGCCACCCG CAGCGAGGGC  1140
GGAGCCGGCC CCAGGTGCTC CCCTGACAGT CCCTCCTCTC CGGAGCATTT TGATACCAGA  1200
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TCACACCGGA AGGTTTTTAA ACACTAAAAT ATATAATTTA TAGTTAAGGC TAAAAAGTAT  2520
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TTAAACACAC AGATACACAC ACACACACAC ACACACACAC AAACCTTCTG CCTTTGATGT  2640
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CACATCTTGG CTATGTAATT CTTGTAATTT TTATTTAGGA AGTGTTGAAG GGAGGTGGCA  2940
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CCGAGGGGAA GGGGCGGTGC CCACACCGGG GACAGGCCGC AGCTCCATTT TCTTATTGCG  3060
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AGGCCGCGTG CGTGAGAACC GCGCCGGTGT CCCCAGAGAC CAGGCTGTGT CCCTCTTCTC  3480
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GATGATTGGA ATAGCTTCTG GAATTTGTTC AAGTTTTGGG TATGTTTAAT CTGTTATGTA  3720
CTAGTGTTCT GTTTGTTATT GTTTTGTTAA TTACACCATA ATGCTAATTT AAAGAGACTC  3780
CAAATCTCAA TGAAGCCAGC TCACAGTGCT GTGTGCCCCG GTCACCTAGC AAGCTGCCCA  3840
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CATCCTGTGC TCGGAGGCCA TCTCGGGCAC AGGCCCACCC CGCCCCACCC CTCCAGAACA  3960
CGGCTCACGC TTACCTCAAC CATCCTGGCT GCGGCGTCTG TCTGAACCAC GCGGGGGCCT  4020
TGAGGGACGC TTTGTCTGTC GTGATGGGGC AAGGGCACAA GTCCTGGATG TTGTGTGTAT  4080
CGAGAGGCCA AAGGCTGGTG GCAAGTGCAC GGGGCACAGC GGAGTCTGTC CTGTGACGCG  4140
CAAGTCTGAG GGTCTGGGCG GCGGGCGGCT GGGTCTGTGC ATTTCTGGTT GCACCGCGGC  4200
GCTTCCCAGC ACCAACATGT AACCGGCATG TTTCCAGCAG AAGACAAAAA GACAAACATG  4260
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Seq ID NO: B2 Protein sequence
Protein Accession #: NP_444284.1

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1          11         21         31         41         51
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ATWMLEVCEE QKCEEEVFPL AMNYLDRFLS LEPVKKSRLQ LLGATCMFVA SKMKETIPLT   120
AEKLCIYTDN SIRPEELLQM ELLLVNKLKW NLAAMTPHDF IEHFLSKMPE AEENKQIIRK   180
HAQTFVALCA TDVKFISNPP SMVAAGSVVA AVQGLNLRSP NNFLSYYRLT RFLSRVIKCD   240
PDCLRACQEQ IEALLESSLR QAQQNMDPKA AEEEEEEEEE VDLACTPTDV RDVDI

Seq ID NO: B3 DNA sequence
Nucleic Acid Accession #: XM_044166
Coding sequence: 1..1576

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CGCCCTTCAG CTGGCTCTCG ATCAACTCTG CCTCCTGGGT TTGGGGGAGC CCCCCGCCCC   180
CAGGGCGGGC GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCCGCGCAGC CGACAGCCCC   240
CCCGCAGCCG GCGCCCGCCC CGCCGCCCGC GGCGCCCCCG GCCGCCCCGA CGACGGCCCC   300
CGCAGCGCAG ACGCCCCAGC CCCCCACCGC CCCCAAAGGG GCGAGCCACG CCAAGCTCTG   360
CGCTCTCTAC AAAGAGGCCG AGCTGCGCCT GAAGGGCAGC AGCAACACCA CGGAGTGTGT   420
TCCCGTGCCC ACCTCCGAGC ACGTGGCCGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA   480
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GGCTCCTGCT CTGCCCGGCC AGGTGACCAT CCGTGTGCGG GTGCCCTACC GCGTGGTGGG   720
GCTGGTGGTG GGCCCCAAAG GGGCAACCAT CAAGCGCATC CAGCAGCAAA CCAACACATA   780
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CGAGTACAAC AATGAAAACG ACTTCCTGGC GGGGAGCCCC GACGCAGCAA TCGATAGCCG   960
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CAAGCAGGAT GTGTACTACG GCGTGGCCGA GACTAGCCCC CCGCTGTGGG CGGGCCAGGA  1200
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AGAAAACAAA AATAGCAAAA AAAAAAAAAA AAAGCAGTTC TTTATAATTT AATATTCTAT  3420
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Seq ID NO: B4 Protein sequence
Protein Accession #: XP_044166.2

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RAGEDGGGGG GGAPAQPTAP PQPAPPPPPA APPAAPTTAP AAQTPQPPTA PKGASDAKLC   120
ALYKEAELRL KGSSNTTECV PVPTSEHVAE IVGRQGCKIK ALRAKTNTYI KTPVRGEEPV   180
FMVTGRREDV ATARREIISA AEHFSMIRAS RNKSGAAFGV APALPGQVTI RVRVPYRVVG   240
LVVGPKGATI KRIQQQTNTY IITPSRDRDP VFEITGAPGN VERARBEIET HIAVRTGKIL   300
EYNNENDPLA GSPDAAIDSR YSDAWRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFEAPRL   360
GEQGGDFGYG GYLFPGYGVG KQDVYYGVAE TSPPLWAGQE NATPTSVLFS SASSSSSSSA   420
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KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPLQGFSKLG GGGLRSPGGG RDCMVCFESE   480
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Seq ID NO: B5 DNA sequence
Nucleic Acid Accession #: NM_000909.1
Coding sequence: 209..1363

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AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTTGTCTAAA   180
ATAATCTATA ACAACCAAAC CAATCAAAAT GAATTCAACA TTATTTTCCC AGGTTGAAAA   240
TCATTCAGTC CACTCTAATT TCTCAGAGAA GAATGCCCAG CTTCTGGCTT TTGAAAATGA   300
TGATTGTCAT CTGCCCTTGG CCATGATATT TACCTTAGCT CTTGCTTATG GAGCTGTGAT   360
CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAAC AAAAGGAGAT   420
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CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC   540
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GGTTCTCATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA   660
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GCCTTTCCTG ATCTACCAAG TAATGACTGA TGAGCCGTTC CAAAATGTAA CACTTGATGC   780
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Seq ID NO: B6 Protein sequence
Protein Accession #: NP_000900.1

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LIIIILKQKE MRNVTNILIV NLSFSDLLVA IMCLPFTFVY TLMDHWVFGE AMCKLNPFVQ   120
CVSITVSIFS LVLIAVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT   180
DEPFQNVTLD AYKDKYVCFD QFPSDSHRLS YTTLLLVLQY FGPLCFIFIC YFKIYIRLKR   240
RNNMMDKMRD NKYRSSETKR INIMLLSIVV AFAVCWLPLT IFNTVFDWNH QIIATCNHNL   300
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KTSLKQASPV AFKKINNNDD NEKI

Seq ID NO: B7 DNA sequence
Nucleic Acid Accession #: NM_002590.2
Coding sequence: 204..3416

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TTCCGAGAGC CTGAGACTGA CGCCCGACCT GGAAACCAGA GAAGACTTCC TTAGCCTTTC   180
GGATCGCACT TGAGGCTGGA GGCATGAGTC CTGTGAGGCG TTGGGGCAGC CCCTGCCTTT   240
TCCCCTTGCA GCTCTTCAGC CTCTGCTGGG TGCTCTCAGT GGCCCAGAGC AAAACAGTCC   300
GATACAGCAC CTTCGAGGAG GATGCCCCCG GCACGGTCAT CGGGACCCTG GCCGAGGACC   360
TGCATATGAA AGTATCGGGT GACACAAGCT TCCGCCTGAT GAAGCAATTC AACAGCTCTC   420
TGCTCCGGGT GCGCGAAGGC GACGGGCAGC TGACCGTCGG GGACGCCGGC CTGGACCGCG   480
AGCGGCTGTG TGGCCAGGCC CCGCAGTGCG TGCTGGCCTT CGATGTGGTC AGCTTCTCGC   540
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AGGAGCAGTT CCGGCTGGTG CACGTGGAGG TAGAGGTGAG GGACGTCAAC GACCACGCGC   600
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Seq ID NO: B8 Protein sequence
Protein Accession #: NP_002581.2

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VEVEVRDVND HAPRFPRAQI PVEVSEGAAV GTRIPLEVPV DEDVGANGLQ TVRLAEPHSP   180
FRVELQTRAD GAQCADLVLL QELDRESQAA YSLELVAQDG GRPPRSATAA LSVRVLDAND   240
HSPAFPQGAV AEVELAEDAP VGSLLLDLDA ADPDEGPNGD VVFAFGARTP PEARRLFRLD   300
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RPYTVRVGDE NDNAPLFTRP VYEVSVRENN PPGAYLATVA ARDRDLGRNG QVTYRLLEAE   540
VGRAGGAVST YVSVDPATGA IYALRSFDYE TLRQLDVRIQ ASDGGSPQLS SSALVQVRVL   600
DQNDHAPVLV HPAPANGSLE VAVPGRTAKD TVVARVQARD ADEGANGELA FELQQQEPRE   660
AFAIGRRTGE ILLTGDLSQE PPGRVFRALL VISDGGRPPL TTTATVSFVV TAGGGRGPAA   720
PASAGSPERS RPPGSRLGVS GSVLQWDTPL IVIIVLAGSC TLLLAAIIAI ATTCNRRKKE   780
VRKGGALREE RPGAAGGGAS APGSPEEAAR GAGPRPNMFD VLTFPGTGKA PFGSPAADAP   840
PPAVAAAEVP GSEGGSATGE SACHFEGQQR LRGAHAEPYG ASPGFGKEPA PPVAVWKGHS   900
FNTISGREAE KFSGKDSGKG DSDFNDSDSD ISGDALKKDL INHMQSGLWA CTAECKILGH   960
SDRCWSPSCS GPNAHPSPHP PAQMSTFCKS TSLPRDPLRR DNYYQAQLPK TVGLQSVYEK  1020
VLHRDYDRTV TLLSPPRPGR LPDLQEIGVP LYQSPPGRYL SPKKGANENV
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Seq ID NO: B9 DNA sequence
Nucleic Acid Accession #: AL121939.12
Coding sequence: 185..1426

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1          11         21         31         41         51
|          |          |          |          |          |
AGCGGAGTST CAGTGGCGAG CTCCGGGTGC TGTGGCCCGG CCTTGGCGGG GCGGCCTCCG    60
GCTCAGGCTG GCTGAGAGGC TCCCAGCTGC AGCGTCCCCG CCCGCCTCCT CGGGAGCTCT   120
GATCTCAGCT GACAGTGCCC TCGGGGACCA AACAAGCCTG GCAGGACAAA ATTAGAAGAT   180
CAAAATGGAA AATATGCTGC TTTGGTTGAT ATTTTTCACC CCTGGGTGGA CCCTCATTGA   240
TGGATCTGAA ATCGAATGGG ATTTTATGTG GCACTTGAGA AAGGTACCCC GGATTGTCAG   300
TGAAAGGACT TTCCATCTCA CCAGCCCCGC ATTTGAGGCA GATGCTAAGA TGATGGTAAA   360
TACAGTGTGT GGCATCGAAT GCCAGAAAGA ACTCCCAACT CCCAGCCTTT CTGAATTGGA   420
GGATTATCTT TCCTATGAGA CTGTCTTTGA GAATGGCACC CGAACCTTAA CCAGGGTGAA   480
AGTTCAAGAT TTGGTTCTTG AGCCGACTCA AAATATCACC ACAAAGGGAG TATCTGTTAG   540
GAGAAAGAGA CAGGTGTATG GCACCGACAG CAGGTTCAGC ATCTTGGACA AAAGGTTCTT   600
AACCAATTTC CCTTTCAGCA CAGCTGTGAA GCTTTCCACG GGCTGTAGTG GCATTCTCAT   660
TTCCCCTCAG CATGTTCTAA CTGCTGCCCA CTGTGTTCAT GATGGAAAGG ACTATGTCAA   720
AGGGAGTAAA AAGCTAAGGG TAGGGTTGTT GAAGATGAGG AATAAAAGTG GAGGCAAGAA   780
ACGTCGAGGT TCTAAGAGGA GCAGGAGAGA AGCTAGTGGT GGTGACCAAA GAGAGGGTAC   840
CAGAGAGCAT CTGCAGGAGA GAGCGAAGGG TGGGAGAAGA AGAAAAAAAT CTGGCCGGGG   900
TCAGAGGATT GCCGAAGGGA GGCCTTCCTT TCAGTGGACC CGGGTCAAGA ATACCCACAT   960
TCCGAAGGGC TGGGCACGAG GAGGCATGGG GGACGCTACC TTGGACTATG ACTATGCTCT  1020
TCTGGAGCTG AAGCGTGCTC ACAAAAAGAA ATACATGGAA CTTGGAATCA GCCCAACGAT  1080
CAAGAAAATG CCTGGTGGAA TGATCCACTT CTCAGGATTT GATAACGATA GGGCTGATCA  1140
GTTGGTCTAT CGGTTTTGCA GTGTGTCYGA CGAATCCAAT GATCTCCTTT ACCAATAYTG  1200
CGATGCTGAG TCGGGCTCCA CCGGTTCGGG GGTCTATCTG CGTCTGAAAG ATCCAGACAA  1260
AAAGAATTGG AAGCGCAAAA TCATTGCGGT CTACTCAGGG CACCAGTGGG TGGATGTCCA  1320
CGGGGTTCAG AAGGACTACA ACGTTGCTGT TCGCATCACT CCCCTAAAAT ACGCCCAGAT  1380
TTGCCTCTGG ATTCACGGGA ACGATGCCAA TTGTGCTTAC GGCTAACAGA GACCTGAAAC  1440
AGGGCGGTGT ATCATCTAAA TCACAGAGAA AACCAGCTCT GCTTACCGTA GTGAGATCAC  1500
TTCATAGGTT ATGCCTGGAC TTGAACTCTG TCAATAGCAT TTCWACATTT TTCAAAATCA  1560
GGAGATTTTC GTCCATTTAA AAAATGTATA GGTGCAGATA TTGAAACTAG GTGGGCACTT  1620
CAATGCCAAG TATATACTCT TCTTTACATG GTGATGAGTT TCATTTGTAG AAAAATTTTG  1680
TTGCCTTCTT AAAAATTAGA CACACTTTAA ACCTTCAAAC AGGTATTATA AATAACATGT  1740
GACTCCTTAA TGGACTTATT CTCAGGGTCC TACTCTAAGA AGAATCTAAT AGGATGCTGG  1800
TTGTGTATTA AATGTGAAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA  1860
ATAGAGACAG AAAGTTACAA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGCTCAT  1920
GCCCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGGGA CATTTAGTTT AGTTTTTTTG  1980
AAGAATTACA AATCAGAAGA AAAAGCAAGC ATTATAAACA AAACTAATAA CTGTTTTACT  2040
GCTTTAAGAA ATAACAATTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTTCT  2100
ATGAAATAAA CCTAGTTTAG AAATAGGGAA GCTGAGACAT TTTAAGATCT CAAGTTTTTA  2160
TTTAACTAAT ACTCAAAATA TGGACTTTTC ATGTATGCAT AGGGAAGACA CTTCACAAAT  2220
TATGAATGAT CATGTGTTGA AAGCCACATT ATTTTATGCT ATACATTCTA TGTATGAGGT  2280
GCTACATTTT TAGGACAAAG AATTCTGTAA TCTTTTTCAA GAAAGAGTCT TTTTCTCCTT  2340
GACAAAATCC AGCTTTTGTA TGAGGACTAT AGGGTGAATT CTCTGATTAG TAATTTTAGA  2400
TATGTCCTTT CCTAAAAATG AATAAAATTT ATGAATATGA CTTAAAAAAA AAARWCGACG  2460
CGGCCGCGAA TTTAGTAGTA GTAGTCGACC CGGGAATTCC GGACCGGTAC CTGCAGGCGT  2520
ACCAGC
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Seq ID NO: B10 Protein sequence
Protein Accession #: CAC35071.1

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1          11         21         31         41         51
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MENMLLWLIF FTPGWTLIDG SEMEWDFMWH LRKVPRIVSE RTFHLTSPAF EADAKMMVNT    60
VCGIECQKEL PTPSLSELED YLSYETVFEN GTRTLTRVKV QDLVLEPTQN ITTKGVSVRR   120
KRQVYGTDSR FSILDKRFLT NPPFSTAVKL STGCSGILIS PQHVLTAAHC VHDGKDYVKG   180
SKKLRVGLLK MRNKSGGKKR RGSKRSRREA SGGDQREGTR EHLRERAKGG RRRKKSGRGQ   240
RIAEGRPSFQ WTRVKNTHIP KGWARGGMGD ATLDYDYALL ELKRAHKKKY MELGISPTIK   300
KMPGGMIHFS GFDNDRADQL VYRFCSVSDE SNDLLYQYCD AESGSTGSGV YLRLKDPDKK   360
NWKRKIIAVY SGHQWVDVHG VQKDYNVAVR ITPLKYAQIC LWIHGNDANC AYG
```

Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_002035.1
Coding sequence: 108..1106

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1          11         21         31         41         51
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CCGGCGGCCC CCGCCCGGCC GCTCCGGGCC CCTGGCCCCG CGGAGCGATG CTGCTGCTGG   120
CTGCCGCCTT CCTCGTGGCC TTCGTGCTGC TGCTGTACAT GGTGTCTCCG CTCATCAGCC   180
CCAAGCCCCT CGCCCTGCCC GGGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG   240
GGAAGTGCAT TGCTATCGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGCACGAA   300
ATGAGGATAA GCTGCTGCAG GCAAAGAAAG AAATTGAAAT GCACTCTATT AATGACAAAC   360
AGGTGGTGCT TTGCATATCA GTTGATGTAT CTCAAGACTA TAACCAAGTA GAGAATGTCA   420
TAAAACAAGC ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAAATTGT GCAGGAATGG   480
CAGTGTCAGG AAAATTTGAA GATCTTGAAG TTAGTACCTT TGAAAGGTTA ATGAGCATCA   540
ATTACCTGGG CAGCGTGTAC CCCAGCCGGG CCGTGATCAC CACCATGAAG GAGCGCCGGG   600
TGGGCAGGAT CGTGTTTGTG TCCTCCCAGG CAGGACAGTT GGGATTATTC GGTTTCACAG   660
CCTACTCTGC ATCCAAGTTT GCCATAAGGG GATTGGCAGA AGCTTTGCAG ATGGAGGTGA   720
AGCCATATAA TGTCTACATC ACAGTTGCTT ACCCACCAGA CACAGACACA CCTGGCTTTG   780
CCGAAGAAAA CAGAACAAAG CCTTTGGAGA CTCGACTTAT TTCAGAGACC ACATCTGTGT   840
GCAAACCAGA ACAGGTGGCC AAACAAATTG TTAAAGATGC CATACAAGGA AATTTCAACA   900
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GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA   960
CTTCTATTAC TGAGGGGCTC CAGCAGGTGG TCACCATGGG CCTTTTCCGC ACTATTGCTT  1020
TGTTTTACCT TGGAAGTTTT GACAGCATAG TTCGTCGCTG CATGATGCAG AGAGAAAAAT  1080
CTGAAAATGC AGACAAAACT GCCTAATCTT CTTACCCCTT GGAAGAAGAC TGTTTCCAAA  1140
TAATTTGAAC AGCTTGCTGC TAAATGGGAC CCAATTTTTG GCCTATAGAC ACTTATGTAT  1200
TGTTTTCGAA TACGTCAGAT TGGACCAGTG CTCTTCAGGA ATGTGGCTGC AAGCAAGGGG  1260
CTAGAAGTTC ACCTCCTGAC AGTATTATTA ATACTATGCA AATATGGAAT AGGAGACCAT  1320
TTGATTTTCT AGGCTTTGTG GTAGAGAGGT GAAGGTATGA GAATTAATAG CGTGTGAACA  1380
AAGTAAAGAA CAGGATTCCA GAATGATCAT TAAATTTGTT TCTATTTATT CTTTTTTGCC  1440
CCCCTAGAGA TTAAGTCCAG AAATGTACTT TCTGGCACAT AAAGAAATCT TGAGGACTTT  1500
GTTTAAACCT TCCATAAAAA AACAATTTTC GGTTTCTCGG GTTCTCTCTC TCTGTCTCTC  1560
TGTCTCTCTG TCTCTCTGTC TCTCTGTCTC TCTCTCTCTC TCTCTTTCTT TCTTTGTGTA  1620
TTTTATTCAA GATGAGTTGG ACCCATTGCC AGTGAGTCTG AATGTCACTG ACAGCCCTGT  1680
GTTGTGCTCA GGACTCACTC TGCTGCTGGT GGAAACTCAT GGCTTCTCTC TCTCTTTGAT  1740
CCCATAAAGC TACGAGGGGG ACGGGAGAGG GCAGTGCAAT GGGAAGTAAA GAGATATTTT  1800
CCAGTAGGAA AAGCAATGCT TTCTTGTCTT TAGACTCAAA TGCTTAGGGA ACGTTTCATT  1860
TCTCATTCAT GGGGAAAGGC AGCCTCCTTA AATGTTTTCT GAAGAGCGGT AAAATCTAGA  1920
AGCTTAAGAA TTTACAGTTC CTTCAATAAC CATGATGACC TGAAGTTCAC CTATCCCATT  1980
TTAGCATCTA CTTGTTTTTC CCATCTCTTC CTTTCCAATT TTGCTTATAC TGCTGTAATA  2040
TTTTTGTAAA AAAAAAAAAA AAGGAAAAAA AAGACCAGCT AAAATTTTCG ACTTGACTTT  2100
TTAACTTAAC TCATGAATTA ATTAAAGCAA ATGAAAAAAT TAAAAAGTGT GACTTTTTCT  2160
CGGAGCATAT ATGTAGCTTT TAGGAAAGGC TGATGATGGT ATAAAGTTTG CTCATTAAGA  2220
AAAAAAGACA AGGCTGATTT TGAAGAGAGT TGCTTTTGAA ATAAAATGAT CA
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Seq ID NO: B12 Protein sequence
Protein Accession #: NP_002026.1

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1          11         21         31         41         51
|          |          |          |          |          |
MLLLAAAFLV AFVLLLYMVS PLISPKPLAL PGAHVVVTGG SSGIGKCIAI ECYKQGAFIT    60
LVARNEDKLL QAKKEIEMHS INDKQVVLCI SVDVSQDYNQ VENVIKQAQE KLGPVDMLVN   120
CAGMAVSGKF EDLEVSTFER LMSINYLGSV YPSRAVITTM KERRVGRIVF VSSQAGQLGL   180
FGFTAYSASK FAIRGLAEAL QMEVKPYNVY ITVAYPPDTD TPGFAEENRT KPLETRLISE   240
TTSVCKPEQV AKQIVKDAIQ GNFNSSLGSD GYMLSALTCG MAPVTSITEG LQQVVTMGLF   300
RTIALFYLGS FDSIVRRCMM QREKSENADK TA
```

Seq ID NO: B13 DNA sequence
Nucleic Acid Accession #: CAT Cluster

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1          11         21         31         41         51
|          |          |          |          |          |
CTTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTTAA TTTTTAAAAT    60
CGGCAAAATA TTGGTGCCTT TCCCGAAATT TGGTCCCGGG CTCCCTTATA GGATAATTGG   120
TTTGGATTGG TTAAGTCCAA TTATTAAATG CTGCGGTTTC AAATTCCCAG CTGGAAGGAC   180
CACCCATTTA AAAACTTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAAAATT   240
CCAGGCATTG GTTTGACATA TTTCCAGAGC TCAAATCTGC AGTGTTCCAC ATGCACATAC   300
AAGATCCAGA GTCTCATGTT AAAATCACTT ACATACCCAG AAAGACCACC ACTTTGCAGG   360
TATAATATTG TACTTAAAGA CAGAGACGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA   420
AAGAACACAT AAGATGCCTT CTTCCATCAA ATGCACTTGC TTGTGAATTA ATGGACTTGT   480
AAATGAAACA ATGCAATCAG TCTTTTATAA TGCACTGTTC AATTTGAGAT TCAAGTATTT   540
CTATTTCTTG GAAAAAATTT TAAGAATCAA AAATAAAGAA AATAAAAAGT GCATACAGTT   600
AAACATTCCA AAAAAAAAAA AA
```

Seq ID NO: B14 DNA sequence
Nucleic Acid Accession #: XM_086767.1
Coding sequence: 276..611

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1          11         21         31         41         51
|          |          |          |          |          |
CTTGTTCATG GCATCTTTAG AAACAAACTG CAATTTTATT TCATTTCCTT GTCGTTCATA    60
CAAAGATTAC AAGACTAGCT TATGTGTGGA CTGTGACTGT TTTAAGGAAA AATCATGTCC   120
TCGGCTGGGT TATCAAGCCA AGCTATTTAA AGGTGTTTTA AAAGAAAGGA TGGAAGGAAG   180
ACCTCTTAGG ACCACTGTGT TTTTGGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT   240
ATTTTGTTCT CAGTATAATT GTTCCAGATA AAACTATGAT GGATGGCTCG TTTTCATTTA   300
AATTATTAAA TCAGCTTGGA ATGATTGAAG AGCCAAGGCT TTATGAAAAG AACAAACCAT   360
TTTATAAACT TCAAGAAGTC AAGATTCTTG CTCAATTTTA TAATGACTTT GTAAATATTT   420
CAAGCATTGG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCCACA TGCACATACA   480
AGATCCAGAG ACTCATGTTA AAATCACTTA CATACCCAGA AAGACCACCA CTTTGCAGGT   540
ATAATATTGT ACTTAAAGAC AGAGAGGAAG TGTTTCTTAA TCCAAACACA TGTACACCAA   600
AGAACACATA AGATGCCTTC TTCCATCAAA TGCACTTGCT TGTGAATTAA TGGACTTGTA   660
AATGAAACAA TGCAATCAGT CTTTTATAAT GCACTGTTCA ATTTGAGATT CAAGTATTTC   720
TATTTCTTGG AAAAAATTTT AAGAATCAAA AATAAAGAAA ATAAAAAATG CATACAGTTA   780
AACATTCC
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Seq ID NO: B15 Protein sequence
Protein Accession #: XP_086767.1

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1          11         21         31         41         51
|          |          |          |          |          |
MMDGSFSFKL LNQLGMIEEP RLYEKNKPFY KLQEVKILAQ FYNDFVNISS IGLTYFQSSN    60
LQCSTCTYKI QRLMLKSLTY PERPPLCRYN IVLKDREEVF LNPNTCTPKN T
```

Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

```
1          11         21         31         41         51
|          |          |          |          |          |
TTTTTTTTTT TTTTTTTTTT TTAAATGCAA AGGAGCAACA AAATTTATTG ACTGAATTAA    60
ACACAACAGT AAAATGGCAG TGTTGTAATT TCATTTTCAG ATGTTTGAAT GGAACAAGAA   120
AAGTGCTATT AGCCCAAGCT TCTTACATTC ATTAAAAGAG TGACTATCAA AAACAGCAAC   180
ATGCACAATG GTACATATGC ACAAAATGGA ATTATATCAA CAAATATACA AAATACCCAA   240
AATAAAATAT TTACAGGTTT AAAAATATAA ACATTGATTC CTCTATCCCA TTAAACCATT   300
GGAGTGGAGA AAGGAGGAAA GACCCTATTG CTATTTAGAA TCCTTTTTAA AACAAGTTTT   360
TAAAACATAG AATTAGTTCT AGGAGACAAT TTTTGATGTT TTTCAGGGGT TTAACATTCT   420
ATTATAAAAA TAACATCTAT AAACCTACTA ACAATTTTCC TCCTGTGCAC AAAAATAATA   480
CTGCCAAAAC CTGTCCTCAA AGACATGCCT GACTTTCAGG AAAGCTAATT ATGGAAATGG   540
AGTTTCTCGT TTGGGTTATC TTTGTTACTA TTTTCAAATA ACCAGCAACT CCCTATATTA   600
CACTGAGATA CTTTATATAA ATAACGTGGG CGAAACCTGA AGTTCACAAT GAGCCTGCTA   660
GGTAGCTGGT GTCAAGTACA AATGATAGGA ATTGACTTTG CCAACAACAT CAAAAGCATT   720
TTCCCTGATA TTCCTGATAG ACCTACCACT ATCAGATCCT CCATATTCAA TAAGATTTAT   780
CCTGGAAGCA ATGAAAATGT TAAATATTAC TTTGCTAGAG TTTCTCCTCC TTTATTTAGA   840
AATAAATGTG TAGTGGGGAC CAGTGGTTGT AATGTAGATA CTTGAGAAGT TTCATTGATT   900
CCTTCAGACC CATGCCG
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Seq ID NO: B17 DNA sequence
Nucleic Acid Accession #: NM_022898.1
Coding sequence: 268..2739

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1          11         21         31         41         51
|          |          |          |          |          |
TTTTCTTGCT TTTCTTCCCT TTTTTTTCTT TTTGCAAACA AAACAAAAAA CAGCATAGAA    60
GAAAGAGCAA AATAAAGAAG AAGAAGAGGA GGAAGAGAGG GAAAGAGAGG AAGGGAAAAA   120
AAACACCAAC CCGGGCAGAG GAGGAGGTGC GGCGGCGGCG GCGGCGGCGG CAGCGGCGGC   180
AGCGGCGCGG CGGCGGCTCG GACCCCCTCC CCCGGCTCCC CCCATCAGTG CAGCTCTCCG   240
GGCGATGCCA GAATAGATGC CGGGGCAATG TCCCGCCGCA AACAGGGCAA CCCGCAGCAC   300
TTGTCCCAGA GGGAGCTCAT CACCCCAGAG GCTGACCATG TGGAGGCCGC CATCCTCGAA   360
GAAGACGAGG GTCTGGAGAT AGAGGAGCCA AGTGGCCTGG GGCTGATGGT GGGTGGCCCC   420
GACCCTGACC TGCTCACCTG TGGCCAGTGT CAAATGAACT TCCCCTTGGG GGACATCCTG   480
GTTTTTATAG AGCACAAAAG GAAGCAGTGT GGCGGCAGCT TGGGTGCCTG CTATGACAAG   540
GCCCTGGACA AGGACAGCCC GCCACCCTCC TCACGCTCCG AGCTCAGGAA AGTGTCCGAG   600
CCGGTGGAGA TCGGGATCCA AGTCACCCCC GACGAAGATG ACCACCTGCT CTCACCCACG   660
AAAGGCATCT GTCCCAAGCA GGAGAACATT GCAGGTAAAG ATGAGCCTTC CAGCTACATT   720
TGCACAACAT GCAAGCAGCC CTTCAACAGC GCGTGGTTCC TGCTGCAGCA CGCGCAGAAC   780
ACGCACGGCT TCCGCATCTA CCTGGAGCCC GGGCCGGCCA GCAGCTCGCT CACGCCGCGG   840
CTCACCATCC CGCCGCCGCT CGGGCCGGAG GCCGTGGCGC AGTCCCCGCT CATGAATTTC   900
CTGGGCGACA GCAACCCCTT CAACCTGCTG CGCATGACGG GCCCCATCCT GCGGGACCAC   960
CCGGGCTTCG GCGAGGGCCG CCTGCCGGGC ACGCCGCCTC TCTTCAGTCC CCCGCCGCGC  1020
CACCACCTGG ACCCGCACCG CCTCAGTGCC GAGGAGATGG GGCTCGTCGC CCAGCACCCC  1080
AGTGCCTTCG ACCGAGTCAT GCGCCTGAAC CCCATGGCCA TCGACTCGCC CGCCATGGAC  1140
TTCTCCGCGC GGCTCCGCGA GCTGGCGGGC AACAGCTCCA CGCCGCCGCC CGTGTCCCCG  1200
GGCCGCGGCA ACCCTATGCA CCGGCTCCTG AACCCCTTCC AGCCCAGCCC CAAGTCCCCG  1260
TTCCTGAGCA CGCCGCCGCT GCCGCCCATG CCCCCTGGCG GCACGCCGCC CCCGCAGCCG  1320
CCAGCCAAGA GCAAGTCGTG CGAGTTCTGC GGCAAGACCT TCAAGTTCCA GAGCAATCTC  1380
ATCGTGCACC GGCGCAGTCA CACGGGCGAG AAGCCCTACA AGTGCCAGCT GTGCGACCAC  1440
GCGTGCTCGC AGGCCAGCAA GCTCAAGCGC CACATGAAGA CGCACATGCA CAAGGCCGGC  1500
TCGCTGGCCG GCCGCTCCGA CGACGGGCTC TCGGCCGCCA GCTCCCCCGA GCCCGGCACC  1560
AGCGAGCTGG CGGGCCAGGG CCTCAAGGCG GCCGACGGTG ACTTCCGCCA CCACGAGAGC  1620
GACCCGTCGC TGGGCCACGA GCCGGAGGAG GAGGACGAGG AGGAGGAGGA CGAGGAGGAG  1680
GAGCTGCTAC TGGAGAACGA GAGCCGGCCC GAGTCGAGCT TCAGCATGGA CTCGGAGCTG  1740
AGCCGCAACC GCGAGAACGG CGGTGGTGGG GTGCCCGGGG TCCCGGGCGC GGGGGGCGGC  1800
GCGGCCAAGG CGCTGGCTGA CGAGAAGGCG CTGGTGCTGG GCAAGGTCAT GGAGAACGTG  1860
GGCCTAGGCG CACTGCCGCA GTACGGCGAG CTCCTGGCCG ACAAGCAGAA GCGCGGCGCC  1920
TTCCTGAAGC GTGCGGCGGG CGGCGGGGAC GCGGGCGACG ACGACGACGC GGGCGGCTGC  1980
GGGGACGCGG GCGCGGGCGG CGCGGTCAAC GGGCCCGGGG GCGGCTTCGC GCCAGGCACC  2040
GAGCCCTTCC CCGGGCTCTT CCCGCGCAAG CCCGCGCCGC TGCCCAGCCC CGGGCTCAAC  2100
AGCGCCGCCA AGCGCATCAA GGTGGAGAAG GACCTGGAGC TGCCGCCCGC CGCGCTCATC  2160
CCGTCCGAGA ACGTGTACTC GCAGTGGCTG GTGGGCTACG CGGCGTCGCG GCACTTCATG  2220
AAGGACCCCT TCCTGGGCTT CACGGACGCA CGACAGTCGC CCTTCGCCAC GTCGTCCGAG  2280
CACTCGTCCG AGAACGGCAG CCTGCGCTTC TCCACGCCGC CCGGGGACCT GCTGGACGGC  2340
GGCCTCTCGG GCCGCAGCGG CACGGCCAGC GGAGGCAGCA CCCCGCACCT GGGCGGCCCG  2400
GGCCCCGGGC GGCCCAGCTC CAAGGAGGGC CGCCGCAGCG ACACGTGCGA GTACTGCGGC  2460
AAGGTGTTCA AGAACTGCAG CAACTTGACG GTGCACCGGC GGAGCCACAC CGGCGAGCGG  2520
CCTTACAAGT GCGAGCTGTG CAACTACGCG TGCGCGCAGA GCAGCAAGCT CACGCGCCAC  2580
ATGAAGACGC ACGGGCAGAT CGGCAAGGAG GTGTACCGCT GCGACATCTG CCAGATGCCC  2640
TTCAGCGTCT ACAGCACCCT GGAGAAACAC ATGAAAAAGT GGCACGGCGA GCACTTGCTG  2700
ACTAACGACG TCAAAATCGA GCAGGCCGAG AGGAGCTAAG CGCGCGGGCC CCGGCGCCCC  2760
GCACCTGTAC AGTGGAACCG TTGCCAACCG AGAGAATGCT GACCTGACTT GCCTCCGTGT  2820
CACCGCCACC CCGCACCCCG CGTGTCCCCG GGGCCCAGGG GAGGCGGCAC TCCAACCTAA  2880
CCTGTGTCTG CGAAGTCCTA TGGAAACCCG AGGGTTGATT AAGGCAGTAC AAATTGTGGA  2940
GCCTTTTAAC TGTGCAATAA TTTCTGTATT TATTGGGTTT TGTAATTTTT TTGGCATGTG  3000
CAGGTACTTT TTATTATTAT TTTTTCTGTT TGAATTCCTT TAAGAGATTT TGTTGGGTAT  3060
CCATCCCTTC TTTGTTTTTT TTTTAACCCG GTAGTAGCCT GAGCAATGAC TCGCAAGCAA  3120
TGTTAGAGGG GAAGCATATC TTTTAAATTA TAATTTGGGG GGAGGGGTGG TGCTGCTTTT  3180
TTGAAATTTA AGCTAAGCAT GTGTAATTTC TTGTGAAGAA GCCAACACTC AAATGACTTT  3240
TAAAGTTGTT TACTTTTTCA TTCCTTCCTT TTTTTTGTCC TGAAATAAAA AGTGGCATGC  3300
AGTTTTTTTT TTAATTATTT TTTAATTTTT TTTTTGGTTT TTGTTTTTGG GGTGGGGGGT  3360
GTGGATGTAC AGCGGATAAC AATCTTTCAA GTCGTAGCAC TTTGTTTCAG AACTGGAATG  3420
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GAGATGTAGC ACTCATGTCG TCCCGAGTCA AGCGGCCTTT TCTGTGTTGA TTTCGGCTTT 3480
CATATTACAT AAGGGAAACC TTGAGTGGTG GTGCTGGGGG AGGCACCCCA CAGACTCAGC 3540
GCCGCCAGAG ATAGGGTTTT TGGAGGGCTC CTCTGGGAAA TGGCCCGACA GCATTCTGAG 3600
GTTGTGCATG ACCAGCAGAT ACTATCCTGT TGGTGTGCCC TGGGGTGCCA TGGCTGCTAT 3660
TCGCTGTAGA TTAGGCTACA TAAAATGGGC TGAGGGTACC TTTTTGGGGA GATGGGGTGG 3720
CCTGCAGTGA CACAGAAAGG AAGAAACTAG CGGTGTTCTT TTAGGCGTTT TCTGGCTTGA 3780
CGGCTTCTCT CTTTTTTTAA ATCACCCCCA CCACATAAAT CTCAAATCCT ATGTTGCTAC 3840
AAGGGGTCAT CCATCATTTC CCAAGCAGAC GAATGCCCTA ATTAATTGAA GTTAGTGTTC 3900
TCTCATTTAA TGCACACTGA TGATATTGTA GGGATGGGTG GGGTGGGGAT CTTGCAAATT 3960
TCTATTCTCT TTTACTGAAA AAGCAGGGGA TGAGTTCCAT CAGAAGGTGC CCAGCGCTAC 4020
TTCCCAGGTT TTTATTTTTT TTTTCCTATC TCATTAGGTT GGAAGGTACT AAATATTGAA 4080
CTGTTAAGAT TAGACATTTG AATTCTGTTG ACCCGCACTT TAAAGCTTTT GTTTGCATTT 4140
AAATTAAATG GCTTCTAAAC AAGAAATTGC AGCATATTCT TCTCTTTGGC CCAGAGGTGG 4200
GTTAAACTGT AAGGGACAGC TGAGATTGAG TGTCAGTATT GCTAAGCGTG GCATTCACAA 4260
TACTGGCACT ATAAAGAACA AAATAAAATA ATAATTTATA GGACAGTTTT TCTACTGCCA 4320
TTCAATTTGA TGTGAGTGCC TTGAAAACTG ATCTTCCTAT TTGAGTCTCT TGAGACAAAT 4380
GCAAAACTTT TTTTTGAAA TGAAAAGACT TTTTAAAAAA GTAAAACAAG AAAAGTACAT 4440
TCTTTAGAAA CTAACAAAGC CACATTTACT TTAAGTAAAA AAAAAAAAAA TTCTGGTTGA 4500
AGATAGAGGA TATGAAATGC CATAAGACCC AATCAAATGA AGAAATAAAC CCAGCACAAC 4560
CTTGGACATC CATTAGCTGA ATTATCCTCA GCCCCTTTTG TTTTTGGGAC AACGCTGCTT 4620
AGATATGGAG TGGAGGTGAT TTACTGCTGA ATTAAAACTC AAGTGACACA AGTTACAAGT 4680
TGATATCGTT GAATGAAAAG CAAAACAAAA ACAATTCAGG AACAACGGCT AATTTTTTCT 4740
AAAGTTAAAT TTAGTGCACT CTGTCTTAAA AATACGTTTA CAGTATTGGG TACATACAAG 4800
GGTAAAAAAA AAATTGTGTG TATGTGTGTT GGAGCGATCT TTTTTTTTCA AAGTTTGCTT 4860
AATAGGTTAT ACAAAAATGC CACAGTGGCC GCGTGTATAT TGTTTTCTTT TGGTGACGGG 4920
GTTTTAGTAT ATATTATATA TATTAAAATT TCTTGATTAC TGTAAAAGTG GACCAGTATT 4980
TGTAATAATC GAGAATGCCT GGGCATTTTA CAAAACAAGA AAAAAAATAC CCTTTTCTTT 5040
TCCTTGAAAA TGTTGCAGTA AAATTTAAAT GGTGGGTCTA TAAATTTGTT CTTGTTACAG 5100
TAACTGTAAA GTCGGAGTTT TAGTAAATTT TTTTCTGCCT TGGGTGTTGA ATTTTTATTT 5160
CAAAAAAAAT GTATAGAAAC TTGTATTTGG GGATTCAAAG GGGATTGCTA CACCATGTAG 5220
AAAAAGTATG TAGAAAAAAA GTGCTTAATA TTGTTATTGC TTTGCAGAAA AAAAAAAAAT 5280
CACATTTCTG ACCTGTACTT ATTTTTCTCT TCCCGCCTCC CTCTGGAATG GATATATTGG 5340
TTGGTTCATA TGATGTAGGC ACTTGCTGTA TTTTTACTGG AGCTCGTAAT TTTTTAACTG 5400
TAAGCTTGTC CTTTTAAAGG GATTTAATGT ACCTTTTTGT TAGTGAATTT GGAAATAAAA 5460
AGAAAAAAAA AACAAAAACA AACAGGCTGC CATAATATAT TTTTTTAATT TGGCAGGATA 5520
AAATATTGCA AAAAAAACAC ATTTGTATGT TAAGTCCTAT TGTACAGGAG AAAAAGGGTT 5580
GTTTGACAAC CTTTGAGAAA AAGAAACAAA AGGAAGTAGT TAAATGCTTT GGTTCACAAA 5640
TCATTTAGTT GTATATATTT TTTGTCGGAA TTGGCCTACA CAGAGAACCG TTCGTGTTGG 5700
GCTTCTCTCT GAACGCCCCG AACCTTGCAT CAAGGCTCCT TGGTGTGGCC ACAGCAGACC 5760
AGATGGGAAA TTATTTGTGT TGAGTGGAAA AAAATCAGTT TTTGTAAAGA TGTCAGTAAC 5820
ATTCCACATC GTCCTCCCTT TCTCTAAGAG GCCATCTCTA AGATGTCAGA TGTAGAGGAG 5880
AGAGAGCGAG AGAACATCTT CCTTCTCTAC CATCACTCCT GTGGCGGTCA CCACCACCAC 5940
CTCTCCCGCC CTTACCAGCA GAAAGCAATG CAAACTGAGC TGCTTTAGTC CTTGAGAAAT 6000
TGTGAAACAA ACACAAATAT CATAAAAGGA GCTGGTGATT CAGCTGGGTC CAGGTGAAGT 6060
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ACCTTTCGTG CCATGGAGAG TGTTGGCCTC TTGTCTTTCT TCCCTGCTTT GCTGCTTTGC 6180
TCTCTGAAAC CTACATTCCG TCAGTTTCCG AATGCGAGGG CCTGGGATGA ATTTGGTGCC 6240
TTTCCATATC TCGTTCTCTC TCCTTCCCCT GCGTTTCCTC TCCATCCTTC ATCCTCCATT 6300
GGTCCTTTTT TTTTCTTTCA TTTTTTATTT AATTTCTTTT CTTCCTGTCT GTTCCTCCCC 6360
TAATCCTCTA TTTTATTTTT ATTTTTTGTA AAGCCAAGTA GCTTTAAGAT AAAGTGGTGG 6420
TCTTTTGGAT GAGGGAATAA TGCATTTTTA AATAAAATAC CAATATCAGG AAGCCATTTT 6480
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CTCTGTGACT GCAGAGAAGA GAGAATTTTG CTTCTGTTTT GTGTTTAAAA AACCAACACG 6900
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TTAGAGGGTC TTTCATGGGG AGAGAAGGAG ACTGAATTAC TCTAAGCAAA ATGTGAAAAG 7080
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ACAGGCAAAC CCGTGATTTT GGTGCTCCTT GTAACTCAGC CCTGCAAAGC AAAGTCCCAT 7200
TGATTTAAGT TGTTTGCATT TGTACTGGCA AGGCAAAATA TTTTTATTAC CTTTTCTATT 7260
ACTTATTGTA TGAGCTTTTG TTGTTTACTT GGAGGTTTTG TCTTTTACTA CAAGTTTGGA 7320
ACTATTTATT ATTGCTTGGT ATTTGTGCTC TGTTTAAGAA ACAGGCACTT TTTTTTATTA 7380
TGGATAAAAT GTTGAGATGA CAGGAGGTCA TTTCAATATG GCTTAGTAAA ATATTTATTG 7440
TTCCTTTATT CTCTGTACAA GATTTTGGGC CTCTTTTTTT CCTTAATGTC ACAATGTTGA 7500
GTTCAGCATG TGTCTGCCAT TTCATTTGTA CGCTTGTTCA AAACCAAGTT TGTTCTGGTT 7560
TCAAGTTATA AAAATAAATT GGACATTTAA CTTGATCTCC AAA

Seq ID NO: B18 Protein sequence
Protein Accession #: NP_075049.1

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CQMNFPLGDI LVFIEHKRKQ CGGSLGACYD KALDKDSPPP SSRSELRKVS EPVEIGIQVT   120
PDEDDHLLSP TKGICPKQEN IACKDEPSSY ICTTCKQPFN SAWFLLQHAQ NTHGFRIYLE   180
PGPASSSLTP RLTIPPPLGP EAVAQSPLMN FLGDSNPFNL LRMTGPILRD HPGFGEGRLP   240
GTPPLFSPPP RHHLDPHRLS AEEMGLVAQH PSAFDRVMRL NPMAIDSPAM DFSRRLRELA   300
GNSSTPPPVS PGRGNPMHRL LNPFQPSPKS PFLSTPPLPP MPPGGTPPPQ PPAKSKSCEF   360
CGKTFKFQSN LIVHRRSHTG EKPYKCQLCD HACSQASKLK RHMKTHMHKA GSLAGRSDDG   420
LSAASSPEPG TSELAGEGLK AADGDFRHHE SDPSLGHEPE EEDEEEEEEE EELLLENESR   480
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PESSFSMDSE LSRNRENGGG GVPGVPGAGG GAAKALADEK ALVLGKVMEN VGLGALPQYG   540
ELLADKQKRG AFLKRAAGGG DAGDDDDAGG CGDAGAGGAV NGRGGGFAPG TEPFPGLFPR   600
KPAPLPSPGL NSAAKRIKVE KDLELPPAAL IPSENVYSQW LVGYAASRHF MKDPFLGFTD   660
ARQSPFATSS EHSSENGSLR FSTPPGDLLD GGLSGRSGTA SGGSTPHLGG PGPGRPSSKE   720
GRRSDTCEYC GKVFKNCSNL TVHRRSHTGE RPYKCELCNY ACAQSSKLTR HMKTHGQIGK   780
EVYRCDICQM PFSVYSTLEK HMKKWHGEHL LINDVKIEQA ERS

Seq ID NO: B19 DNA sequence
Nucleic Acid Accession #: NM_000399.2
Coding sequence: 339..1769

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TGGCAAATAG ACATTTTTCT TATTTCTTAA AAAACAGCAA CTTGTTTGCT ACTTTTATTT   180
CTGTTGATTT TTTTTTCTTG GTGTGTGTGG TGGTTGTTTT TAAGTGTGGA GGGCAAAAGG   240
AGATACCATC CCAGGCTCAG TCCAACCCCT CTCCAAAACG GCTTTTCTGA CACTCCAGGT   300
AGCGAGGGAG TTGGGTCTCC AGGTTGTGCG AGGAGCAAAT GATGACCGCC AAGGCCGTAG   360
ACAAAATCCC AGTAACTCTC AGTGGTTTTG TGCACCAGCT GTCTGACAAC ATCTACCCGG   420
TGGAGGACCT CGCCGCCACG TCGGTGACCA TCTTTCCCAA TGCCGAACTG GGAGGCCCCT   480
TTGACCAGAT GAACGGAGTG GCCGGAGATG GCATGATCAA CATTGACATG ACTGGAGAGA   540
AGAGGTCGTT GGATCTCCCA TATCCCAGCA GCTTTGCTCC CGTCTCTGCA CCTAGAAACC   600
AGACCTTCAC TTACATGGGC AAGTTCTCCA TTGACCCTCA GTACCCTGGT GCCAGCTGCT   660
ACCCAGAAGG CATAATCAAT ATTGTGAGTG CAGGCATCTT GCAAGGGGTC ACTTCCCCAG   720
CTTCAACCAC AGCCTCATCC AGCGTCACCT CTGCCTCCCC CAACCCACTG GCCACAGGAC   780
CCCTGGGTGT GTGCACCATG TCCCAGACCC AGCCTGACCT GGACCACCTG TACTCTCCGC   840
CACCGCCTCC TCCTCCTTAT TCTGGCTGTG CAGGAGACCT CTACCAGGAC CCTTCTGCGT   900
TCCTGTCAGC AGCCACCACC TCCACCTCTT CCTCTCTGGC CTACCCACCA CCTCCTTCCT   960
ATCCATCCCC CAAGCCAGCC ACGGACCCAG GTCTCTTCCC AATGATCCCA GACTATCCTG  1020
GATTCTTTCC ATCTCAGTGC CAGAGAGACC TACATGGTAC AGCTGGCCCA GACCGTAAGC  1080
CCTTTCCCTG CCCACTGGAC ACCCTGCGGG TGCCCCCTCC ACTCACTCCA CTCTCTACAA  1140
TCCGTAACTT TACCCTGGGG GGCCCCAGTG CTGGGGTGAC CGGACCAGGG GCCAGTGGAG  1200
GCAGCGAGGG ACCCCGGCTG CCTGGTAGCA GCTCAGCAGC AGCAGCAGCC GCCGCCGCCG  1260
CCGCCTATAA CCCACACCAC CTGCCACTGC GGCCCATTCT GAGGCCTCGC AAGTACCCCA  1320
ACAGACCCAG CAAGACGCCG GTGCACGAGA GGCCCTACCC GTGCCCAGCA GAAGGCTGCG  1380
ACCGGCGGTT CTCCCGCTCT GACGAGCTGA CACGGCACAT CCGAATCCAC ACTGGGCATA  1440
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ATATCCGCAC CCACACCGGT GAGAAGCCCT TCGCCTGTGA CTACTGTGGC CGAAAGTTTG  1560
CCCGGAGTGA TGAGAGGAAG CGCCACACCA AGATCCACCT GAGACAGAAA GAGCGGAAAA  1620
GCAGTGCCCC CTCTGCATCG GTGCCAGCCC CCTCTACAGC CTCCTGCTCT GGGGGCGTGC  1680
AGCCTGGGGG TACCCTGTGC AGCAGTAACA GCAGCAGTCT TGGCGGAGGG CCGCTCGCCC  1740
CTTGCTCCTC TCGGACCCGG ACACCTTGAG ATGAGACTCA GGCTGATACA CCAGCTCCCA  1800
AAGGTCCCGG AGGCCCTTTG TCCACTGGAG CTGCACAACA AACACTACCA CCCTTTCCTG  1860
TCCCTCTCTC CCTTTGTTGG GCAAAGGGCT TTGGTGGAGC TAGCACTGCC CCCTTTCCAC  1920
CTAGAAGCAG GTTCTTCCTA AAACTTAGCC CATTCTAGTC TCTCTTAGGT GAGTTGACTA  1980
TCAACCCAAG GCAAAGGGGA GGCTCAGAAG GAGGTGGTGT GGGGATCCCC TGGCCAAGAG  2040
GGCTGAGGTC TGACCCTGCT TTAAAGGGTT GTTTGACTAG GTTTTGCTAC CCCACTTCCC  2100
CTTATTTTGA CCCATCACAG GTTTTTGACC CTGGATGTCA GAGTTGATCT AAGACGTTTT  2160
CTACAATAGG TTGGGAGATG CTGATCCCTT CAAGTGGGGA CAGCAAAAAG ACAAGCAAAA  2220
CTGATGTGCA CTTTATGGCT TGGGACTGAT TTGGGGGACA TTGTACAGTG AGTGAAGTAT  2280
AGCCTTTATG CCACACTCTG TGGCCCTAAA ATGGTGAATC AGAGCATATC TAGTTGTCTC  2340
AACCCTTGAA GCAATATGTA TTATATACTC AGAGAACAGA AGTGCAATGT GATGGGAGGA  2400
ACGTAGCAAT ATCTGCTCCT TTTCGAGTTG TTTGAGAAAT GTAGGCTATT TTTTCAGTGT  2460
ATATCCACTC AGATTTTGTG TATTTTTGAT GTACCCACAC TGTTCTCTAA ATTCTGAATC  2520
TTTGGGAAAA AATGTAAAGC ATTTATGATC TCAGAGGTTA ACTTATTTAA GGGGGATGTA  2580
CATATTCTCT GAAACTAGGA TGCATGCAAT TGTGTTGGAA GTGTCCTTGG TCGCCTTGTG  2640
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TAGAAAGTAT ATTTTTGTAT GCTTTGTTTT GTGACTTAAA AGTGTTACCT TTGTAGTCAA  2820
ATTTCAGATA AGAATCTACA TAATGTTACC GGAGCTGATT TGTTTGGTCA TTAGCTCTTA  2880
ATAGTTGTGA AAAAATAAAT CTATTCTAAC GCAAAACCAC TAACTGAAGT TCAGATATAA  2940
TGGATGGTTT GTGACTATAG TGTAAATAAA TACTTTTCAA CAAT

Seq ID NO: B20 Protein sequence
Protein Accession #: NP_000390.2

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MMTAKAVDKI PVTLSGFVHQ LSDNIYPVED LAATSVTIFP NAELGGPFDQ MNGVAGDGMI    60
NIDMTGEKRS LDLPYPSSFA PVSAPRNQTF TYMGKFSIDP QYPGASCYPE GIINIVSAGI   120
LQGVTSPAST TASSSVTSAS PNPLATGPLG VCTMSQTQPD LDHLYSPPPP PPPYSGCAGD   180
LYQDPSAFLS AATTSTSSSL AYPPPPSYPS PKPATDPGLF PMIPDYPGFF PSQCQRDLHG   240
TAGPDRKPFP CPLDTLRVPP PLTPLSTIRN FTLGGPSAGV TGPGASGGSE GPRLPGSSSA   300
AAAAAAAAAY NPHHLPLRPI LRPRKYPNRP SKTPVHERPY PCPAEGCDRR FSRSDELTRH   360
IRIHTGHKPF QCRICMRNFS RSDHLTTHIR THTGEKPFAC DYCGRKFARS DERKRHTKIH   420
LRQKERKSSA PSASVPAPST ASCSGGVQPG GTLCSSNSSS LGGGPLAPCS SRTRTP

Seq ID NO: B21 DNA sequence
Nucleic Acid Accession #: NM_004962.2
Coding sequence: 457..1893

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CCTCGAAGCA GCCGGGCCGG GCGCGCAGTG GGCTACAAAC TTTCGCAGCG CGAGTCCGCC   180
AAGGCAGCGC GCCGACTCGG GCTCGGCTCG GCTCTGCGCT GCTCCGGACG GCTGTGACCG   240
CTGGCCGGGG GCTCGGGCCG CCGGTACCCA CGGACCGCGC GCCCGGGTGC CTGCTCCGCT   300
AAGCCCCTCG CCCCGCGCGG ACCTCGGTAT CCAGCGCCCT GCTGCCCGGG CTCTCCCCGC   360
GCGCCCTACT GCCGCGAGGT CAGTCCGCAG CCTCCGGTGC GCCAGCGCTC GCCTTCCTCC   420
TCCTGGACTT CGGCCCTTTG CCGCCCTCAC CACGCCATGG CTCATGTCCC CGCTCGGACC   480
AGCCCGGGAC CCGGGCCCCA GCTGCTGCTG CTGCTGCTGC CGTTGTTTCT GCTGTTGCTC   540
CGGGATGTGG CCGGCAGCCA CAGGGCCCCC GCCTGGTCCG CACTGCCCGC GGCCGCCGAC   600
GGCCTGCAGG GGGACAGGGA TCTCCAGCGG CACCCTGGGG ACGCGGCCGC CACGTTGGGC   660
CCCAGCGCCC AGGACATGGT CGCTGTCCAC ATGCACAGGC TCTATGAGAA GTACAGCCGG   720
CAGGGCGCGC GGCCGGGAGG GGGCAACACG GTCCGCAGCT TCAGGGCCAG GCTGGAAGTG   780
GTCGACCAGA AGGCCGTGTA TTTCTTCAAC CTGACTTCCA TGCAAGACTC GGAAATGATC   840
CTTACGGCCA CTTTCCACTT CTACTCAGAG CCGCCTCGGT GGCCTCGAGC GCTCGAGGTG   900
CTATGCAAGC CGCGGGCCAA GAACGCTTCA GGCCGCCCGC TGCCCCTGGG CCCGCCCACA   960
CGCCAGCACC TGCTCTTCCG CAGCCTCTCG CAGAACACGG CCACACAGGG GCTACTCCGC  1020
GGGGCCATGG CCCTGGCGCC CCCACCGCGC GGCCTGTGGC AGGCCAAGGA CATCTCCCCC  1080
ATCGTCAAGG CGGCCCGCCG GGATGGCGAG CTGCTCCTCT CCGCCCAGCT GGATTCTGAG  1140
GACAGGGACC CGGGGGTGCC CCGGCCCAGC CCCTATGCGC CCTACATCCT AGTCTATGCC  1200
AACGATCTGG CCATCTCGGA GCCCAACAGC GTGGCAGTGA CGCTGCAGAG ATACGACCCC  1260
TTCCCTGCCG GAGACCCCGA GCCCCGCGCA GCCCCCAACA ACTCAGCGGA CCCCCGCGTG  1320
CCCCGAGCCG CGCAGGCCAC TGGGCCCCTC CAGGACAACG AGCTGCCGGG GCTGGATGAG  1380
AGGCCGCCGC GCGCCCACGC ACAGCACTTC CACAAGCACC AGCTGTGGCC CAGCCCCTTC  1440
CGGGCGCTGA AACCCCGGCC AGGGCGCAAA GACCGCAGGA AGAAGGGCCA GGAGGTGTTC  1500
ATGGCCGCCT CGCAGGTGCT GGACTTTGAC GAGAAGACGA TGCAGAAAGC CCGGAGGAAG  1560
CAGTGGGATG AGCCGAGGGT GTGCTCCCGG AGGTACCTGA AGGTGGACTT CGCAGACATC  1620
GGCTGGAATG AATGGATAAT CTCACCGAAA TCTTTTGATG CCTACTACTG CGCGGGAGCA  1680
TGTGAGTTCC CCATGCCTAA GATCGTTCGT CCATCCAACC ATGCCACCAT CCAGAGCATT  1740
GTCAGGGCTG TGGGCATCAT CCCTGGCATC CCAGAGCCCT GCTGTGTTCC CGATAAGATG  1800
AACTCCCTTG GGGTCCTCTT CCTGGATGAG AATCGGAATG TGGTTCTGAA GGTGTACCCC  1860
AACATGTCCG TGGACACCTG TGCCTGCCGG TGAGACCACT CCAGGGTGGA AAGAAGCCAC  1920
GCCCAGCAGA GCTGCCTTCT CGGAGCCTTC TGCAACCAGG ACTTGTGGTG CAGCTGCAGA  1980
CACAGAGCAC AGCTCATGGG CAACATCACT GGGGCCCAGA GAGAGCTGTC CGCCAGTGCA  2040
TCATTAGGGG GTCTTTCATT GCTAGTGACT AGCCCCTTAA ATGCCAGCCT GAGTACCTGA  2100
AGGAATCTGG GAATTAGCCC TGGCCTGAAA GTGGCCCATC ATTCATACCC ACTGTTCTGA  2160
AGGCTTGAAA ACAAAACATA TCCACAACAT TGGCTTGATG TGATCATCAT CTCATAACTG  2220
AGCAAGAAGA CTATGCAAAT CTTAGGGCGC TCGCTCCCTG CACACGGAAA GAACTCTGTT  2280
TAAATGCTCA GTTCAGAACA CTTTGGGCCA CATAGTGATT TTGGAAAACA GGATAATCGT  2340
GGTGTAAATG AGTGTTTCCT TTCAAAGTCC ACTGCAGAGC TTTTATCCAT ATGGTATGCA  2400
CATGTAGCCA ATATTGGTTT CTTTTTCTTA ATATATATAT TTTATTTTAA AACAACAAAA  2460
AGGGAGGGCG TTGACACCAT TCCCCACAGA GATAGTCATG CTGAGTGTGG GTTGTTTAAA  2520
CATGCATATT GAAATAACAC ATATAGTAAC GTGGGAATAC TAAAAAATAA CCAAGATTTT  2580
ATATTTTTGT AAATTATACT TTCTATACTG TAGATTGTGT ATGTTATGTG TTTTTATGGA  2640
AAGCTAATAA ATTAAAGGTA CAGTGGTATC TTGA
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Seq ID NO: B22 Protein sequence
Protein Accession #: NP_004953.1

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GDAAATLGPS AQDMVAVHMH RLYEKYSRQG ARPGGGNTVR SFRARLEVVD QKAVYFFNLT   120
SMQDSEMILT ATFHFYSEPP RWPRALEVLC KPRAKNASGR PLPLGPPTRQ HLLFRSLSQN   180
TATQGLLRGA MALAPPPRGL WQAKDISPIV KAARRDGELL LSAQLDSEER DPGVPRPSPY   240
APYILVYAND LAISEPNSVA VTLQRYDPFP AGDPEPRAAP NNSADPRVRR AAQATGPLQD   300
NELPGLDERP PRAHAQHFHK HQLWPSPFRA LKPRPGRKDR RKKGQEVFMA ASQVLDFDEK   360
TMQKARRKQW DEPRVCSRRY LKVDFADIGW NEWIISPKSF DAYYCAGACE FPMPKIVRPS   420
NHATIQSIVR AVGIIPGIPE PCCVPDKMNS LGVLFLDENR NVVLKVYPNM SVDTCACR
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Seq ID NO: B23 DNA sequence
Nucleic Acid Accession #: AK026322.1

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TCCATCATCT GTCATTTTTG CATCTGTTTT TATTGACTAA CTTTCTTCCT CATCATGGTC   120
ACATATCCTT GCTTCTTCCC ATATTTAGTA AAGTTTAGTT GGATGCTGGA TTGTTTTAAT   180
TTAGCATTTT GGAGTGACTG CTTTTGCACT TGCCTTTAAA AGTATTGGAC TTCGTTTTGA   240
TAGTTGAATT ACTTGCAAAT CAGCTTGATC ATTCTGAGAC TTGTTTTTAA CTTTTGTCGA   300
AAAGGCTATG CTACTTCAAG TATAATAAAA CCTAGTTTTA GTTTTATCCT ATAACTAAGG   360
CATGTGTTCA ATTTGAATGT CTCCAACCCT GTGTGAACTC TGAAAATTGT TCAGCTCCCA   420
ATTTCGCAGT AATTTTTTTT GTTCAGCCTT GCAGTCTCAT CCTACTCAAG TGTGGCTCTG   480
TATCCAACAA CAGTCTTGGA GATCTCATGA AGATTTCTGA AACTTTTGCT CTGCAGGATA   540
CCTTCCTTTG TGGTTATGTG CCCTGAAAAC TCCAGCCTCC GTGTCTTCAA TTCAGTGAAA   600
CTACTACTCT GCTTGGATTC CCCTCTTATA CAATGGTCTA CCAAGTGACT GCAAACAGAA   660
ATCTAAGGGA ATTTCAGGAG TCACCTCATT TATTTTCCTT TTTTTCAGGG ATTATAGTAG   720
TACTATACCA CCTGTCAGCC AATGTGTGAG AATGGTGGTT TCATACATTT TCTCCAATTC   780
TTTCTTGTTA CAGGAGCCTC CATTACTTTT CAAACAGTAA TGCAGTTGCA GTTGCCTCTC   840
CTTTTCTTCA TTATGTGTTT ATCTCTGGCA GTTTGAGCCA AGAGAGGGCA CGGAGAAGTA   900
CAATGACTAG AGAGCACTTC TGTTGAGGCT CATTCATTGA CCCCTACCCC AGTGCTTTAT   960
GAATGTGTGC TGCAGATGTC ATACAGCATC ACAGCTTCTT CTCTAATTTA TGAGCCATAA  1020
TTTTTTTTTT TGTATTTTTA TTGTATTACC TGCTTGGTTG CAAGAGGATG ATGAGGAGGA  1080
CTACTATAGG ATAAATTTGT TTTTATAGAG CAATTTCTCA TGGGTCACGA GGGATAGTAC  1140
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TCCATTTTCC TCACTGATAT CGGCTTGATC ATCTGAGTCA GTCGGCTCAT TGTGGAAACA 1200
TATGGAATCC TTTATGCTTT TTCTCAGGCT GCTTCTGTTA CATGAAATAA AGCCAGAGTT 1260
GATTGTGAAA AAAAAAAAAA AAAA

Seq ID NO: B24 DNA sequence
Nucleic Acid Accession #: cat cluster

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CTTTCCCACT CTGATGATTT GTGCTCTTAT TTTTCCTAGA TTTACCTCAT CTAGGGCATA  180
TTCTTTTCCC TCTTCCTCTT TACCTTTCCT GGTCCTGATC CCTCTGTACT CAGTTCCCCT  240
AAATTATTGG ACTACAAACT AATATACTAG AAAAGCATAC ACTTATTTTA TTTGAATGCA  300
GAAATGCTAT CTATCAGTAT ATATACATAA GAATGTATAT TACAGTATAT CTATATATAC  360
TTAACACTGT AACTTTCAGT ATTCCCCAGT TAGCGTACCT AACTCTCCTG TGGGTTATGT  420
TAATTCTTAT TAGACTACTA GAGAAAAACC AACTGGCAGT TTGCTAAGCA TATCTACTGG  480
TGTTGTTTCT GCGCCCTCTT TTGGCTAATT GATGTAATTA TACTGGCTCT AAAGATTTAC  540
TGCCCCATAA GTAAATAGTA TAGCCACATT CTGAACATAT CAAAAGTACA AACTTAGGAG  600
GAGTGTATGT ACAAAAATGT AAAATTTTAT GAAAATGAAC ATGTTTTTAT GATGTTATTT  660
CTAGTTCATA AGAATGTGAT GACTGCTTTG CTTCATTTAT GTACGTTCCC ATTATATTCT  720
TGCTGTCAAT CAATCACAAA TTTATATCAG ATTAGGATAA ACTAAGCCAT TTTATGTATT  780
TTATTTTAAA CCTTATTTTG GCAGAGTAAT TCCTTAGAAT TGGAAAAGCT GTTACTTTGA  840
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ATTTTCCTTT TCTTTGTTCT TTTTTTTACA TTTCGCAGAG TTATATCTAT AGTTTTAGTA 1080
ACAATTTCTT ATGTATTCTG GATAACTGAA AACAACTAAA GGTGTTGGGC ATTAGAAAAT 1140
AATTGTGAGC AGTAAGATTA CTGATGTAAT ATGTATGTTG GACTGAAGTA TTTCTTTATA 1200
AACATTCTAT TTGATTTTAA GCAAAATGTA TGTTAAAGCA TGTTTTTACA TCAGTAAAGT 1260
CATTTGTCGA CCTTCTGGAA ATGAAAGGTT TTTACCTAGA TACTGTAAGT TACACCTCCT 1320
TAACAATCAT ATTTGTCATT GTTGTTTTCT GCAAACAAAA ATGTTTATGG GCTTCATGTA 1380
GGCTTAAGAT TGTAGGCAAA AATGGACTGA GTTCAGGACC CTTCAAGCAG TAGGCATTCA 1440
GTTACAGAGC AGTTGGTACT TTGTAACCCA GACTTACAGT TTAAAAATAT CAAGTTAGCT 1500
GATGTTTCAT TATAATAAAA ATACTATTTT GCTTAAGAGT TGTATTACAA ATATTTGTGC 1560
TTAACATTAG AAATAGCTGT TTTAAATTGT AGTTAACATA TTAACTTTTT CAGAAAAAAA 1620
GCATGGTTTA TTTTTAATAA TGAAATAGAG AACATAATAC GTAATGTTCA GTATAACAGC 1680
TGAGTTAAAA CATCTGCCAG GATTAACATC AGTGCGTTTT TGCCAATGCA TAGAGGCATT 1740
TTTCTCTAAG TATGATGGCT AATGATAACT ATTCTTTGTT ACACATTCAA GTCACTCCCA 1800
TACAAGTAAC TAGTGGGTGA TATGTTTCAC TCCAAAGGGT GTATTAATTC TGAATGCTAA 1860
TCATGAAGAC TTAAGTTAGG ACAACACTTC AAACCAGGAA GTGTGAACTG ATTTA
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Seq ID NO: B25 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1144

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGAGCGCG GGATGCACCT CGGTGCAGCG GCCGCCGGCG AGGACGACCT CTTCCTGCAC   60
AAGAGCCTGA GCGCCTCCAC CTCCAAGCGC TTGGAAGCGG CTTTCCGCTC CACGCCCCCG  120
GGCATGGACC TGTCCCTGGC GCCGCCGCCT CGGGAACGCC CGGCGTCCTC CTCCTCGTCG  180
CCCCTGGGCT GCTTCGAGCC GGCTGACCCC GAGGGGGCAG GGCTGCTGTT GCCGCCGCCT  240
GGAGGAGGCG GCGGCGGCAG CGCGGGAAGT GGCGGCGGCG GCGGCGGCGG GGTGGGTGTC  300
CCCGGGCTGC TAGTAGGTTC AGCCGGCGTT GGGGGCGACC CTAGCCTAAG CAGCCTGCCG  360
GCCGGGGCCG CCCTTTGCCT CAAGTACGGC GAAAGCGCGA GCCGGGGCTC GGTGGCCGAG  420
AGCAGCGGCG GCGAGCAGAG CCCCGACGAC GACAGCGACG GTCGCTGCGA GCTCGTGCTG  480
CGGGCCGGAG TAGCCGACCC GCGGGCCTCC CCGGGAGCGG GAGGTGGTGG CGCGAAGGCA  540
GCCGAGGGCT GCTCCAATGC CCACCTCCAC GGCGGCGCCA GCGTCCCCCC GGGGGGCCTG  600
GGCGGCGGCG GCGGCGGGGG TAGCAGCAGC GGTAGCAGTG GCGGCGGTGG CGGTAGCGGT  660
AGCGGCAGCG GCGGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAAGAAATC CAAAGAGCAA  720
AAGGCGCTGC GGCTTAACAT CAATGCCCGA GAGCGCCGGC GGATGCACGA CCTGAACGAC  780
GCGCTGGACG AGCTGCGCGC GGTGATCCCC TACGCGCACA GCCCCTCGGT GCGAAAGCTC  840
TCCAAGATCG CCACGCTGCT GCTCGCCAAG AACTACATCC TCATGCAGGC GCAGGCCCTG  900
GAGGAGATGC GGCGCCTAGT CGCCTACCTC AACCAGGGCC AGGCCATCTC GGCTGCCTCC  960
CTGCCCAGCT CGGCGGCTGC AGCGGCAGCA GCTGCTGCCC TGCACCCGGC GCTCGGCGCC 1020
TACGAGCAGG CAGCCGGCTA CCCGTTCAGC GCCGGACTGC CCCCGGCTGC CTCCTGCCCG 1080
GAGAAGTGCG CCCTGTTTAA CAGCGTCTCC TCCAGCCTCT GCAAACAGTG CACGGAGAAG 1140
CCTT
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Seq ID NO: B26 Protein sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
MERGMHLGAA AAGEDDLFLH KSLSASTSKR LEAAFRSTPP GMDLSLAPPP RERPASSSSS   60
PLGCFEPADP EGAGLLLPPP GGGGGGSAGS GGGGGGGVGV PGLLVGSAGV GGDPSLSSLP  120
AGAALCLKYG ESASRGSVAE SSGGEQSPDD DSDGRCELVL RAGVADPRAS PGAGGGGAKA  180
AEGCSNAHLH GGASVPPGGL GGGGGGGSSS GSSGGGGGSG SGSGGSSSSS SSSSKKSKEQ  240
KALRLNINAR ERRRMHDLND ALDELRAVIP YAHSPSVRKL SKIATLLLAK NYILMQAQAL  300
EEMRRLVAYL NQGQAISAAS LPSSAAAAAA AAALHPALGA YEQAAGYPFS AGLPPAASCP  360
EKCALFNSVS SSLCKQCTEK P
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Seq ID NO: B27 DNA sequence
Nucleic Acid Accession #: cat cluster

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1          11         21         31         41         51
|          |          |          |          |          |
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TAGATACACA TACAAATGGT CGTACATAGC TGTCATAGTC TGATTGACCT ATTTAATATA  120
TATATCATTC TTTACACATC CAAAACCCGC CAACAGATCC ATCACAGCTC CCAACTCACC  180
ATCCAACCTG ACAAACTGAA TTTGTATTAT CTGCAAGGAG TGGAAAATAG CAGGACTCCA  240
TTTTTAAAAA AGATTTTCTT GATTTTCATA GGGCGGAAAG GCAGTCAAAC AGCCATGCAA  300
AACTAAAACT GAAAGCTCAC TTTGGGTAAA TAGCTTCTTG TTCTTCCTTA GTTTTCTTTC  360
TTTTTAAATT TTATTTTTTT AGAAAAAATAA CAAAGGATTT CACACCATAG GCAAATCAAA  420
CCAGTCTTTT AACTTAAATA ATTCTCCACA GTTAAAATAA CATATATGTA CATATATATT  480
AAAAGCAATT AAATTAGACC TTTTAAAAAT GCACAGCACA GCCTGGAAAA ATATTTGCTT  540
AGCATGTTCT TACGTATAGC AACTATTGCT GTGATGTTTT TCCCTTTTGG AATGTAAAGG  600
AGTCCCCTTT CAAAAAAGAG ATCAATTCAT TCATCAATTA AGAATACACC TTTCCTGTAA  660
TTTTTGGACT GAAGCAATTT ATTAAAGCTC AATTTAAATA CAGGCATGAT GCAACTGAAA  720
ATATCCAGGT GACCTTTCAT AAACCTAAGC AGCTCAGATA CATCAATATT TCTCTTCATA  780
CTTGTTGGCA AATAAACCTT TAAACACTTG GCACACAGCA TAAGTAATCT ATAAAACAAT  840
TTTAGAGGCA TTAAAAAAAT CTGCACATAA GACCCATGAC TTTAACACAT GATAAATACT  900
GTTGATGTGG AAGGGTCATT GAAGAATAAC AAATAAATAC CATGAATTGT TAATACATCA  960
TTGCAGAGTA GAAAGTAACA AGGTGCACAT AAATATTTTT AAATGCAATT CTTTCAGCCA 1020
CAGTCAGTTT TTTTATATCA CTCTCGCCAA AACTTTGAGC ATTTTCACAG GATTAAAGTT 1080
CAGAGACAAT AAAAAATACA AGTCTTTCAT AGTAACATGT TCTCTCTCTC TCGCTCTGGG 1140
TTTTATTTCC CCCTCACTTA AGTCAACATT TCAAGTTTTT CTCCTGGCTC AGAATCAAAA 1200
TTTATTTTCA AGTGCCCTTT CTGATTTGTC TGAATGAATA TTCCATCTCT CATGCTACCG 1260
ATCCGCT
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Seq ID NO: B28 DNA sequence
Nucleic Acid Accession #: NM_002581.2
Coding sequence: 368..5251

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CAGATAAAGG AGCGGGGAGA GAAATTAATT GCCAACCAGG AGGAGTTGGG CTGTATTTTT   180
CAAAGGTGGG GAGAGTGGAG CACACACCTT GAGGAGGAAA GCGAGAAAGA AAAGAAAAAA   240
GCAAGTGAAG GGGGGCTCGC CCAAGAAGGG TGAAGAAGCG AAGAAAGTCG AGGCGCCGAG   300
GCTCCCAAAG CTGGCAGCTC CGGGTGGCGG TGCAGGGGCG AAGGGGGGGG CGGGGGGAAC   360
GTCGGACATG CGGCTCTGGA GTTGGGTGCT GCACCTGGGG CTGCTGAGCG CCGCGCTGGG   420
CTCCGGGCTG GCCGAGCGTC CCCGCCGGGC CCGGAGAGAC CCGCGGGCCG GCCGACCCCC   480
GCGCCCCGCC GCCGGCCCGG CCACCTGCGC CACCCGCGGC CCGCGGCCGC CGCGCCTCGC   540
CGCCGCCGCC GCCGCCGCCG GGCGTGCCTG GGAAGCCGTG CGCGTCCCCC GGCGGCGGCA   600
GCAGCGGGAG GCGAGGGGCG CCACCGAGGA GCCGAGCCCG CCGAGCCGGG CGCTCTATTT   660
CAGCGGGCGA GGCGAGCAGC TGCGAGTCCT CCGGGCCGAC CTCGAGCTGC CCCGGGACGC   720
GTTCACGCTG CAAGTGTGGC TGCGAGCGGA GGGGGGCCAG AGGTCTCCGG CAGTGATCAC   780
AGGGCTGTAT GACAAATGTT CTTATATCTC ACGTGACCGA GGATGGGTCG TGGGCATTCA   840
CACCATCAGT GACCAAGACA ACAAAGACCC ACGCTACTTT TTCTCCTTGA AGACAGACCG   900
AGCCCGGCAA GTGACCACCA TCAATGCCCA CCGCAGCTAC CTCCCAGGCC AGTGGGTATA   960
CCTAGCTGCC ACCTATGATG GGCAGTTCAT GAAGCTCTAT GTGAATGGTG CCCAGGTGGC  1020
CACCTCTGGG GAACAAGTGG GTGGCATATT CAGCCCACTG ACCCAGAAGT GCAAAGTGCT  1080
CATGTTAGGG GGCAGTGCCC TGAATCACAA CTACCGGGGC TACATCGAGC ACTTCAGTCT  1140
GTGGAAGGTG GCCAGGACTC AGCGGGAGAT ACTGTCTGAC ATGGAAACCC ATGGCGCCCA  1200
CACTGCTCTA CCTCAGCTCC TCCTCCAGGA GAACTGGGAC AATGTGAAGC ATGCCTGGTC  1260
CCCCATGAAG GATGGCAGCA GCCCCAAAGT GGAATTCAGC AATGCCCACG GCTTTCTGCT  1320
GGACACGAGT CTGGAGCCTC CTCTGTGCGG ACAGACATTG TGTGACAACA CAGAGGTCAT  1380
TGCCAGCTAC AATCAGCTCT CAAGTTTCCG CCAGCCCAAG GTGGTGCGCT ACCGCGTGGT  1440
CAACCTCTAT GAAGATGATC ATAAGAACCC GACGGTGACG CGCGAGCAGG TGGACTTCCA  1500
GCACCATCAG CTGGCTGAGG CCTTCAAGCA ATACAACATC TCCTGGGAGC TGGACGTGCT  1560
GGAGGTGAGC AACTCCTCCC TTCGCCGCCG CCTCATCCTG GCCAACTGTG ACATCAGCAA  1620
GATTGGGGAT GAGAACTGTG ACCCCGAGTG CAACCACACG CTGACGGGCC ACGACGGCGG  1680
GGATTGCCGC CACCTGCGCC ACCCTGCCTT CGTGAAGAAG CAGCACAACG GGGTGTGTCA  1740
CATGGACTGC AACTATGAAC GGTTCAACTT TGATGGTGGA GAGTGCTGTG ACCCTGAAAT  1800
CACCAATGTC ACTCAGACTT GCTTTGACCC CGACTCTCCA CACAGAGCCT ACTTGGATGT  1860
TAATGAGCTG AAGAACATTC TTAAATTGGA TGGATCAACA CATCTCAATA TTTTCTTTGC  1920
AAAATCCTCA GAGGAGGAGT TGGCAGGAGT AGCAACTTGG CCATGGGACA AGGAGGCCCT  1980
GATGCACTTA GGTGGCATTG TCTTGAACCC ATCTTTCTAT GGCATGCCTG GGCACACCCA  2040
CACCATGATC CATGAGATTG GTCACAGCCT GGGCCTCTAT CACGTCTTCC GAGGCATCTC  2100
AGAAATCCAG TCCTGCAGTG ACCCCTGCAT GGAGACAGAG CCCTCCTTCG AGACTGGAGA  2160
CCTCTGCAAT GATACCAACC CAGCCCCTAA ACACAAGTCC TGTGGTGACC CAGGGCCAGG  2220
AAATGACACC TGTGGCTTTC ATAGCTTCTT CAACACTCCT TACAACAACT TCATGAGCTA  2280
TGCAGATGAC GACTGTACGG ACTCCTTCAC GCCCAATCAA GTCGCCAGAA TGCACTGTTA  2340
CCTGGACCTG GTCTACCAGG GCTGGCAGCC CTCCAGGAAA CCAGCGCCTG TTGCCCTCGC  2400
CCCCCAAGTT CTGGGCCACA CAACGGACTC TGTGACACTG GAGTGGTTCC CACCTATAGA  2460
TGGCCATTTC TTTGAAAGAG AATTGGGATC AGCATGTCAT CTTTGCCTGG AAGGGAGAAT  2520
CCTGGTGCAG TATGCTTCCA ACGCTTCCTC CCCAATGCCC TGCAGCCCAT CAGGACACTG  2580
GAGCCCTCGT GAAGCAGAAG GTCATCCTGA TGTTGAACAG CCCTGTAAGT CCAGTGTCCG  2640
CACCTGGAGC CCAAATTCAG CTGTCAACCC ACACACGGTT CCTCCAGCCT GCCCTGAGCC  2700
TCAAGGCTGC TACCTCGAGC TGGAGTTCCT CTACCCCTTG GTCCCTGAGT CTCTGACCAT  2760
TTGGGTGACC TTTGTCTCCA CTGACTGGGA CTCTAGTGGA GCTGTCAATG ACATCAAACT  2820
GTTGGCTGTC AGTGGGAAGA ACATCTCCCT GGGTCCTCAG AATGTCTTCT GTGATGTCCC  2880
ACTGACCATC AGACTCTGGG ACGTGGGCGA GGAGGTGTAT GGCATCCAAA TCTACACGCT  2940
GGATGAGCAC CTGGAGATCG ATGCTGCCAT GTTGACCTCC ACTGCAGACA CCCCACTCTG  3000
TCTACAGTGT AAGCCCCTGA AGTATAAGGT GGTCCGGGAC CCTCCTCTCC AGATGGATGT  3060
GGCCTCCATC CTACATCTCA ATAGGAAATT CGTAGACATG GATCTAAATC TTGGCAGTGT  3120
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GTACCAGTAT TGGGTCATAA CTATTTCAGG AACTGAAGAG AGTGAGCCAT CACCTGCTGT  3180
CACATACATC CATGGACGTG GGTACTGTGG CGATGGCATT ATACAAAAAG ACCAAGGTGA  3240
ACAATGCGAC GACATGAATA AGATCAATGG TGATGGCTGC TCCCTTTTCT GCCGACAAGA  3300
AGTCTCCTTC AATTGTATTG ATGAACCCAG CCGGTGCTAT TTCCATGATG GTGATGGGGT  3360
ATGTGAGGAG TTTGAACAAA AAACCAGCAT TAAGGACTGT GGTGTCTACA CGCCCCAGGG  3420
ATTCCTGGAT CAGTGGGCAT CCAATGCTTC AGTATCTCAT CAAGACCAGC AATGCCCAGG  3480
CTGGGTCATC ATCGGACAGC CAGCAGCATC CCAGGTGTGT CGAACCAAGG TGATAGATCT  3540
CAGTGAAGGC ATTTCCCAGC ATGCCTGGTA CCCTTGCACC ATCAGCTACC CATATTCCCA  3600
GCTGGCTCAG ACCACTTTTT GGCTCCGGGC GTATTTTTCT CAACCAATGG TTGCCGCAGC  3660
TGTCATTGTC CACCTGGTGA CGGATGGGAC ATATTATGGG GACCAAAAGC AGGAGACCAT  3720
CAGCGTGCAG CTGCTTGATA CCAAAGATCA GAGCCACGAT CTAGGCCTCC ATGTCCTGAG  3780
CTGCAGGAAC AATCCCCTGA TTATCCCTGT GGTCCATGAC CTCAGCCAGC CCTTCTACCA  3840
CAGCCAGGCG GTACGTGTGA GCTTCAGTTC GCCCCTGGTC GCCATCTCGG GGGTGGCCCT  3900
CCGTTCCTTC GACAACTTTG ACCCCGTCAC CCTGAGCAGC TGCCAGAGAG GGGAGACCTA  3960
CAGCCCTGCC GAGCAGAGCT GCGTGCACTT CGCATGTGAG AAAACTGACT GTCCAGAGCT  4020
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TACTGTGAGC TGCCGGACAG GCTACGTGCT CCAGATACGG CGGGATGATG AGCTGATCAA  4140
GAGCCAGACG GGACCCAGCG TCACAGTGAC CTGTACAGAG GGCAAGTGGA ATAAGCAGGT  4200
GGCCTGTGAG CCAGTCGACT GCAGCATCCC AGATCACCAT CAAGTCTATG CTGCCTCCTT  4260
CTCCTGCCCT GAGGCCACCA CCTTTGGCAG TCAATGTTCC TTCCAGTGCC GTCACCCTGC  4320
ACAATTGAAA GGCAACAACA GCCTCCTGAC CTGCATGGAG GATGGGCTGT GGTCCTTCCC  4380
AGAGGCCCTG TGTGAGCTCA TGTGCCTCGC TCCACCCCCT GTGCCCAATG CAGACCTCCA  4440
GACCGCCCGG TCCCGAGAGA ATAAGCACAA GGTGGGCTCC TTCTGCAAAT ACAAATGCAA  4500
GCCTGGATAC CATGTGCCTG GATCCTCTCG GAAGTCAAAG AAACGGGCCT TCAAGACTCA  4560
GTGTACCCAG GATGGCAGCT GGCAGGAGGG AGCTTGTGTT CCTGTGACCT GTGACCCACC  4620
TCCACCAAAA TTCCATGGGC TCTACCAGTG TACTAATGGC TTCCAGTTCA ACAGTGAGTG  4680
TAGGATCAAG TGTGAAGACA GTGATGCCTC CCAGGGACTT GGGAGCAATG TCATTCATTG  4740
CCGGAAAGAT GGCACCTGGA ACGGCTCCTT CCATGTCTGC CAGGAGATGC AAGGCCAGTG  4800
CTCGGTTCCA AACGAGCTCA ACAGCAACCT CAAACTGCAG TGCCCTGATG GCTATGCCAT  4860
AGGGTCGGAG TGTGCCACCT CGTGCCTGGA CCACAACAGC GAGTCCATCA TCCTGCCAAT  4920
GAACGTGACC GTGCGTGACA TCCCCCACTG GCTGAACCCC ACACGGGTAG AGAGAGTTGT  4980
CTGCACTGCT GGTCTCAAGT GGTATCCTCA CCCTGCTCTG ATTCACTGTG TCAAAGGCTG  5040
TGAGCCCTTC ATGGGAGACA ATTATTGTGA TGCCATCAAC AACCGAGCCT TTTGCAACTA  5100
TGACGGTGGG GATTGCTGCA CCTCCACAGT GAAGACCAAA AAGGTCACCC CATTCCCTAT  5160
GTCCTGTGAC CTACAAGGTG ACTGTGCTTG TCGGGACCCC CAGGCCCAAG AACACAGCCG  5220
GAAAGACCTC CGGGGATACA GCCATGGCTA AGGAAGGACA AGAAGTTGTC AAAGAATTCC  5280
CAACGCCAGG ACCCACATCC CTTTGGTATT GATTTCACAG TCAGCTGCTC AACGGAATGG  5340
CCTCTCCACA CCAGGGATCC TTAGCACCCA ACCGGTCTGC CTTTAATTTT ACCCAGGAAG  5400
GACTCACATT GGGGCGAATG AACCAAGTTT CGCCATGCTG GATGATGAAA TGGATTCCCA  5460
TCCCAAAGTC TGAGATGGAT TGCATATACA GTGTGCAGTC CCAGAGCCTC CTAAAATTCT  5520
AGCCATTTGT CACACAACCA CAGCAAAAAA AAA
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Seq ID NO: B29 Protein sequence
Protein Accession #: NP_002572.1

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MRLWSWVLHL GLLSAALGCG LAERPRRARR DPRAGRPPRP AAGPATCATR GPRPPRLAAA    60
AAAAGRAWEA VRVPRRRQQR EARGATEEPS PPSRALYFSG RGEQLRVLRA DLELPRDAFT   120
LQVWLRAEGG QRSPAVITGL YDKCSYISRD RGWVVGIHTI SDQDNKDPRY FFSLKTDRAR   180
QVTTINAHRS YLPGQWVYLA ATYDGQFMKL YVNGAQVATS GEQVGGIFSP LTQKCKVLML   240
GGSALNHNYR GYIEHFSLWK VARTQREILS DMETHGAHTA LPQLLLQENW DNVKHAWSPM   300
KDGSSPKVEF SNAHGFLLDT SLEPPLCGQT LCDNTEVIAS YNQLSSFRQP KVVRYRVVNL   360
YEDDHKNPTV TREQVDFQHH QLAEAFKQYN ISWELDVLEV SNSSLRRRLI LANCDISKIG   420
DENCDPECNH TLTGHDGGDC RHLRHPAFVK KQHNGVCDMD CNYERFNFDG GECCDPEITN   480
VTQTCFDPDS PHRAYLDVNE LKNILKLDGS THLNIFFAKS SEEELAGVAT WPWDKEALMH   540
LGGIVLNPSF YGMPGHTHTM IHEIGHSLGL YHVFRGISEI QSCSDPCMET EPSFETGDLC   600
NDTNPAPKHK SCGDPGPGND TCGFHSFFNT PYNNFMSYAD DDCTDSFTPN QVARMHCYLD   660
LVYQGWQPSR KPAPVALAPQ VLGHTTDSVT LEWFPPIDGH FFERELGSAC HLCLEGRILV   720
QYASNASSPM PCSPSGHWSP REAEGHPDVE QPCKSSVRTW SPNSAVNPHT VPPACPEPQG   780
CYLELEFLYP LVPESLTIWV TFVSTDWDSS GAVNDIKLLA VSGKNISLGP QNVFCDVPLT   840
IRLWDVGEEV YGIQIYTLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVVR DPPLQMDVAS   900
ILHLNRKFVD MDLNLGSVYQ YWVITISGTE ESEPSPAVTY IHGRGYCGDG IIQKDQGEQC   960
DDMNKINGDG CSLFCRQEVS FNCIDEPSRC YFHDGDGVCE EPEQKTSIKD CGVYTPQGFL  1020
DQWASNASVS HQDQQCPGWV IIGQPAASQV CRTKVIDLSE GISQHAWYPC TISYPYSQLA  1080
QTTFWLRAYF SQPMVAAAVI VHLVTDGTYY GDQKQETISV QLLDTKDQSH DLGLHVLSCR  1140
NNPLIIPVVH DLSQPFYHSQ AVRVSFSSPL VAISGVALRS FDNFDPVTLS SCQRGETYSP  1200
AEQSCVHFAC EKTDCPELAV ENASLNCSSS DRYHGAQCTV SCRTGYVLQI RRDDELIKSQ  1260
TGPSVTVTCT EGKWNKQVAC EPVDCSIPDH HQVYAASFSC PEGTTFGSQC SFQCRHPAQL  1320
KGNNSLLTCM EDGLWSFPEA LCELMCLAPP PVPNADLQTA RCRENKHKVG SFCKYKCKPG  1380
YHVPGSSRKS KKRAFKTQCT QDGSWQEGAC VPVTCDPPPP KFHGLYQCTN GFQFNSECRI  1440
KCEDSDASQG LGSNVIHCRK DGTWNGSFHV CQEMQGQCSV PNELNSNLKL QCPDGYAIGS  1500
ECATSCLDHN SESIILPMNV TVRDIPHWLN PTRVERVVCT AGLKWYPHPA LIHCVKGCEP  1560
FMGDNYCDAI NNRAFCNYDG GDCCTSTVKT KKVTPFPMSC DLQGDCACRD PQAQEHSRKD  1620
LRGYSHG
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Seq ID NO: B30 DNA sequence
Nucleic Acid Accession #: NM_032808.1
Coding sequence: 61..1008

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1          11         21         31         41         51
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ATGTTGCATG AGCTGCTCCG GCTGCAGGAG ATCCAGCTGG TGGGCGGGCA GCTGGCCGTG   120
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GTGGAGCCCT ATGCCTTCCG CGGCCTCAAC TACCTGCGCG TGCTCAATGT CTCTGGCAAC   180
CAGCTGACCA CACTGGAGGA ATTAGTCTTC CACTCGGTGG GCAACCTGGA GACACTCATC   240
CTGGACTCCA ACCCGCTGGC CTGCGACTGT CGGCTCCTGT GGGTGTTCCG GCGCCGCTGG   300
CGGCTCAACT TCAACCGGCA GCAGCCCACG TGCGCCACGC CCGAGTTTGT CCAGGGCAAG   360
GAGTTCAAGG ACTTCCCTGA TGTGCTACTG CCCAACTACT TCACCTGCCG CCGCGCCCGC   420
ATCCGGGACC GCAAGGCCCA GCAGGTGTTT GTGGACGAGG GCCACACGGT GCAGTTTGTG   480
TGCCGGGCCG ATGGCGACCC GCCGCCCGCC ATCCTCTGGC TCTCACCCCG AAAGCACCTG   540
GTCTCAGCCA AGAGCAATGG GCGGCTCACA GTCTTCCCTG ATGGCACGCT GCAGGTGCGC   600
TACGCCCAGG TACAGGACAA CGGCACGTAC CTGTGCATCG CGGCCAACGC GGGCGGCAAC   660
GACTCCATGC CCGCCCACCT GCATGTGCGC AGCTACTCGC CCGACTGGCC CCATCAGCCC   720
AACAAGACCT TCGCTTTCAT CTCCAACCAG CCGGGCGAGG GAGACGCCAA CAGCACCCGC   780
GCCACTGTGC CTTTCCCCTT CGACATCAAG ACCCTCATCA TCGCCACCAC CATGGGCTTC   840
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AAGGGCAACA CAAAGCACAA CATCGAGATC GAGTATGTGC CCCGAAAGTC GGACGCAGGC   960
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GGGCACGGAC CCCCGGCCGG CCGGGCAGGG GAAGGGCCCT GGCCGCCACC TGCTCACTCT  1080
CCAGTCCTTC CCACCTCCTC CCTACCCTTC TACACACGTT CTCTTTCTCC CTCCCGCCTC  1140
CGTCCCCTGC TGCCCCCCGC CAGCCCTCAC CACCTGCCCT CCTTCTACCA GGACCTCAGA  1200
AGCCCAGACC TGGGGACCCC ACCTACACAG GGGCATTGAC AGACTGGAGT TGAAAGCCGA  1260
CGAACCGACA CGCGGCAGAG TCAATAATTC AATAAAAAAG TTACGAACTT TCTCTGTAAC  1320
TTGGGTTTCA ATAATTATGG ATTTTTATGA AAACTTGAAA TAATAAAAAG AGAAAAAAAC  1380
TATTTCCTAT AGCTAGTCGG AATGCAAACT TTTGACGTCC TGATTGCTCC AGGGCCCTCT  1440
TCCAACTCAG TTTCTTGTTT TTCTCTTCCT CCTCCTCCTC TTCTTCCTCC TTTCTCTTCT  1500
CTTCCCCAGT GGGGAGGGAT CACTCAGGAA AACAGGAAAG GAGGTTCCAG CCCCACCCAC  1560
CTGCCCACCC CGCCCCAGGC ACCATCAGGA GCAGGCTAGG GGGCAGGCCT GGGCCCAGCT  1620
CCGGGCTGGC TTTTTGCAGG GCGCAGGTGG AGGGGACAGG TCTGCCGATG GGGGTGGGAG  1680
CCTGTCTGCT GGGCTGCCAG GCGGCACCAC TGCAACGGGT GGGAGCCTGG CTTGGGTGTG  1740
GCTGAGACTC TGGACAGAGG CTGGGGTCCT CCTGGGGGAC AGCACAGTCA GTGGAGAGAG  1800
CCAGGGGCTG GAGGTGGGGC CCACCCCAGC CTCTGGTCCC AGCTCTGCTG CTCACTTGCT  1860
GTGTGGCCTC AAGCAGGTCA CTGGCCTCTC TGGGCCTCAG TCTCCACATC TGTACAAATG  1920
GGAACATTAC CCCCTGCCCT GCCTACCTCA CAGGGCTGTT GTGAGGAATT GATGAGATCA  1980
TGTATGTGAA ACACTTTGTA ACCTGTAAAG CGCTGTGCAC ACGTG
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Seq ID NO: B31 Protein sequence
Protein Accession #: NP_116197.1

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1          11         21         31         41         51
|          |          |          |          |          |
MLHELLRLQE IQLVGGQLAV VEPYAFRGLN YLRVLNVSGN QLTTLEELVF HSVGNLETLI    60
LDSNPLACDC RLLWVFRRRW RLNFNRQQPT CATPEFVQGK EFKDFPDVLL PNYFTCRRAR   120
IRDRKAQQVF VDEGHTVQFV CRADGDPPPA ILWLSPRKHL VSAKSNGRLT VFPDGTLEVR   180
YAQVQDNGTY LCIAANAGGN DSMPAHLHVR SYSPDWPHQP NKTFAFISNQ PGEGEANSTR   240
ATVPFPFDIK TLIIATTMGF ISFLGVVLFC LVLLFLWSRG KGNTKHNIEI EYVPRKSDAG   300
ISSADAPRKF NMKMI
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Seq ID NO: B32 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
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CAGCACATAC AAGAAACATA CAGTGTACCT CAAAAGGGGC CCTTGAAATG TCATCAAAGG    60
GTAATAACCT AGTGAGTGAG TTGTGATGTC ATCTGGAACA TAGGAAATGG GGCTCTTAGC   120
GTATTCGGTA CGAAGGAAGC CAGGCTGGTC CTGGCAGGAA GTAAATGATA ATCTTTGGGA   180
AACCAGGACC CTGCCTCCCA GCCCAGAGGT GGAGGAGGGC GGTCAGGGTG GGGTCTACAG   240
TGGCACAGCA CTGACAAAGG TAGAGGGAAA TGTAATAGCA CATCTACGCT GCAGTCTGGT   300
GAAAGTGCCC GGGGTGGTCC TTGGAAAACA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC   360
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GGGTATAGAA A
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Seq ID NO: B33 DNA sequence
Nucleic Acid Accession #: NM_006174.1
Coding sequence: 71..1408

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AGACTATAAT ATGGATTTAG AGCTCGACGA GTATTATAAC AAGACACTTG CCACAGAGAA   120
TAATACTGCT GCCACTCGGA ATTCTGATTT CCCAGTCTGG GATGACTATA AAAGCAGTGT   180
ACATGACTTA CAGTATTTTC TGATTGGGCT CTATACATTT GTAAGTCTTC TTGGCTTTAT   240
GGGGAATCTA CTTATTTTAA TGGCTCTCAT GAAAAAGCGT AATCAGAAGA CTACGGTAAA   300
CTTCCTCATA GGCAATCTGG CCTTTTCTGA TATCTTGGTT GTGCTGTTTT GCTCACCTTT   360
CACACTGACG TCTGTCTTGC TGGATCAGTG GATGTTTGGC AAAGTCATGT GCCATATTAT   420
GCCTTTTCTT CAATGTGTGT CAGTTTTGGT TTCAACTTTA ATTTTAATAT CAATTGCCAT   480
TGTCAGGTAT CATATGATAA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA   540
CTTTCTGATA GCTACTGTCT GGACACTAGG TTTTGCCATC TGTTCTCCCC TTCCAGTGTT   600
TCACAGTCTT GTGGAACTTC AAGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATTT   660
ATGTGTTGAG TCATGGCCAT CTGATTCATA CAGAATTGCC TTTACTATCT CTTTATTGCT   720
AGTTCAGTAT ATTCTGCCCT TAGTTTGTCT TACTGTAAGT CATACAAGTG TCTGCAGAAG   780
TATAAGCTGT GGATTGTCCA ACAAAGAAAA CAGACTTGAA GAAAATGAGA TGATCAACTT   840
AACTCTTCAT CCATCCAAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG   900
GAGTTATTCA TTCATCAAAA AACACAGAAG AAGATATAGC AAGAAGACAG CATGTGTGTT   960
ACCTGCTCCA GAAAGACCTT CTCAAGAGAA CCACTCCAGA ATACTTCCAG AAAACTTTGG  1020
CTCTGTAAGA AGTCAGCTCT CTTCATCCAG TAAGTTCATA CCAGGGGTCC CCACTTGCTT  1080
TGAGATAAAA CCTGAAGAAA ATTCAGATGT TCATGAATTG AGAGTAAAAC GTTCTGTTAC  1140
```

AAGAATAAAA AAGAGATCTC GAACTGTTTT CTACAGACTG ACCATACTGA TATTAGTATT 1200
TGCTGTTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAATCT 1260
TATTTCAAAT AGGCATTTCA AGTTGGTGTA TTGCATTTGT CATTTGTTGG GCATGATGTC 1320
CTGTTGTCTT AATCCAATTC TATATGGGTT TCTTAATAAT GGGATTAAAG CTGATTTAGT 1380
GTCCCTTATA CACTGTCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence
Protein Accession #: NP_006165.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDLELDEYYN KTLATENNTA ATRNSDFPVW DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL    60
LILMALMKKR NQKTTVNFLI GNLAFSDILV VLFCSPFTLT SVLLDQWMFG KVMCHIMPFL   120
QCVSVLVSTL ILISIAIVRY HMIKHPISNN LTANHGYFLI ATVWTLGFAI CSPLPVFHSL   180
VELQETFGSA LLSSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC   240
GLSNKENRLE ENEMINLTLH PSKKSGPQVK LSGSHKWSYS FIKKHRRRYS KKTACVLPAP   300
ERPSQENHSR ILPENFGSVR SQLSSSSKFI PGVPTCFEIK PEENSDVHEL RVKRSVTRIK   360
KRSRSVFYRL TILILVFAVS WMPLHLFHVV TDFNDNLISN RHFKLVYCIC HLLGMMSCCL   420
NPILYGFLNN GIKADLVSLI HCLHM
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Seq ID NO: B35 DNA sequence
Nucleic Acid Accession #: NM_014279.1
Coding sequence: 286..1689

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1          11         21         31         41         51
|          |          |          |          |          |
GCGCGGGGGA GCCATTAGGA GGCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC    60
CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG   120
CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG   180
GGGACACGAG CCAGGCGCCG CCGCCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG   240
TCCGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CCTGCATGCC AGGTCGTTGG   300
AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG   360
ATGGGCACTG AACTCACTCA AGTGCTGCCC ACCAACCCTG AGGAGAGCTG GCAGGTGTAC   420
AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC   480
ATGTGTTCAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC   540
ATCTCTCAAT CCATAGAGGT CTTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG   600
AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT   660
AAGCAACACC TGGCCAGGCA GTTTAAGGCG ATAAAAGCGA AAATGGATGA ACTTAGGCCT   720
TTGATACCTG TGTTGGAAGA GTACAAGGCC GATGCCAAAT TGGTATTGCA GTTTAAAGAG   780
GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATTGG CGCCTATGAC   840
TACGATGAAC TTCAGAGCAG AGTGTCCAAT CTTGAAGAAA GGCTCCGTGC ATGCATGCAA   900
AAACTAGCTT GCGGGAAGTT GACGGGCATC AGTGACCCCG TGACTGTCAA GACCTCCGGC   960
TCGAGGTTCG GATCCTGGAT GACAGACCCT CTCGCCCCTG AAGGCGATAA CCGGGTGTGG  1020
TACATGGACG GCTATCACAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTTGACTTC  1080
ATGAACACGG ACAATTTCAC CTCCCACCGT CTCCCCCACC CCTGGTCGGG CACGGGGCAG  1140
GTGGTCTACA ACGGTTCTAT CTACTTCAAC AAGTTCCAGA GCCACATCAT CATCAGGTTT  1200
GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCCGG TTACAACAAC  1260
ATGTACCACT ACGCCTGGGG TGGCCACTCG GACATCGACC TCATGGTGGA CGAGAGCGGG  1320
CTGTGGGCCG TGTACGCCAC CAACCAGAAC GCTGGCAACA TCGTGGTCAG TAGGCTGGAC  1380
CCCGTGTCCC TGCAGACCCT GCAGACCTGG AACACGAGCT ACCCCAAGCG CAGCGCCGGG  1440
GAGGCCTTCA TCATCTGCGG CACGCTGTAC GTCACCAACG GCTACTCAGG GGGTACCAAG  1500
GTCCACTATG CATACCAGAC CAATGCCTCC ACCTATGAAT ACATCGACAT CCCATTCCAG  1560
AACAAATACT CCCACATCTC CATGCTGGAC TACAACCCCA AGGACCGGGC CCTGTATGCC  1620
TGGAACAACG GCCACCAGAT CCTCTACAAC GTGACCCTCT TCCACGTCAT CCGCTCCGAC  1680
GAGTTGTAGC TCCCTCCTCC TGGAAGCCAA GGGCCCACGT CCTCACCACA AAGGGACTCC  1740
TGTGAAACTG CTGCCAAAAA GATACCAATA ACACTAACAA TACCGATCTT GAAAAATCAT  1800
CAGCAGTGCG GATTCTGACA TCGAGGGATG GCATTACCTC CGTGTTTCTC CCTTTCGAGC  1860
CGGCGGGCCA CAGACGTCGG AAGAAACTCC CGTATTTGCA GCTGGAACTG CAGCCCACGG  1920
CGCCCCGGTT TTCCTCCCCG CCCTGTCCCT CTCTGGTCAA ACAACATACT AAAGAGGCGA  1980
GGCAATGACT GTTGGCCAGT TCTCACCGGG GAAAAACCCA CTGTTAGGAT GGCATGAACA  2040
TTTCCTTAGA TCGTGGTCAG CTCCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG  2100
GCTGCACCCG GCCGTAGGCT AGTGTAACTC GCATCCCATT GCAGTGCCGT TTCTTGACTG  2160
TGTTGCTGTC TCTTAGATTA ACCGTGCTGA GGCTCCACAT AGCTCCTGGA CCTGTGTCTA  2220
GTACATACTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGCTGTGCCC ACATTGTTTG  2280
AACTCGCGTA CCCCGTAGAT ACATTGTGCA ACGTTCTTCT GTTATTCCCT TGAGGTGGTA  2340
ACTTCGTATG TTCAGTTTAT GCGATGATTG TTGTAAATGC AATGCCGTAG TTTGGATTAA  2400
TAAGTGGATG GTTTTTGTTT CTAAAAAGAA AAAAAAAATC AGTGTTCACC CTTATAGAGA  2460
CATAGTCAAG TTCATGTTGA TAATAATCAA AGGAATTACT CTCTTCTTGT TAAATTAGCT  2520
AAATCATGTA ACCGCAGATA GGAAGGGCTC ACCTGGGGAA ACTCTGGTTT CCGATGGGAC  2580
AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTTAAGTAA AAAACAAAGG  2640
CAAACTTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAAAA  2700
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A
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Seq ID NO: B36 Protein sequence
Protein Accession #: NP_055094.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPEE SWQVYSSAQD SEGRCICTVV    60
APQQTMCSRD ARTKQLRQLL EKVQNMSQSI EVLDRRTQRD LQYVEKMENQ MKGLESKFKQ   120
VEESHKQHLA RQFKAIKAKM DELRPLIPVL EEYKADAKLV LQFKEEVQNL TSVLNELQEE   180
IGAYDYDELQ SRVSNLEERL RACMQKLACG KLTGISDPVT VKTSGSRFGS WMTDPLAPEG   240
DNRVWYMDGY HNNRFVREYK SMVDFMNTDN FTSHRLPHPW SGTGQVVYNG SIYFNKFQSH   300
IIIRFDLKTE TILKTRSLDY AGYNNMYHYA WGGHSDIDLM VDESGLWAVY ATNQNAGNIV   360
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VSRLDPVSLQ TLQTWNTSYP KRSAGEAFII CCTLYVTNGY SGGTKVHYAY QTNASTYEYI   420
DIPFQNKYSH ISMLDYNPKD RALYAWNNGH QILYNVTLFH VIRSDEL

Seq ID NO: B37 DNA sequence
Nucleic Acid Accession #: NM_006334.1
Coding sequence: 286..693

1          11         21         31         41         51
|          |          |          |          |          |
GCGCGGGGGA GCCATTAGGA GGCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC    60
CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG   120
CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG   180
GGGACACGAG CCAGGCGCCG CCGCCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG   240
TCCGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CCTGCATGCC AGGTCGTTGG   300
AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG   360
ATGGGCACTG AACTCACTCA AGTGCTGCCC ACCAACCCTG AGGAGAGCTG GCAGGTGTAC   420
AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC   480
ATGTGTTCAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC   540
ATGTCTCAAT CCATAGAGGT CTTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG   600
AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT   660
AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACTTAAAA GAGTTTTTTC AATGCTGCAG   720
TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTTGCA   780
CCATGCATTT TTACTATTAT TTTCCAATAC TTAGCACCAT TTCACTAAGG AACCTTGAAT   840
ACAACCAGGA TCCTCCTTTG CATGCGACTG TAGCTGCATT TCATGAATAG TTTGAACCCT   900
TGTCAATGCA TTTTTTGAAA AAGAAAGAAA AAAAAAACTT CGTGTATGTG ACTCAAAGCA   960
TGTAACCTTA AGATGTTGCA TTCTAAACTG ACAATAAAGA CCTTTCCCC

Seq ID NO: B38 Protein sequence
Protein Accession #: NP_006325.1

1          11         21         31         41         51
|          |          |          |          |          |
MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPEE SWQVYSSAQD SEGRCICTVV    60
APQQTMCSRD ARTKQLRQLL EKVQNMSQSI EVLDRRTQRD LQYVEKMENQ MKGLESKFKQ   120
VEESHKQHLA RQFKG

Seq ID NO: B39 DNA sequence
Nucleic Acid Accession #: NM_058199.1
Coding sequence: 286..795

1          11         21         31         41         51
|          |          |          |          |          |
GCGCGGGGGA GCCATTAGGA GGCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC    60
CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG   120
CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG   180
GGGACACCAG CCAGGCGCCG CCGCCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG   240
TCCGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CCTGCATGCC AGGTCGTTGG   300
AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG   360
ATGGGCACTG AACTCACTCA AAATAAAAGA GAAAACAAAG CAGAGAAGAT GGGAGGGCCA   420
GAGAGCGAGA GGAAGACCAC AGGAGAGAAG ACACTGAACG AGCTTCCCTT GTTTTGCCTG   480
GAAGCCCACG CTGGCTCCCT GGCTCTGCCC AGGATGTGCA GTCCAAATCC CAATCCAGCA   540
GTGGGGTTAT GTCGTCCCGC TTACCCTCAG AGCCCTTCTC CTGGTGCTGC CCAGACGATC   600
AGCCAGTCCC TCCTGGAGAG GTTCTGCATG GCCTCTAGGA GAGAAGTTTT CTTGGCCCCA   660
GGAAGGCCTG GTGGAGGGTG GTGGTTGTGC ACTGTTGCTG GACAGATGCA TTCATTCATG   720
TGCACACACA CACACACACA TGCACACACA GGGGAGCAGA TACCTGCAGA GAAGAGCCAA   780
CCAGGTCCTG ATTAGTGGCA AGCTGCCCCA CAAAGGGCTA TGCCTGTGTC TTATTGAGAC   840
ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCCTGGAC ATGGCCGCAC CCAAGGGCCC   900
TCCAAGCCTT AATGGCACCC TGAAGCCTCC ATGCCCAGGC CAAAAGATGC TTTTCCTCCC   960
TAAAAAAAAA AAAAAAAAAA

Seq ID NO: B40 Protein sequence
Protein Accession #: NP_478106.1

1          11         21         31         41         51
|          |          |          |          |          |
MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQNKRENKAE KMGGPESERK TTGEKTLNEL    60
PLFCLEAHAG SLALPRMCSP NPNPAVGLCR PAYPQSPSPG AAQTISQSLL ERFCMASRRE   120
VFLAPGRPGG GWWLCTVAGQ MHSFMCTHTH THAHTGEQIP AEKSQPGPD

Seq ID NO: B41 DNA sequence
Nucleic Acid Accession #: AY038071.1
Coding sequence: 1..1686

1          11         21         31         41         51
|          |          |          |          |          |
ATGAGCAATC AGTACCAGGA GGAGGCCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT    60
CCAACTTTGC TCTCCTCCTA CTGCATCGAC AGCATCCTGG GCCGGAGGAG CCCGTGCAAA   120
ATGCGGTTGC TGGGAGCCGC GCAGAGCTTG CCTGCTCCGC TGACCAGCCG CGCCGACCCG   180
GAAAAGGCCG TGCAAGGCTC CCCTAAGAGC AGCAGCGCCC CGTTCGAGGC CGAGCTGCAC   240
CTGCCGCCCA AGCTGCGGCG CCTGTACGGC CCGGGCGGGG GCCGCCTCCT TCAGGGTGCG   300
GCAGCGGCGG CGGCGGCGGC GGCGGCGGCG GCGGCAGCGG CCGCCACGGC CACGGCGGGT   360
CCACGCGGGG AGGCCCCTCC GCCGCCACCG CCAACCGCGC GGCCCGGGGA ACGGCCGGAC   420
GGCGCAGGGG CCGCCGCGGC AGCCGCGGCC GCGGCCGCCG CGGCCTGGGA CACGCTCAAG   480
ATCAGCCAGG CGCCGCAGGT GAGCATCAGC CGCAGCAAGT CGTACCGCGA GAACGGGGCG   540
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CCCTTCGTGC CGCCGCCGCC CGCGCTCGAC GAGCTGGGCG GCCCGGGGGG CGTCACGCAC   600
CCGGAGGAGC GCCTCGGCGT GGCCGGCGGC CCGGGCAGCG CCCCGGCTGC GGGTGGTGGC   660
ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAGATGA GGACGAGGAA   720
GAGGAACTGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACGACGCCCG CGCGCTGCTC   780
AAGGAGCCCC GGCGCTGTCC TGTGGCCGCC ACTGGCGCCG TGGCCGCAGC AGCTGCCGCT   840
GCAGTGGCCA CAGAGGGCGG GGAGCTGTCA CCCAAGGAGG AGCTGCTGCT GCACCCGGAA   900
GACGCTGAGG GCAACGACGG CGAGGACAGC GTGTGCCTCT CTGCGGGCAG CGACTCGGAG   960
GAGGGGCTGC TGAAACGCAA ACAGAGGCGC TACCGCACCA CGTTCACCAG CTACCAGCTG  1020
GAGGAACTGG AGCGGGCCTT CCAGAAGACG CACTACCCGG ACGTCTTCAC CAGGGAGGAA  1080
CTGGCCATGA GGCTGGACTT GACCGAGGCC CGAGTCCAGG TCTGGTTCCA GAACCGTCGG  1140
GCCAAGTGGC GCAAGCGGGA GAAGGCAGGC GCGCAGACCC ACCCCCCTGG GCTGCCCTTC  1200
CCGGGGCCGC TCTCCGCCAC CCACCCGCTC AGCCCCTACC TGGACGCCAG CCCCTTCCCT  1260
CCGCACCACC CGGCGCTCGA CTCCGCTTGG ACTGCCGCTG CCGCCGCCGC CGCCGCCGCC  1320
TTCCCGAGCC TACCTCCGCC TCCGGGCTCG GCCAGCCTGC CGCCCAGCGG GGCGCCGCTG  1380
GGCCTGAGCA CTTTCCTCGG AGCGGCAGTG TTCCGACACC CAGCTTTCAT CAGCCCGGCA  1440
TTCGGCAGGC TCTTTTCCAC AATGGCCCCC CTGACCAGCG CGTCGACCGC GGCCGCGCTC  1500
CTGAGACAGC CCACACCCGC CGTGGAGGGC GCAGTGGCAT CGGGCGCCCT GGCCGACCCG  1560
GCCACGGCGG CCGCAGACAG ACGCGCCTCT AGCATAGCCG CGCTGAGGCT CAAGGCCAAG  1620
GAGCACGCGG CGCAGCTCAC GCAGCTCAAC ATCCTGCCGG GCACCAGCAC GGGCAAGGAG  1680
GTGTGC
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Seq ID NO: B42 Protein sequence
Protein Accession #: AAK93901.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSNQYQEEGC SERPECKSKS PTLLSSYCID SILGRRSPCK MRLLGAAQSL PAPLTSRADP    60
EKAVQGSPKS SSAPFEAELH LPPKLRRLYG PGGGRLLQGA AAAAAAAAAA AAAAATATAG   120
PRGEAPPPPP PTARPGERPD GAGAAAAAAA AAAAAWDTLK ISQAPQVSIS RSKSYRENGA   180
PFVPPPPALD ELGGPGGVTH PEERLGVAGG PGSAPAAGGG TGTEDDEEEL LEDEEDEDEE   240
EELLEDDEEE LLEDDARALL KEPRRCPVAA TGAVAAAAAA AVATEGGELS PKEELLLHPE   300
DAEGKDGEDS VCLSAGSDSE EGLLKRKQRR YRTTFTSYQL EELERAFQKT HYPDVFTREE   360
LAMRLDLTEA RVQVWFQNRR AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASPFP   420
PHHPALDSAW TAAAAAAAAA FPSLPPPPGS ASLPPSGAPL GLSTFLGAAV FRHPAFISPA   480
FGRLFSTMAP LTSASTAAAL LRQPTPAVEG AVASGALADP ATAAADRRAS SIAALRLKAK   540
EHAAQLTQLN ILPGTSTGKE VC
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Seq ID NO: B43 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
CGCCTGCCCC CCCGTTGCTT CTCTCTCTTC CCTTCTGCCT GCGTGCTCGC CCGTCTTTGG    60
TTCCGCCGGT TCCGTGCGCC CTCTCTGGGC TTCGGCTTCA CCCTCCGTCT GGCTGTCGCT   120
CTGCTCTCCT CCGCTCTCAT GCCCCTTTCA GCTCCTACTC TGGTGTCGTC CCCCTCCCTC   180
GCTCGTTTCT CTTGTTCCTC TCCTTCCCGG TTCGTGTTCT GCTTCTTCGT GTTCCCTCTC   240
GTCTGTGTTT GTGGGTCGTC CTCTGCGTCC TGCCTCTTTC TCTTGCGTTT CCGCGCGCTT   300
CCTGTTTTGG TCCCCCTGGT TCTCGCGCGG TTCTGTGTGC GCGGGCCGCC CCGTTCTTTC   360
TTGGTGCTTT GCTCCTGCTC TCTGTCTGGT GTTCTCCGCC GTCTGTGTCT TTCTCCTTTT   420
ATCTTCTGTT TTCTCTTTTT CTTGTTTCTT CTTGTTTTTT TTTGTCTTTG TTTTCTCTTA   480
GCTGAGGTTG GGGAGAGATA ACGCTGTAAA CTTTTATTTT TCAGGAAATC TGGAAACCTA   540
CAGTCTCCAT GCCTGCTCAG CCAAGAAGGA GCTCACTGTG GGCACCAGAG ACAGGGACCC   600
AATGTGGAGA CCTGTGAGCC TGTGTCCGGC CCTGAACTCT CAAGCACAGG GCAGGCTTCC   660
TGAGCATTGA AGAGAATATG TGGGAGAACA AAACAGAAAC TGAAAGAATA TGCAAGGTGT   720
CTTTCTTGGA TGTTATTCCA TGATAGATAG TAGGGGCAGG AGTGAGAGAG GCTGACTAGG   780
TCTGGACATG GAGGCTGGAA GAGTCAGGGT GTGATTCGGA GAGGCGCATG AGAAGGAAGG   840
TGGATTTTAA GGCTGGAAAT CTGAGGGTCA GTGGTCCAAG TCACTCAGAG ACAGAATCAC   900
AGCATAGCCC TTGCTGATGG CAA
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Seq ID NO: B44 DNA sequence
Nucleic Acid Accession #: NM_014421.1
Coding sequence: 718..1497

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1          11         21         31         41         51
|          |          |          |          |          |
CCACGCGTCC GGCGGGAGCC CGCGGCGAGC GTAGCGCAAG TCCGCTCCCT AGGCATCGCT    60
GCGCTGGCAG CGATTCGCTG TCTCTTGTGA GTCAGGGGAC AACGCTTCGG GGCAACTGTG   120
AGTGCGCGTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTCGGTC CGGGGACGTC   180
TCCTGATCCC CTACTAAAGC GCCTGCTAAC TTTGAAAAGG AGCACTGTGT CCTGCAAAGT   240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTTGA AGGAGAAGGA   300
GCTGATGCGG GCCTCCTGAT CAATTAAGAG GAGAGTTAAA CCGCCGAGAT CCCGGCGGGA   360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTTCT   420
TGCACCTTGG GTCACGCCTC CTTGGCCAGA AAGCGCCTCG CATTTGATTG CTTCCAGTTA   480
TTGCAGAACT TCCTGTCCTG GTGGAGAAGC GGGTCTCGCT TGGGTTCCGC TAATTTCTGT   540
CCTGAGGCGT GAGACTGAGT TCATAGGGTC CTGGGTCCCC GAACCAGGAA GGGTTGAGGG   600
AACACAATCT GCAAGCCCCC GCGACCCAAG TGAGGGGCCC CGTGTTGGGG TCCTCCCTCC   660
CTTTGCATTC CCACCCCTCC GGGCTTTGCG TCTTCCTGGG GACCCCCTCG CCGGGAGATG   720
GCCGCGTTGA TGCGGAGCAA GGATTCGTCC TGCTGCCTGC TCCTACTGGC CGCGGTGCTG   780
ATGGTGGAGA GCTCACAGAT CGGCAGTTCG CGGGCCAAAC TCAACTCCAT CAAGTCCTCT   840
CTGGGCGGGG AGACGCCTGG TCAGGCCGCC AATCGATCTG CGGGCATGTA CCAAGGACTG   900
GCATTCGGCG GCAGTAAGAA GGGCAAAAAC CTGGGGCAGG CCTACCCTTG TAGCAGTGAT   960
AAGGAGTGTG AAGTTGGGAG GTATTGCCAC AGTCCCCACC AAGGATCATC GGCCTGCATG  1020
GTGTGTCGGA GAAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCCC CAGTACCCGC  1080
TGCAATAATG GCATCTGTAT CCCAGTTACT GAAAGCATCT TAACCCCTCA CATCCCGGCT  1140
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CTGGATGGTA CTCGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200
TGGCAGAATC TAGGAAGACC ACACACTAAG ATGTCACATA TAAAAGGGCA TGAAGGAGAC 1260
CCCTGCCTAC GATCATCAGA CTGCATTGAA GGGTTTTGCT GTGCTCGTCA TTTCTGGACC 1320
AAAATCTGCA AACCAGTGCT CCATCAGGGG GAAGTCTGTA CCAAACAACG CAAGAAGGGT 1380
TCTCATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGGCCTGTC TTGCAAAGTA 1440
TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTCAGAA AATTTGATCA 1500
CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560
GGTGGAAAAT AAGGTTCAGA TGCAGAAGAA TGGCTAAAAT AAGAAACGTG ATAAGAATAT 1620
AGATGATCAC AAAAAGGGAG AAAGAAAACA TGAACTGAAT AGATTAGAAT GGGTGACAAA 1680
TGCAGTGCAG CCAGTGTTTC CATTATGCAA CTTGTCTATG TAAATAATGT ACACATTTGT 1740
GGAAAATGCT ATTATTAAGA GAACAAGCAC ACAGTGGAAA TTACTGATGA GTAGCATGTG 1800
ACTTTCCAAG AGTTTAGGTT GTGCTGGAGG AGAGGTTTCC TTCAGATTGC TGATTGCTTA 1860
TACAAATAAC CTACATCCCA GATTTCTATT CAACGTTAGA GTTTAACAAA ATACTCCTAG 1920
AATAACTTGT TATACAATAG GTTCTAAAAA TAAAATTGCT AAACAAGAAA TGAAAACATG 1980
GAGCATTGTT AATTTACAAC AGAAAATTAC CTTTTGATTT GTAACACTAC TTCTGCTGTT 2040
CAATCAAGAG TCTTGGTAGA TAAGAAAAAA ATCAGTCAAT ATTTCCAAAT AATTGCAAAA 2100
TAATGGCCAG TTGTTTAGGA AGGCCTTTAG GAAGACAAAT AAATAACAAA CAAACAGCCA 2160
CAAATACTTT TTTTTCAAAA TTTTAGTTTT ACCTGTAATT AATAAGAACT GATACAAGAC 2220
AAAAACAGTT CCTTCAGATT CTACGGAATG ACAGTATATC TCTCTTTATC CTATGTGATT 2280
CCTGCTCTGA ATGCATTATA TTTTCCAAAG TATACCCATA AATTGTGACT AGTAAAATAC 2340
TTACACAGAG CAGAATTTTC ACAGATGGCA AAAAAATTTA AAGATGTCCA ATATATGTGG 2400
GAAAAGAGCT AACAGAGAGA TCATTATTTC TTAAAGATTG GCCATAACCT GTATTTTGAT 2460
AGAATTAGAT TGGTAAATAC ATGTATTCAT ACATACTCTG TGGTAATAGA GACTTGAGCT 2520
GGATCTGTAC TGCACTGGAG TAAGCAAGAA AATTGGGAAA ACTTTTTCGT TTGTTCAGGT 2580
TTTGGCAACA CATAGATCAT ATGTCTGAGG CACAAGTTGG CTGTTCATCT TTGAAACCAG 2640
GGGATGCACA GTCTAAATGA ATATCTGCAT GGGATTTGCT ATCATAATNT TTCCTATGCN 2700
GNTGAATTCN GTGTGAGGTC CTGTGTCCGT CCTATCCTCA AATTATTTAT TTTATAGTGC 2760
TGAGATCCTC AAATAATCTC AATTTCGGAG GTTTCACAAA ATGGACTCCT GAAGTAGACA 2820
GAGTAGTGAG GTTTCATTGC CCTCTATAAG CTTCTGACTA GCCAATGGCA TCATCCAATT 2880
TTCTTCCCAA ACCTCTGCAG CATCTGCTTT ATTGCCAAAG GGCTAGTTTC GGTTTTCTGC 2940
CAGCCATTGC GGTTAAAAAA TATAAGTAGG ATAACTTGTA AAACCTGCAT ATTGCTAATC 3000
TATAGACACC ACAGTTTCTA AATTCTTTGA AACCACTTTA CTACTTTTTT TAAACTTAAC 3060
TCAGTTCTAA ATACTTTGTC TGGAGCACAA AACAATAAAA GGTTATCTTA TAGTTGTGAC 3120
TTTAAACTTT TGTAGACCAC AATTCACTTT TTAGTTTTCT TTTACTTAAA TCCCATCTGC 3180
AGTCTCAAAT TTAAGTTCTC CCAGTAGAGA TTGAGTTTGA GCCTGTATAT CTATTAAAAA 3240
TTTCAACTTC CCACATATAT TTACTAAGAT GATTAAGACT TACATTTTCT GCACAGGTCT 3300
GCAAAAACAA AAATTATAAA CTAGTCCATC CAAGAACCAA AGTTTGTATA AACAGGTTGC 3360
TATAAGCTTG GTGAAATGAA AATGGAACAT TTCAATCAAA CATTTCCTAT ATAACAATTA 3420
TTATATTTAC AATTTGGTTT CTGCAATATT TTTCTTATGT CCACCCTTTT AAAAATTATT 3480
ATTTGAAGTA ATTTATTTAC AGGAAATGTT AATGAGATGT ATTTTCTTAT AGAGATATTT 3540
CTTACAGAAA GCTTTGTAGC AGAATATATT TGCAGCTATT GACTTTGTAA TTTAGGAAAA 3600
ATGTATAATA AGATAAAATC TATTAAATTT TTCTCCTCTA AAAACTGAAA AAAAAAAAAA 3660
AAAAAAAAAA A

Seq ID NO: B45 Protein sequence
Protein Accession #: NP_055236.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAALMRSKDS SCCLLLLAAV LMVESSQIGS SRAKLNSIKS SLGGETPGQA ANRSAGMYQG   60
LAFGGSKKGK NLGQAYPCSS DKECEVGRYC HSPHQGSSAC MVCRRKKKRC HRDGMCCPST  120
RCNNGICIPV TESILTPHIP ALDGTRHRDR NHGHYSNHDL GWQNLGRPHT KMSHIKGHEG  180
DPCLRSSDCI EGFCCARHFW TKICKPVLHQ GEVCTKQRKK GSHGLEIFQR CDCAKGLSCK  240
VWKDATYSSK ARLHVCQKI
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Seq ID NO: 46 DNA sequence
Nucleic Acid Accession #: NM_019885.1
Coding sequence: 1..1539

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCTCTTTG AGGGCTTGGA TCTGGTGTCG GCGCTGGCCA CCCTCGCCGC GTGCCTGGTG    60
TCCGTGACGC TGCTGCTGGC CGTGTCGCAG CAGCTGTGGC AGCTGCGCTG GGCCGCCACT   120
CGCGACAAGA GCTGCAAGCT GCCCATCCCC AAGGGATCCA TGGGCTTCCC GCTCATCGGA   180
GAGACCGGCC ACTGGCTGCT GCAGGGTTCT GGCTTCCAGT CGTCGCGGAG GGAGAAGTAT   240
GGCAACGTGT TCAAGACGCA TTTGTTGGGG CGGCCGCTGA TACGCGTGAC CGGCGCGGAG   300
AACGTGCGCA AGATCCTCAT GGGCGAGCAC CACCTCGTGA GCACCGAGTG GCCTCGCAGC   360
ACCCGCATGT TGCTGGGCCC CAACACGGTG TCCAATTCCA TTGGCGACAT CCACCGCAAC   420
AAGCGCAAGG TCTTCTCCAA GATCTTCAGC CACGAGGCCC TGGAGAGTTA CCTGCCCAAG   480
ATCCAGCTGG TGATCCAGGA CACACTGCGC GCCTGGAGCA GCCACCCCGA GGCCATCAAC   540
GTGTACCAGG AGGCGCAGAA GCTGACCTTC CGCATGGCCA TCCGGGTGCT GCTGGGCTTC   600
AGCATCCCTG AGGAGGACCT TGGGCACCTC TTTGAGGTCT ACCAGCAGTT TGTGGACAAT   660
GTCTTCTCCC TGCCTGTCGA CCTGCCCTTC AGTGGCTACC GGCGGGGCAT TCAGGCTCGG   720
CAGATCCTGC AGAAGGGGCT GGAGAAGGCC ATCCGGGAGA AGCTGCAGTG CACACAGGGC   780
AAGGACTACT TGGACGCCCT GGACCTCCTC ATTGAGAGCA GCAAGGAGCA CGGGAAGGAG   840
ATGACCATGC AGGAGCTGAA GGACGGGACC CTGGAGCTGA TCTTTGCGGC CTATGCCACC   900
ACGGCCAGCG CCAGCACCTC ACTCATCATG CAGCTGCTGA AGCACCCCAC TGTGCTGGAG   960
AAGCTGCGGG ATGAGCTGCG GGCTCATGGC ATCCTGCACA GTGGCGGCTG CCCCTGCGAG  1020
GGCACACTGC GCCTGGACAC GCTCAGTGGG CTGCGCTACC TGGACTGCGT CATCAAGGAG  1080
GTCATGCGCC TGTTCACGCC CATTTCCGGC GGCTACCGCA CTGTGCTGCA GACCTTCGAG  1140
CTTGATGGTT TCCAGATCCC CAAAGGCTGG AGTGTCATGT ATAGCATCCG GGACACCCAT  1200
GACACAGCGC CCGTGTTCAA AGACGTGAAC GTGTTCGACC CCGATCGCTT CAGCCAGGCG  1260
CGGAGCGAGG ACAAGGATGG CCGCTTCCAT TACCTCCCGT TCGGTGGCGG TGTCCGGACC  1320
TGCCTGGGCA AGCACCTGGC CAAGCTGTTC CTGAAGGTGC TGGCGGTGGA GCTGGCTAGC  1380
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ACCAGCCGCT TTGAGCTGGC TACACGGACC TTCCCCCGCA TCACCTTGGT CCCCGTCCTG  1440
CACCCCGTGG ATGGCCTCAG CGTCAAGTTC TTTGGCCTGG ACTCCAACCA GAACGAGATC  1500
CTGCCGGAGA CGGAGGCCAT GCTGAGCGCC ACAGTCTAAC CCAAGACCCA CCCGCCTCAG  1560
CCCAGCCCAG GCAGCGGGGT GGTGGTTGTG GGAGGTAGAA ACCTGTGTGT GGGAGGGGGC  1620
CGGAACGGGG AGGGCGAGTG GCCCCCATAC TTGCCCTCCC TTGCTCCCCC TCCCTGGCAA  1680
ACCCTACCCA AAGCCAGTGG GCCCCATTCC TAGGGCTGGG CTCCCCTTCT GGCTCCAGCT  1740
TCCCTCCAGC CACTCCCCAT TTACCATCAG CTCAGCCCCT GGGAAGGGCG TGGCAGGGGC  1800
TCTGCATGCC CGTGACAGTG TTAGGTGTCA GCGCGTGCTA CAGTGTTTTT GTGATGTTCT  1860
GAACTGCTCC CTTCCCTCCG TTCCTTTCGG ACCCTTTTAG CTGGGGTTGG GGGACGGGAA  1920
GAGCCGTGCC CCCTTGGGCG CACTCTTCAG CGTCTCCTCC TCCTGCGCCC CCACTGCGTC  1980
TGCCCAGGAA CAGCATCCTG GGTAGCAGAA CAGGAGTCAA CCTTGGCGGG GCGGGGGCTG  2040
CGTCCAACCT GGAGATTGCC CTTCCCTATG CCACGGTTCC CACCCTCCCT CACCAGTTTG  2100
GACAATTTGA AATTACCTAT TGCTGCTACT TGTTCTGTCC TCTGACCTTG GGGCAAAGGA  2160
GCCCCAGGCC CTGTCTCCCC AGCATCCTCC CTGGTGGCCC TGGGCAGGTG CACTGACACC  2220
CCCACCTTCC CATCCCCTGC TGAACCAGGC CCTGTTACAC ACAGCCGCCT AAGGCCCGCG  2280
GCTCATGTGC TGCCCGCCCC CATATTTATT CACTGATAGA GAATCTTGGG GATGCTGGGG  2340
TCTGGAGTGA ACATCTCCTC CCCTTCATGC CCTAGCCTGT GTTCTAGCTG TCCTGGCGAG  2400
ACTTCTGTGA GTGAAGAGGA AGGGGTCTCT GGTCAAACCC AGCCCCCAGG GCCTAGGGTT  2460
GAAAGCCTTC CCCGGCTCCG GGCATTATTT GGGTTTAATC TCGGAGCCTC ACTCCTGGAC  2520
TGAAGTCCGG TGCCTCTGCC TTATCCCTGG TGGAGATGGA ATGTGGCCCA TTGCCTCCTC  2580
CCTCTCCTGT CAAAAACCCT GATCAGGTAG ATTTGGAGGC GGCCACGATT TCCTGTTTGG  2640
CCCCTGTTCA CCCCAGTGCA CTGGCCCTGA CTCCAGGCGT GAGTATGGGG AAGGATACGG  2700
GTTCTTCTGA CGGGGAGCAA GGGCCTCCGT CTTCCCTTCC TTAACTCTCC CCCTTTGCCC  2760
TCCGCCCTGA AAAAGGTGTC CTTGAAGTCC CTTCCACCTC TATGCCACTG TCTGCTTAGC  2820
CCAGCTCAGG GGTGGGGAAG AGGCGAAAGC GTGGGGGAGG TGAGCGCAGC GGCAGTTCTG  2880
CCTCGGAGCT GATTGCAGGG CCCTGTGTGG TCTCCGGACA GCTGCGGGAA GGCTGCCGCA  2940
GCTGAAGCTG AAGAGGCGGC TACGTGCGGT TTGTCAGGGG GATTGGGTTG AAAACTGGCC  3000
AGTCGGGATG ACTGGGTGAA AGAGGAGTAG CTCCTGCCAC TGGCGTTTTG AGTGTTGGCA  3060
ATTTGGGATG CCTCCTGGGG AAGGTTTCCG GGCGTTTGGT GAGTCTCTAG ATTTTTCCTT  3120
GCTTTCTGTG TTTATTGGTT TTTGATGTTG TAAAAGCAAT GAATCCCCTT TACAAGAAAA  3180
TCGAAAACAC AGAAGAATGA AGGACATGCC AGTCCCCGAT CGCTGCTGTG AGCACCTCAG  3240
TGGCTCCCTC AGACCAGATC CCGTAGGCAG CCCCACAGAC CGACCCTGAC CCCACTCACA  3300
GCCACCCTGA AGATAGACTA TAGGAACGGG CCCATACCAC ACAGACTGCT CTCCAATCCC  3360
TGAGTCTCAG ATGTTTCATT TATTTCCTAC TTTTCCACTA CTAAAAAACA GTGTGGAATA  3420
GACATTATTG GCAAAATTGC TCATCCCTAA TCCTGAAAAA CAGGCCAGAA TGGGTAAAGA  3480
CTTGTCAAAG CTTGCAACAT AGCTACATGG TGCACCCGGA CCTGTACCCC CTCCCCCCAA  3540
CACAAAACCA GTGTCTGGGA GGTTCATTTT CCTTTAAACT GATCCAGCTG GCCCTGAACC  3600
AATTGTTTTT GACTGAGTAT CTAGGAGAGC AGTAAGTGGA ACTTCAGACA AGCCCACTGG  3660
GTCTGGTCCA GGTGAGGGGC AGGGGGCATG GGGCTGGGAG GTCTCAGGGG CCTTCCCTGG  3720
GGGTGGCCAG CCTGGTAGGG GGCAGAGAAG GAAAAGCTGA GGGGGGTCCC TGTGAGGGAG  3780
GAAAGAAGGA TCATTTGCCC CGCTGGGTCT CAAAGGCAGT GAGAAGAGAG CTGAAGAAAG  3840
CTCTGGCTGG CTGACAGGAT CCCTGTGTTG TAATTGGTCC CTCCTTTCAG CTCTCTAGTG  3900
AGATGCCCGT GTCTGTGCGT GTGCGTGTGT GTTTCATACA GCTAGCATTA GATGGGTGAT  3960
GTTTCTTACT TATCATCCCT AACTATTGCA ACTTGACCTT AAAAAGACAA AACCCCACAA  4020
AACTCTTCCT GCCACGGGCT TGCAGATTGA AGCACTTTCG ATGTTGGGCG CTGGCGTTTG  4080
TGTTCTGGGC ACCACCGTGA CCCTGCCCAG ATGGCTATAA TATTATTTTA TACACAAACC  4140
TTTTTTTTCA TAAATGTTAT AATTTTGTGT CTGTCTTTAT AAACTATTAT AAGTACTATT  4200
TTTGTTATAA TTCAAAATAG ATATTTAGTA TAAAGTTTTT GCTGTTAAAT ATTTGTTATT  4260
TAGTAAAATA TGAATTTTGC TCTATTGTAA ACATGGTTCA AAATATTAAT ATGTTTTTAT  4320
CACAGTCGTT TTAATATTGA AAAAGCACTT GTGTGTTTTG TTTTGATATG AAACTGGTAC  4380
CGTGTGAGTG TTTTTGCTGT CGTGGTTTTA ATCTGTATAT AATATTCCAT GTTGCATATT  4440
AAAAA
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Seq ID NO: B47 Protein sequence
Protein Accession #: NP_063938.1

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1          11         21         31         41         51
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MLFEGLDLVS ALATLAACLV SVTLLLAVSQ QLWQLRWAAT RDKSCKLPIP KGSMGFPLIG    60
ETGHWLLQGS GFQSSRREKY GNVFKTHLLG RPLIRVTGAE NVRKILMGEH HLVSTEWPRS   120
TRMLLGPNTV SNSIGDIHRN KRKVFSKIFS HEALESYLPK IQLVIQDTLR AWSSHPEAIN   180
VYQEAQKLTF RMAIRVLLGF SIPEEDLGHL FEVYQQFVDN VFSLPVDLPF SGYRRGIQAR   240
QILQKGLEKA IREKLQCTQG KDYLDALDLL IESSKEHGKE MTMQELKDGT LELIFAAYAT   300
TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGCPCE GTLRLDTLSG LRYLDCVIKE   360
VMRLFTPISG GYRTVLQTFE LDGFQIPKGW SVMYSIRDTH DTAPVFKDVN VFDPDRFSQA   420
RSEDKDGRFH YLPFGGGVRT CLGKHLAKLF LKVLAVELAS TSRFELATRT FPRITLVPVL   480
HPVDGLSVKF PGLDSNQNEI LPETEAMLSA TV
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Seq ID NO: B48 DNA sequence
Nucleic Acid Accession #: AB040527.1; AL136582.1
Coding sequence: 94..2319

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1          11         21         31         41         51
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GCGGCTGCGG GGTTCCTGGT GCTGAGGACG GACGCCATTG GAGTTCCCGA GAAGCATGGC    60
TGAGGGAAGC TTCAGCGTGC AATCGGAAAG CTACAGTGTT GAAGACATGG ATGAGGGTAG   120
CGACGAAGTC GGGGAGGAAG AGATGGTTGA AGGCAACGAC TATGAAGAAT TCGGTGCGTT   180
TGGTGGCTAT GGCACCCTCA CCAGCTTTGA CATCCATATC CTCAGAGCCT TCGGAAGCTT   240
GGGTCCAGGC CTTCGCATCT TATCGAATGA GCCCTGGGAA CTGGAAAACC CTGTGCTGGC   300
CCAGACCCTG GTGGAGGCAT TGCAGCTGGA TCCGGAAACA CTTGCCAATG AGACGGCCGC   360
CCGTGCTGCC AACGTAGCCC GCGCCGCCGC CTCCAACCGT GCGGCTCGGG CCGCTGCCGC   420
CGCTGCCCGT ACCGCCTTCA GTCAGGTGGT CGCTAGCCAC CGGGTGGCCA CGCCGCAGGT   480
CTCAGGAGAG GATACCCAGC CCACGACCTA CGCCGCCGAG GCTCAGGGGC CCACCCCTGA   540
GCCACCCCTT GCTTCTCCGC AGACCTCCCA GATGTTAGTC ACCAGTAAGA TGGCTGCCCC   600
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CGAGGCTCCG GCAACCTCCG CACAGTCCCA GACAGGCTCC CCGGCCCAGG AGGCTGCTAC   660
TGAGGGCCCT AGTAGCGCCT GTGCTTTCTC TCAGGCTCCG TGTGCCAGGG AGGTGGACGC   720
CAACCGGCCC AGCACAGCCT TCCTGGGCCA GAATGATGTC TTCGATTTCA CTCAGCCGGC   780
AGGTGTCAGT GGCATGGCCT TCCCGCGCCC CAAGAGACCT GCCCCAGCCC AAGAGGCTGC   840
CACAGAGGGC CCCAGTGCTG CCTCTGGTGT GCCCCAGACG GGACCTGGCA GGGAGGTGGC   900
AGCCACCCGG CCCAAGACCA CCAAGTCGGG GAAGGCGCTG GCCAAGACTC GGTGGGTGGA   960
GCCTCAGAAT GTTGTGGCAG CAGCTGCTGC CAAGGCCAAG ATGGCCACGA GCATCCCTGA  1020
GCCGGAGGGT GCAGCTGCTG CCACTGCTCA GCACAGTGCT GAGCCCTGGG CCAGGATGGG  1080
AGGCAAGAGG ACCAAGAAGT CCAAGCACCT GGATGATGAG TATGAGAGCA GCGAGGAGGA  1140
GAGAGAGACT CCCGCGGTCC CACCCACCTG GAGAGCATCA CAGCCCTCAT TGACGGTGCG  1200
GGCTCAGTTG GCCCCTCGGC CCCCGATGGC CCCGAGGTCC CAGATACCCT CAAGGCACGT  1260
ACTGTGCCTG CCCCCCCGCA ACGTGACCCT TCTGCAGGAG AGGGCAAATA AGTTGGTGAA  1320
ATACCTGATG ATTAAGGACT ACAAGAAGAT CCCCATCAAG CGCGCAGACA TGCTGAAGGA  1380
TGTCATCAGA GAATATGATG AACATTTCCC TGAGATCATT GAACGAGCAA CGTACACCCT  1440
GGAAAAGAAG TTTGGGATCC ACCTGAAGGA GATCGACAAG GAAGAACACC TGTATATTCT  1500
TGTCTGCACA CGGGACTCCT CAGCTCGCCT CCTTGGAAAA ACCAAGGACA CTCCCAGGCT  1560
GAGTCTCCTC TTGGTGATTC TGGGCGTCAT CTTCATGAAT GGCAACCGTG CCAGCGAGGC  1620
TGTCCTCTGG GAGGCACTAC GCAAGATGGG ACTGCGCCCT GGGGTGAGGC ACCCATTCCT  1680
CGGCGATCTG AGGAAGCTCA TCACAGATGA CTTTGTGAAG CAGAAGTACC TGGAATACAA  1740
GAAGATCCCC AACAGCAACC CACCTGAGTA TGAATTCCTC TGGGGCCTGC GAGCCCGCCA  1800
TGAGACCAGC AAGATGAGGG TCCTGAGATT CATCGCCCAG AATCAGAACC GAGACCCCCG  1860
GGAATGGAAG GCTCATTTCT TGGAGGCTGT GGATGATGCT TTCAAGACAA TGGATGTGGA  1920
TATGGCCGAG GAACATGCCA GGGCCCAGAT GAGGGCCCAG ATGAATATCG GGGATGAAGC  1980
GCTGATTGGA CGGTGGAGCT GGGATGACAT ACAAGTCGAG CTCCTGACCT GGGATGAGGA  2040
CGGAGATTTT GGCGATGCCT GGGCCAGGAT CCCCTTTGCT TTCTGGGCCA GATACCATCA  2100
GTACATTCTG AATAGCAACC GTGCCAACAG GAGGGCCACG TGGAGAGCTG GCGTCAGCAG  2160
TGGCACCAAT GGAGGGGCCA GCACCAGCGT CCTAGATGGC CCCAGCACCA GCTCCACCAT  2220
CCGGACCAGA AATGCTGCCA GAGCTGGCGC CAGCTTCTTC TCCTGGATCC AGCACCGTTG  2280
ACGAACTGCA GCGATCTTAC TGGCCAAGCC AGAGCGCCTC CTCTCAGATT CCTTCTCGAC  2340
ACAGCACCCT AGGCGGCTTC TTCCTGTCAG TCGGAGGTGG CATGCAAGAT GAAGCTCTCT  2400
TTGCTCTTCC TGCTTTCATT TTGTGCTTTT CCTTGTGTTT TCATGTTTTG GGTATCAGTG  2460
TTACATTAAA GTTGCAAAAT TAAA
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Seq ID NO: B49 Protein sequence
Protein Accession #: BAB33378.1; CAB66517.1

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1          11         21         31         41         51
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MAEGSFSVQS ESYSVEDMDE GSDEVGEEEM VEGNDYEEPG APGGYGTLTS FDIHILRAPG    60
SLGPGLRILS NEPWELENPV LAQTLVEALQ LDPETLANET AARAANVARA AASNRAARAA   120
AAAARTAFSQ VVASHRVATP QVSGEDTQPT TYAAEAQGPT PEPPLASPQT SQMLVTSKMA   180
APEAPATSAQ SQTGSPAQEA ATEGPSSACA FSQAPCAREV DANRPSTAFL GQNDVFDFTQ   240
PAGVSGMAFP RPKRPAPAQE AATEGPSAAS GVPQTGPGRE VAATRPKTTK SGKALAKTRW   300
VEPQNVVAAA AAKAKMATSI PEPEGAAAAT AQHSAEPWAR MGGKRTKKSK HLDDEYESSE   360
EERETPAVPP TWRASQPSLT VRAQLAPRPP MAPRSQIPSR HVLCLPPRNV TLLQERANKL   420
VKYLMIKDYK KIPIKRADML KDVIREYDEH FPEIIERATY TLEKKFGIHL KEIDKEEHLY   480
ILVCTRDSSA RLLGKTKDTP RLSLLLVILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP   540
FLGDLRKLIT DDFVKQKYLE YKKIPNSNPP EYEFLWGLRA RHETSKMRVL RFIAQNQNRD   600
PREWKAHFLE AVDDAFKTMD VDMAEEHARA QMRAQMNIGD EALIGRWSWD DIQVELLTWD   660
EDGDFGDAWA RIPFAFWARY HQYILNSNRA NRRATWRAGV SSGTNGGAST SVLDGPSTSS   720
TIRTRNAARA GASFFSWIQH R
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Seq ID NO: B50 DNA sequence
Nucleic Acid Accession #: XM_084965.1
Coding sequence: 356..2014

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1          11         21         31         41         51
|          |          |          |          |          |
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GCTGGGCTTA GTGCACCAAT GCTAAGGACA GACATGAAGG GCTTGGGAAA GGCATGAAGA   120
TGCAGGGAGT CTAGGAGAGA GGATAAGAAA AACAAGCATT TTGTGGTGGG TTGAATTGCG   180
TTGTCGTTTT TAGAGGCATT TCGTGATCCA TGGTTGCGCT CCCGTGAAGA GCGAGTCTAC   240
AGAAGGAATC CGAAGCGGCG GCGGCGAGCG CGGCTCAGGT TGATTTAGAA TACGGGTGAC   300
AGTGGCCTGG CGCGAGCCCA CTGCTGACGA AAGCGGCTTA TCCCGCGCGG TTTCCATGGA   360
GACGAGCCGG AGCCGCGGCG GCGGCGGGGC TGTCAGCGAG CGCGGCGGAG CTGGCGCGTC   420
CGTGGGGGTC TGCAGGAGGA AGGCGGAGGC CGGGGCCGGG ACCGGGACCC TCGCGGCAGA   480
CATGGACTTG CATTGTGACT GTGCCGCCGA AACGCCGGCC GCCGAGCCGC CGTCGGGGAA   540
GATTAATAAA GCTGCCTTCA AATTATTCAA GAAGAGGAAA TCGGGTGGCA CCATGCCCAG   600
CATTTTTGGG GTCAAAAACA AAGGGGACGG GAAAAGCTCG GGTCCGACGG GGCTGGTGAG   660
GAGCAGGACC CACGACGGAC TTGCCGAGGT GCTGGTGCTG GAGAGCGGCA GGAAGGAGGA   720
GCCGCGCGGC GGGGGCGACA GCGGCGGGGG CGGCCGGGGG CGGCCGAACC CGGGGCCCCC   780
CAGAGCCGCA GGGCCCGGCG GGGGCTCCCT CGCCAGCAGC TCGGTGGCCA AGTCGCACAG   840
CTTCTTCTCG CTGCTGAAGA AGAACGGGCG CTCGGAAAAC GGCAAGGGAG AGCCTGTGGA   900
CGCGAGCAAG GCCGCCGCCA AACAAAAGCG GGGGCTGCGG GGGCTGTTCA GCGGCATGCG   960
CTGGCACAGG AAAGACAAGC GGGCCAAGGC GGAGGCCGCG GAGGGGCGCG CGCCCGGGGG  1020
CGGCTTGATC CTACCCGGCT CGCTCACCGC CAGCCTGGAG TGCGTCAAGG AGGAGACGCC  1080
CAGAGCCGCG CGCGAGCCGG AGGAGCCCAG CCAGGACGCC CCGCGAGACC CAGCAGGCTG  1140
TGGAGATATT ATTGCAGACC AAGAGGAAGA GGCAGGTCCC AGCTGTGACA AGCATGTCCC  1200
CGGGCCAGGC AAGCCGGCTC TGTCTAAAAA GAACCCCGGC GTGGTGGCCT ACCAAGGAGG  1260
CGGGGAAGAG ATGGCCAGCC CGGACGAGGT GGACGACACC TATCTACAGG AGTTCTGGGA  1320
CATGCTCTCC CAGACCGAGG AGCAGGGACC CGAGCCCCAG GAGGGCGCGG CTAAGGTGGC  1380
AGCTGCGCTG GAAACCAAGG TGGTGCCCGA GACCCCCAAA GACACCAGGT GTGTGGAAGC  1440
GGCCAAGGAC GCGTCCTCGG TCAAGCGCAG GAGGCTCAAC CGGATTCCCA TCGAGCCCCA  1500
TCCTAAGGAG GAGCCCAAGC ACCCGGAGAA GGAGCAGCAG GAAGGCGTCC CCAACAGCGA  1560
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CGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA  1620
GAAGGCGGGC ATCCCCCGGG ATAGCTACAG CGGGGACGCG CTCTATGATC TCTATGCTGA  1680
CCCGGACGGA AGTCCAGCAA CCCTTCCTGG AGGGAAGGAC AACGAGGAGA CGTCCTCCCT  1740
GTCCCGGTTA AAGCCCGTAT CTCCAGGCAC CATCACCTGT CCACTGCGAA CACCAGGCAG  1800
CTTGCTGAAG GACTCTAAGA TCCCTATTAG CATCAAGCAC CTGACCAACC TTCCATCTAG  1860
CCATCCCGTG GTGCACCAGC AACCCTCCAG GAGTGAGATG CCCAGAACAA AAATCCCGGT  1920
TTCCAAAGTG CTGGTCCGCA GAGTCAGCAA CCGGGGCTTG GCTGGGACCA CCATCAGAGC  1980
AACGGCCTGC CACGACAGTG CCAAAAAGTT GTGAGGTCTT CCAGGCCAAG GTGGATGGGC  2040
CCCATGCCAA GGAATACAAC TTTTCCCTGG AAACCACTAA AGTAAGTTTT GCTTTTCCTA  2100
AAGAAAGTCT TTTAGGACAC CACCCGTCCC CCGCCCTGCT CCAGAGCGTG GACCGAGGAG  2160
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AAGTTTTTCT TCCTTTTGCT TTAATATACT GAACACTTGG AAGTCACCTT TACTTGCCTT  2340
TGCAGAAAAC AGAACTTAGC CAAACCTAAG TAAGAGTCAT GCCTGGATAT TGGGATAAGC  2400
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ACGTTTCCTT CCTTCCCTTC TTTCCTCTTT CCTTTCCAGT T
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Seq ID NO: B51 Protein sequence
Protein Accession #: XP_084965.1

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METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS    60
GKINKAAFKL FKKRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK   120
EEPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLLKKN GRSENGKGEP   180
VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE   240
TPRAAREPEE PSQDAPRDPA GCGDIIADQE EEAGPSCDKH VPGPGKPALS KKNPGVVAYQ   300
GGGEEMASPD EVDDTYLQEF WDMLSQTEEQ GPEPQEGAAK VAAALETKVV PETPKDTRCV   360
EAAKDASSVK RRRLNRIPIE PHPKEEPKHP EKEQQEGVPN SDEGYWDSTT PGPEEDSSSS   420
GKKAGIPRDS YSGDALYDLY ADPDGSPATL PGGKDNEETS SLSRLKPVSP GTITCPLRTP   480
GSLLKDSKIP ISIKHLTNLP SSHPVVHQQP SRSEMPRTKI PVSKVLVRRV SNRGLAGTTI   540
RATACHDSAK KL
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Seq ID NO: B52 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2016

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GCGTCCGTGG GGGTCTGCAG GAGGAAGGCG GAGGCCGGGG CCGGGACCGG GACCCTCGCG   120
GCAGACATGG ACTTGCATTG TGACTGTGCC GCCGAAACGC CGGCCGCCGA GCCGCCGTCG   180
GGGAAGATTA ATAAAGCTGC CTTCAAATTA TTCAAGAAGA GGAAATCGGG TGGCACCATG   240
CCCAGCATTT TTGGGGTCAA AAACAAAGGG GACGGGAAAA GCTCGGGTCC GACGGGGCTG   300
GTGAGGAGCA GGACCCACGA CGGACTTGCC GAGGTGCTGG TGCTGGAGAG CGGCAGGAAG   360
GAGGAGCCGC GCGGCGGGGG CGACAGCGGC GGGGGCGGCG GGGGGCGGCC GAACCCGGGG   420
CCCCCCAGAG CCGCAGGGCC CGGCGGGGGC TCCCTCGCCA GCAGCTCGGT GGCCAAGTCG   480
CACAGCTTCT TCTCGCTGCT GAAGAAGAAC GGGCGCTCGG AAAACGGCAA GGGAGAGCCT   540
GTGGACGCGA GCAAGGCCGG CGGCAAACAA AAGCGGGGGC TGCGGGGGCT GTTCAGCGGC   600
ATGCGCTGGC ACAGGAAAGA CAAGCGGGCC AAGGCGGAGG CCGCGGAGGG GCGCGCGCCC   660
GGGGGCGGCT TGATCCTACC CGGCTCGCTC ACCGCCAGCC TGGAGTGCGT CAAGGAGGAG   720
ACGCCCAGAG CCGCGCGCGA GCCGGAGGAG CCCAGCCAGG ACGCCCCGCG AGACCCAGCA   780
GGTGAGCCCG CAGGGGGAGA GGAGGTGCCC GCCCCCGCCG ACCGCGCCCC AGCGCGGAGC   840
TGCCGAGAGG CAGAGGGCCT CGCGCACCCC GGCGACACCG GCGCCCCGGG AGAGGACGCC   900
GCGGGGCATC GGCGCGCCGA GCCGGGGCCC GGGGAGGTCC GCACGGCAGA GGACGCTTCC   960
AGGACGGGGG CCGTTCCCGT AAAGACGGTC CCCCTTGTCG ACTCCGAAGG CGGCAGCGGC  1020
CGGGCGCCCG CCGCCCCAGA CCCTGCCTCT GTCGATCCAC CCTCAGACCC GTCGGCAGAT  1080
CGTATTTGTT TGATGTTTTC TGACGTGACT TCACTGAAAA GCTTTGACTC TCTTACAGGC  1140
TGTGGAGATA TTATTGCAGA CCAAGAGGAA GAGGCAGGTC CCAGCTGTGA CAAGCATGTC  1200
CCCGGGCCAG GCAAGCCGGC TCTGTCTAAA AAGAACCCCG GCGTGGTGGC CTACCAAGGA  1260
GGCGGGGAAG AGATGGCCAG CCCGGACGAG GTGGACGACA CCTATCTACA GGAGTTCTGG  1320
GACATGCTCT CCCAGACCGA GGAGCAGGGA CCCGAGCCCC AGGAGGGCGC GGCTAAGGTG  1380
GCAGCTGCGC TGGAAACCAA GGTGGTGCCC GAGACCCCCA AAGACACCAG GTGTGTGGAA  1440
GCGGCCAAGG ACGCGTCCTC GGTCAAGCGC AGGAGGCTCA ACCGGATTCC CATCGAGCCC  1500
CATCCTAAGG AGGAGCCCAA GCACCCGGAG AAGGAGCAGC AGGAAGGCGT CCCCAACAGC  1560
GACGAGGGCT ACTGGGACTC CACCACGCCA GGCCCAGAGG AAGACAGCTC GAGCAGCGGG  1620
AAGAAGGCGG GCATCCCCCG GGATAGCTAC AGCGGGGACG CGCTCTATGA TCTCTATGCT  1680
GACCCGGACG GAAGTCCAGC AACCCTTCCT GGAGGGAAGG ACAACGAGGA GACGTCCTCC  1740
CTGTCCCGGT TAAAGCCCGT ATCTCCAGGC ACCATCACCT GTCCACTGCG AACACCAGGC  1800
AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAGC ACCTGACCAA CCTTCCATCT  1860
AGCCATCCCG TGGTGCACCA GCAACCCTCC AGGAGTGAGA TGCCCAGAAC AAAAATCCCG  1920
GTTTCCAAAG TGCTGGTCCG CAGAGTCAGC AACCGGGGCT TGGCTGGGAC CACCATCAGA  1980
GCAACGGCCT GCCACGACAG TGCCAAAAAG TTGTGA
```

Seq ID NO: B53 Protein sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS    60
GKINKAAFKL FKKRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK   120
EEPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLLKKN GRSENGKGEP   180
VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE   240
TPRAAREPEE PSQDAPRDPA GEPAGGEEVP APADRAPARS CREAEGLAHP GDTGARGEDA   300
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AGHRRAEPGP GEVRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPPSDPSAD   360
RICLMFSDVT SLKSFDSLTG CGDIIADQEE EAGPSCDKHV PGPGKPALSK KNPGVVAYQG   420
GGEEMASPDE VDDTYLQEFW DMLSQTEFQG PEPQEGAAKV AAALETKVVP ETPKDTRCVE   480
AAKDASSVKR RRLNRIPIEP HPKEEPKHPE KEQQEGVPNS DEGYWDSTTP GPEEDSSSSG   540
KKAGIPRDSY SGDALYDLYA DPDGSPATLP GGKDNEETSS LSRLKPVSPG TITCPLRTPG   600
SLLKDSKIPI SIKHLTNLPS SHPVVHQQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR   660
ATACHDSAKK L
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Seq ID NO: B54 DNA sequence
Nucleic Acid Accession #: NM_014138.1
Coding sequence: 60..854

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1          11         21         31         41         51
|          |          |          |          |          |
CTGCAGAGAC TTCCCAGGAA GGTCCAGCGC CCTCTCAGCC TTCGTACTCA GAACAGCCGA    60
TGATGGGCCT CAGTAACCTG AGCCCCGGTC CTGGCCCCAG CCAGGCCGTG CCTCTCCCAG   120
AGGGGCTGCT CCGCCAGCGG TACAGAGAGG AGAAGACCCT GGAAGAGCGG CGGTGGGAGA   180
GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG   240
ATCACATGGC CCCCTATGCT GTTGGGAGGG AAGCCAGAAT CTCCCCATTA GGTGACAGAA   300
GTCAGAATCG ATTCCGATGT GAATGTCGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG   360
GGATCCCTGG GGAGAGTAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGCAGG   420
GCCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACCAGCC CGGGCCTCTG CCTGAAGCGG   480
CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA   540
TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCCATG   600
GGATGGAGAC CCGAAGGGAC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGGTGTGGGC   660
CCATTTTGGG GACCAAACAG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG   720
ACACGTGGGA GTCCTCCCAG CATGATGCTT GACTGACCCG AGGAAGGTCC TCATGTTTCG   780
TGCCTGTCAT TCTCGGATGG CTGTGAGGCA TTCCTTGGCA AGGGACGCTG CGTACCAGCG   840
GTCCTCACCG CATCTCACAT GGCTCCTGTG ATGCATGTTG TCGCTTTCCC ACCCGGGATC   900
TCCATCTCTC TTCCCTTCCT GCTGTCAGTA AGAGATCACA TGTCTGTGTA GTGTGAATGC   960
CTTGTCGCTG TCCTGTGCTT TTGCACCATT GAGTTGACTG CCTCTGAGAA GCAGCACTAG  1020
GCCTGTTGAA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAATGGGC AGGTAAACGC  1080
AGTGTGGGAA AGGAATGTGG AATGAGAACT TGGTGGTTCA CCGCTGTACT ATTTGTGTAA  1140
ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG  1200
TAGTAGTCTC CCTTACAGGA ATTTTTGACG GGGTTCCTCA TCATCAATAC CAAATAAATA  1260
TATGTAGGAA TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  1320
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA  1380
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA
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Seq ID NO: B55 Protein sequence
Protein Accession #: NP_054857.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEFLQRKKA FLRHVRRRHR    60
DHMAPYAVGR EARISPLGDR SQNRFRCECR YCQSHRPNLS GIPGESNRAP HPSSWETLVQ   120
GLSGLTLSLG TNQPGPLPEA ALQPQETEEK RQRERQQESK IMFQRLLKQW LEEN
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Seq ID NO: B56 DNA sequence
Nucleic Acid Accession #: NM_000025.1
Coding sequence: 198..1424

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1          11         21         31         41         51
|          |          |          |          |          |
GCTACTCCTC CCCCAAGAGC GGTGGCACCG AGGGAGTTGG GGTGGGGGGA GGCTGAGCGC    60
TCTGGCTGGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTCGCTCTC ATGCCTTGCT   120
GTCCCCTCCC CTGAGCCAGG TGATTTGGGA GACCCCCTCC TTCCTTCTTT CCCTACCGCC   180
CCACGCGCGA CCCGGGGATG GCTCCGTGGC CTCACGAGAA CAGCTCTCTT GCCCCATGGC   240
CGGACCTCCC CACCCTGGCG CCCAATACCG CCAACACCAG TGGGCTGCCA GGGGTTCCGT   300
GGGAGGCGGC CCTAGCCGGG GCCCTGCTGG CGCTGGCGGT GCTGGCCACC GTGGGAGGCA   360
ACCTGCTGGT CATCGTGGCC ATCGCCTGGA CTCCGAGACT CCAGACCATG ACCAACGTGT   420
TCGTGACTTC GCTGGCCGCA GCCGACCTGG TGATGGGACT CCTGGTGGTG CCGCCGGCGG   480
CCACCTTGGC GCTGACTGGC CACTGGCCGT TGGGCGCCAC TGGCTGCGAG CTGTGGACCT   540
CGGTGGACGT GCTGTGTGTG ACCGCCAGCA TCGAAACCCT GTGCGCCCTG GCCGTGGACC   600
GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GGTCACCAAG CGCTGCGCCC   660
GGACAGCTGT GGTCCTGGTG TGGGTCGTGT CGGCCGCGGT GTCGTTTGCG CCCATCATGA   720
GCCAGTGGTG GCGCGTAGGG GCCGACGCCG AGGCGCAGCG CTGCCACTCC AACCCGCGCT   780
GCTGTGCCTT CGCCTCCAAC ATGCCCTACG TGCTGCTGTC CTCCTCCGTC TCCTTCTACC   840
TTCCTCTTCT CGTGATGCTC TTCGTCTACG CGCGGGTTTT CGTGGTGGCT ACGCGCCAGC   900
TGCGCTTGCT GCGCGGGGAG CTGGGCCGCT TTCCGCCCGA GGAGTCTCCG CCGGCGCCGT   960
CGCGCTCTCT GGCCCCGGCC CCGGTGGGGA CGTGCGCTCC GCCCGAAGGG GTGCCCGCCT  1020
GCGGCCGGCG GCCCGCGCGC CTCCTGCCTC TCCGGGAACA CCGGGCCCTG TGCACCTTGG  1080
GTCTCATCAT GGGCACCTTC ACTCTCTGCT GGTTGCCCTT CTTTCTGGCC AACGTGCTGC  1140
GCGCCCTGGG GGGCCCCTCT CTAGTCCCGG GCCCGGCTTT CCTTGCCCTG AACTGGCTAG  1200
GTTATGCCAA TTCTGCCTTC AACCCGCTCA TCTACTGCCG CAGCCCGGAC TTTCGCAGCG  1260
CCTTCCGCCG TCTTCTGTGC CGCTGCGGCC GTCGCCTGCC TCCGGAGCCC TGCGCCGCCG  1320
CCCGCCCGGC CCTCTTCCCC TCGGGCGTTC CTGCGGCCCG GAGCAGCCCA GCGCAGCCCA  1380
GGCTTTGCCA ACGGCTCGAC GGGGCTTCTT GGGGAGTTTC TTAGGCCTGA AGGACAAGAA  1440
GCAACAACTC TGTTGATCAG AACCTGTGGA AAACCTCTGG CCTCTGTTCA GAATGAGTCC  1500
CATGGGATTC CCCGGCTGTG ACACTCTACC CTCCAGAACC TGACGACTGG GCCATGTGAC  1560
CCAAGGAGGG ATCCTTACCA AGTGGGTTTT CACCATCCTC TTGCTCTCTG TCTGAGAGAT  1620
GTTTTCTAAA CCCCAGCCTT GAACTTCACT CCTCCCTCAG TGGTAGTGTC CAGGTGCCGT  1680
GGAGCAGCAG GCTGGCTTTG GTAGGGGCAC CCATCACCCG GCTTGCCTGT GCAGTCAGTG  1740
AGTGCTTAGG GCAAAGAGAG CTCCCCTGGT TCCATTCCTT CTGCCACCCA AACCCTGATG  1800
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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
AAGATTTGGG GTTTTATCTC TGGTTCCCTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAGGAC TTCGCCAGGG 1980
TTTTGGGAGC TCCAGGGTTC ATAAGAAGGT GAACCATTAG AACAGATCCC TTCTTTTCCT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTCGGCCCA CTTTCCCTCC 2100
GTTTGTTTTC TTTTCATAAT CCACTTACTC CCTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAAACAAAA 2220
AATGAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCCTTCCTG AAACTCTTGA AATCCAGTTG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGCCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGGG 2400
GCATTTGTCC CCTCCATGCT ATAATCCAGT GGTGCCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGCGTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTG CTTGGGTTGG 2520
TCAAATGTCT TGTGTCATAA ATATATTCTG ATGTTTCCCA GCCTTTCCAC AACCTCTACC 2580
TTCCCACTCA CCTTCCCCAG CTACAAAAAT CTGTATTATC CTCTTAAAGT AAAACTGGAG 2640
TTAC

Seq ID NO: B57 Protein sequence
Protein Accession #: NP_000016.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAPWPHENSS LAPWPDLPTL APNTANTSGL PGVPWEAALA GALLALAVLA TVGGNLLVIV    60
AIAWTPRLQT MTNVFVTSLA AADLVMGLLV VPPAATLALT GHWPLGATGC ELWTSVDVLC   120
VTASIETLCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VWVVSAAVSF APIMSQWWRV   180
GADAEAQRCH SNPRCCAFAS NMPYVLLSSS VSFYLPLLVM LFVYARVFVV ATRQLRLLRG   240
ELGRFPPEES PPAPSRSLAP APVGTCAPPE GVPACGRRPA RLLPLREHRA LCTLGLIMGT   300
FTLCWLPFFL ANVLRALGGP SLVPGPAFLA LNWLGYANSA FNPLIYCRSP DFRSAFRRLL   360
CRCGRRLPPE PCAAARPALF PSGVPAARSS PAQPRLCQRL DGASWGVS
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Seq ID NO: B58 DNA sequence
Nucleic Acid Accession #: NM_032553.1
Coding sequence: 37..1038

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1          11         21         31         41         51
|          |          |          |          |          |
CACCATTAGG CAAAGATAGT TTCTCTAGAG AGAATCATGC CTGCTAATTA CACGTGTACC    60
AGGCCAGATG GAGACAATAC AGATTTTCGA TACTTTATTT ATGCAGTGAC ATACACTGTC   120
ATTCTTGTGC CAGGTCTCAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG   180
AAAGAAACAA AACGAGCTGT GATATTTATG ATAAACTTAG CCATTGCTGA CTTACTACAA   240
GTTCTTTCCT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT   300
GGTCTCTGCA TGTTCTGTTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC   360
TTGGTCTGCA TCAGTGTGCG ACGATTTTGG TTTCTCATGT ACCCCTTTCG CTTCCATGAC   420
TGCAAACAGA AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCTTGCC   480
TGTGTACTCT TTCCACTCCT CAGAACCAGT GATGATACCT CTGGCAATAG GACCAAATGC   540
TTTGTGGATC TTCCTACCAG GAATGTCAAC CTGGCCCAGT CCGTTGTTAT GATGACCATT   600
GGCGAGTTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG   660
GTTTTATCAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC   720
TTGAAGATGA TTCTAACCTG TGCAGGGGTA TTCCTAATTT GCTTTGCACC TTATCATTTC   780
AGTTTTCCTT TAGATTTCCT GGTGAAGTCC AATGAAATTA AAAGCTGCCT AGCCAGAAGG   840
GTGATTCTAA TATTTCATTC TGTGGCATTG TGTCTTGCTA GTCTGAATTC ATGTCTTGAC   900
CCAGTCATAT ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCTTTCAAG ACAAGATTTG   960
CATGACAGCA TCCAACTCCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG  1020
ACACCTGAAT TATGCTAAAA CAAAAAACCA AACTGAATGT GACCTGAAAT GCAAGTACAT  1080
CAGAACATAT CTGCAATACC CAAGCCACAG GGAAGAACTT GCAAAACAAC ACAGCTTTTC  1140
AGTTCTGCTC TATCTTACTG CTATGGGGAA TTCACTTCTT CAAAGCAGGA CCTATTTGGA  1200
GCATTACGAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTTT CTTCAAGT
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Seq ID NO: B59 Protein sequence
Protein Accession #: NP_115942.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPANYTCTRP DGDNTDFRYF IYAVTYTVIL VPGLIGNILA LWVFYGYMKE TKRAVIFMIN    60
LAIADLLQVL SLPLRIFYYL NHDWPFGPGL CMFCFYLKYV NMYASIYFLV CISVRRFWFL   120
MYPFRFHDCK QKYDLYISIA GWLIICLACV LFPLLRTSDD TSGNRTKCFV DLPTRNVNLA   180
QSVVMMTIGE LIGFVIPLLI VLYCTWKTVL SLQDKYPMAQ DLGEKQKALK MILTCAGVFL   240
ICFAPYHFSF PLDFLVKSNE IKSCLARRVI LIFHSVALCL ASLNSCLDPV IYYFSTNEFR   300
RRLSRQDLHD SIQLHAKSFV SNHTASTMTP ELC
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Seq ID NO: B60 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
GATTCGGATT TTAATCCGAC TCACTATAGG GAATTTTGGC CCTCGAGGCC AAGAATTCGG    60
CCCGAGGGTT AGACATTTAA CTTGAGTCTT TTCATATCAC GGTATGCTTT TATTTTACCC   120
TCATATATAA TTAATTTTCA TCTGGGCATA TATTTCCAGA TTAGAAATCA TTTCTTTTCA   180
TACATTTTAA GGAATTTATA CATTTGCATC TGAAATTGTA TTCATTATCT TCTAGAAACC   240
AAGAGTGGAC TTGGTATCCG TCTGATTATA TTTTCTTTGT TGGTAAAGAG CCTCTTTTTT   300
CCCTTTTTAT TTTCATCTTC TCTTTCTCTA GTGTTTATAA TCTTATTTTT ATGAATGTAG   360
TCTAATTATT TAGAACACTG TCTCCGAGTA TGTGTTTATT TGGGTTTGTG TTTTGAACAT   420
TGCCTCCAGG TGCGAGTTTA TGTGTGTTTA TGTTTCCTAT TTGAGGTTGG ACACTTAGAA   480
AATTTTCTCA ATTCGAAAAC TATTTTCCTT CAGCACTCAG AAATTTTTAT CAAAGATTAT   540
TTCCACGATT ATTTCCTGTC CTTGGTTTTT CGTGTTCTTA ACCTAGAATT CAATTGTTTA   600
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ATGTTAGACC TTACACATCT TCAATGTATC ATATATATTT CACTCATATT ATTTATTGTC 660
ATATCTTTTG GACTATTGTG TGAAAGCAAT AAATGTATAT TACTTTAAAA AAAAAAAAAA 720
AAAACTHCAT TTTCAAATTT AATACACACA AATTGTGCAT ACCCACACAC ATATACCACA 780
GATATATTCA TTTTCAGGAT TTCTTTAAGT GTTATTTTAA AAATAATCAT ATTCTTATTT 840
TGTGAACTGT GGGATTTCTT GAAACTTTTT GAAAACTCTC ATTAGTCTGT GTTTGTGTGG 900
TTTCTTTAAA TTATCTCTTC CTTCAGAATT ACTTTTGTGT TTTGAATTTG AGTCTTTGCC 960
ATTCATAAGG CGGGCTTTCC TTGAATACCA GATAACTCTG AGTTTCCTGT TCATATTTAA 1020
GAATAAATAA CCTAATTTGA AAAAAAAAAA AAAAA

Seq ID NO: B61 DNA sequence
Nucleic Acid Accession #: NM_014522.1
Coding sequence: 846..3911

1 11 21 31 41 51
| | | | | |
CTGGTGGTCC AGTACCTCCA AAGATATGGA ATACACTCCT GAAATATCCT GAAAACTTTT 60
TTTTTTCAGA ATCCTTTAAT AAGCAGTTAT GTCAATCTGA AAGTTGCTTA CTTGTACTTT 120
ATATTAATAG CTATTCTTGT TTTTCTTATC CAAAGAAAAA TCCTCTAATC CCCTTTTCAC 180
ATGATAGTTG TTACCATGTT TAGGCATTAG TCACATCAAC CCCTCTCCTC TCCCAAACTT 240
CTCTTCTTCA AATCAAACTT TATTAGTCCC TCCTTTATAA TGATTCCTTG CCTCGTTTTA 300
TCCAGATCAA TTTTTTTTCA CTTTGATGCC CAGAGCTGAA GAAATGGACT ACTGTATAAA 360
TTATTCATTG CCAAGAGAAT AATTGCATTT TAAACCCATA TTATAACAAA GAATAATGAT 420
TATATTTTGT GATTTGTAAC AAATACCCTT TATTTTCCCT TAACTATTGA ATTAAATATT 480
TTAATTATTT GTATTCTCTT TAACTATCTT GGTATATTAA AGTATTATCT TTTATATATT 540
TATCAATGGT GGACACTTTT ATAGGTACTC TGTGTCATTT TTGATACTGT AGGTATCTTA 600
TTTCATTTAT CTTTATTCTT AATGTACGAA TTCATAATAT TTGATTCAGA ACAAATTTAT 660
CACTAATTAA CAGAGTGTCA ATTATGCTAA CATCTCATTT ACTGATTTTA ATTTAAAACA 720
GTTTTTGTTA ACATGCATGT TTAGGGTTGG CTTCTTAATA ATTTCTTCTT CCTCTTCTCT 780
CTCTCCTCTT CTTTTGGTCA GTGTTGTGCG GGTTAATACA ACAAACTGTA ACAAGTGTAC 840
CTGGTATGGA CTTGTTGTCC GGGACGTACA TTTTCGCGGT CCTGCTAGCA TGCGTGGTGT 900
TCCACTCTGG CGCCCAGGAG AAAAACTACA CCATCCGAGA AGAAATGCCA GAAAACGTCC 960
TGATAGGCGA CTTGTTGAAA GACCTTAACT TGTCGCTGAT TCCAAACAAG TCCTTGACAA 1020
CTGCTATGCA GTTCAAGCTA GTGTACAAGA CCGGAGATGT GCCACTGATT CGAATTGAAG 1080
AGGATACTGG TGAGATCTTC ACTACTGGCG CTCGCATTGA TCGTGAGAAA TTATGTGCTG 1140
GTATCCCAAG GGATGAGCAT TGCTTTTATG AAGTGGAGGT TGCCATTTTG CCGGATGAAA 1200
TATTTAGACT GGTTAAGATA CGTTTTCTGA TAGAAGATAT AAATGATAAT GCACCATTGT 1260
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CTCTCCCAGC GGCTGTTGAT CCTGACGTAG GAATAAACGG AGTTCAAAAC TACGAACTAA 1380
TTAAGAGTCA AAACATTTTT GGCCTCGATG TCATTGAAAC ACCAGAAGGA GACAAGATGC 1440
CACAACTGAT TGTTCAAAAG GAGTTAGATA GGGAAGAGAA GGATACCTAC GTGATGAAAG 1500
TAAAGGTTGA AGATGGTGGC TTTCCTCAAA GATCCAGTAC TGCTATTTTG CAAGTGAGTG 1560
TTACTGATAC AAATGACAAC CACCCAGTCT TTAAGGAGAC AGAGATTGAA GTCAGTATAC 1620
CAGAAAATGC TCCTGTAGGC ACTTCAGTGA CACAGCTCCA TGCCACAGAT GCTGACATAG 1680
GTGAAAATGC CAAGATCCAC TTCTCTTTCA GCAATCTAGT CTCCAACATT GCCAGGAGAT 1740
TATTTCACCT CAATGCCACC ACTGGACTTA TCACAATCAA AGAACCACTG GATAGGGAAG 1800
AAACACCAAA CCACAAGTTA CTGGTTTTGG CAAGTGATGG TGGATTGATG CCAGCAAGAG 1860
CAATGGTGCT GGTAAATGTT ACAGATGTCA ATGATAATGT CCCATCCATT GACATAAGAT 1920
ACATCGTCAA TCCTGTCAAT GACACAGTTG TTCTTTCAGA AAATATTCCA CTCAACACCA 1980
AAATTGCTCT CATAACTGTG ACGGATAAGG ATGCGGACCA TAATGGCAGG GTGACATGCT 2040
TCACAGATCA TGAAATCCCT TTCAGATTAA GGCCAGTATT CAGTAATCAG TTCCTCCTGG 2100
AGACTGCAGC ATATCTTGAC TATGAGTCCA CAAAAGAATA TGCCATTAAA TTACTGGCTG 2160
CAGATGCTGG CAAACCTCCT TTGAATCAGT CAGCAATGCT CTTCATCAAA GTGAAAGATG 2220
AAAATGACAA TGCTCCAGTT TTCACCCAGT CTTTCGTAAC TGTTTCTATT CCTGAGAATA 2280
ACTCTCCTGG CATCCAGTTG ACGAAAGTAA GTGCAATGGA TGCAGACAGT GGGCCTAATG 2340
CTAAGATCAA TTACCTGCTA GGCCCTGATG CTCCACCTGA ATTCAGCCTG GATTGTCGTA 2400
CAGGCATGCT GACTGTAGTG AAGAAACTAG ATAGAGAAAA AGAGGATAAA TATTTATTCA 2460
CAATTCTGGC AAAAGATAAC GGGGTACCAC CCTTAACCAG CAATGTCACA GTCTTTGTAA 2520
GCATTATTGA TCAGAATGAC AATAGCCCAG TTTTCACTCA CAATGAATAC AACTTCTATG 2580
TCCCAGAAAA CCTTCCAAGG CATGGTACAG TAGGACTAAT CACTGTAACT GATCCTGATT 2640
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ATTCACAAAC TGGTGTCATC CGACCAAATA TTTCATTTGA TAGAGAAAAA CAAGAATCTT 2760
ACACTTTCTA TGTAAAGGCT GAGGATGGTG GTAGAGTATC ACGTTCTTCA AGTGCCAAAG 2820
TAACCATAAA TGTGGTTGAT GTCAATGACA ACAAACCAGT TTTCATTGTC CCTCCTTCCA 2880
ACTGTTCTTA TGAATTGGTT CTACCGTCCA CTAATCCAGG CACAGTGGTC TTTCAGGTAA 2940
TTGCTGTTGA CAATGACACT GGCATGAATG CAGAGGTTCG TTACAGCATT GTAGGAGGAA 3000
ACACAAGAGA TCTGTTTGCA ATCGACCAAG AAACAGGCAA CATAACATTG ATGGAGAAAT 3060
GTGATGTTAC AGACCTTGGT TTACACAGAG TGTTGGTCAA AGCTAATGAC TTAGGACAGC 3120
CTGATTCTCT CTTCAGTGTT GTAATTGTCA ATCTGTTCGT GAATGAGTCG GTGACCAATG 3180
CTACACTGAT TAATGAACTG GTGCGCAAAA GCACTGAAGC ACCAGTGACC CCAAATACTG 3240
AGATAGCTGA TGTATCCTCA CCAACTAGTG ACTATGTCAA GATCCTGGTT GCAGCTGTTG 3300
CTGGCACCAT AACTGTCGTT GTAGTTATTT TCATCACTGC TGTAGTAAGA TGTCGCCAGG 3360
CACCACACCT TAAGGCTGCT CAGAAAAACA AGCAGAATTC TGAATGGGCT ACCCCAAACC 3420
CAGAAAACAG GCAGATGATA ATGATGAAGA AAAAGAAAAA GAAGAAGAAG CATTCCCCTA 3480
AGAACTTGCT GCTTAATTTT GTCACTATTG AAGAAACTAA GGCAGATGAT GTTGACAGTG 3540
ATGGAAACAG AGTCACACTA GACCTTCCTA TTGATCTAGA AGAGCAAACA ATGGGAAAGT 3600
ACAATTGGGT AACTACACCT ACTACTTTCA AGCCCGACAG CCCTGATTTG GCCCGACACT 3660
ACAAATCTGC CTCTCCACAG CCTGCCTTCC AAATTCAGCC TGAAACTCCC CTGAATTCGA 3720
AGCACCACAT CATCCAAGAA CTGCCTCTCG ATAACACCTT TGTGGCCTGT GACTCTATCT 3780
CCAAGTGTTC CTCAAGCAGT TCAGATCCCT ACAGCGTTTC TGACTGTGGC TATCCAGTGA 3840
CGACCTTCGA GGTACCTGTG TCCGTACACA CCAGACCGGT AGGTATCCAA GTTTCTAACA 3900
CAACTTTCTA ACTATTTTTT TATTATTATT TTCAGTTGAT GTAGAACTTT ACAAAATCTA 3960
TTGACTTCAA AGAGGGATCA AAACAATCAT ATTCTACAGA TGTACCCAAT AGATATATGG 4020
ATTCAATTAA GTTTGGTAGA AGATGAGAAC AAAATAACTA CTGATTTAGG AAAATTGGAT 4080
GCAGAATAAT AATTATAGTA GGGGCAATTT TGTCTGTAGA TGGCAGTATG ACAATTCTTG 4140

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CTAGAGAATA TATTGAAAAA AACTTCAACA CAAAGGGTTG TAGCACTGTC CTCAGTACCA  4200
TTGTGTGCAT GACGATCAGA ATAGTCTGGG CTAGATACAT CACATTAAAG CTTTTCAGAA  4260
TCTGATAAAT AGCTCTAAAT ACTAATGATA TTGAGAAGCC TAGCTTCACT TGGGAAAATC  4320
TGTGGCTGTT CACAGAAATT CAGCACCAAG TTATTCCCCC CATACTCTAC CAGGCCTTCA  4380
GGTCCTCATA AAGAAAAGTG TCGTTTTCAG ATTAGGAACT CAAAATTATT TTGGTGCATC  4440
AAATCTACAG TCACACAATA TAACAAGAAT GGGATTAGAA AAATGAAAGC CTACTCATTC  4500
TCATCTTTAA GCCAGAGAAT GAAATATATA TGAGGTCTCT GGATAGCTAT TTAAATATTT  4560
GCATATTTAT GCAAGGTATT TTGAGCCCTT CAGAAGACAT TCT
```

Seq ID NO: B62 Protein sequence
Protein Accession #: NP_055337.1

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          1          11          21          31          41          51
          |           |           |           |           |           |
MDLLSGTYIF AVLLACVVFH SGAQEKNYTI REEMPENVLI GDLLKDLNLS LIPNKSLTTA    60
MQFKLVYKTG DVPLIRIEED TGEIFTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF   120
RLVKIRFLIE DINDNAPLFP ATVINISIPE NSAINSKYTL PAAVDPDVGI NGVQNYELIK   180
SQNIFGLDVI ETPEGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT   240
DTNDNHPVFK ETEIEVSIPE NAPVGTSVTQ LHATDADIGE NAKIHFSFSN LVSNIARRLF   300
HLNATTGLIT IKEPLDREET PNHKLLVLAS DGGLMPARAM VLVNVTDVND NVPSIDIRYI   360
VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCFT DHEIPFRLRP VFSNQFLLET   420
AAYLDYESTK EYAIKLLAAD AGKPPLNQSA MLFIKVKDEN DNAPVFTQSF VTVSIPENNS   480
PGIQLTKVSA MDADSGPNAK INYLLGPDAP PEFSLDCRTG MLTVVKKLDR EKEDKYLFTI   540
LAKDNGVPPL TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYG   600
DNSAVTLSIL DENDDFTIDS QTGVIRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT   660
INVVDVNDNK PVFIVPPSNC SYELVLPSTN PGTVVFQVIA VDNDTGMNAE VRYSIVGGNT   720
RDLFAIDQET GNITLMEKCD VTDLGLHRVL VKANDLGQPD SLFSVVIVNL FVNESVTNAT   780
LINELVRKST EAPVTPNTEI ADVSSPTSDY VKILVAAVAG TITVVVVIFI TAVVRCRQAP   840
HLKAAQKNKQ NSEWATPNPE NRQMIMMKKK KKKKKHSPKN LLLNFVTIEE TKADDVDSDG   900
NRVTLDLPID LEEQTMGKYN WVTTPTTFKP DSPDLARHYK SASPQPAFQI QPETPLNSKH   960
HIIQELPLDN TFVACDSISK CSSSSSDPYS VSDCGYPVTT FEVPVSVHTR PVGIQVSNTT  1020
F
```

Seq ID NO: B63 DNA sequence
Nucleic Acid Accession #: XM_059180.2
Coding sequence: 276..3740

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          1          11          21          31          41          51
          |           |           |           |           |           |
GCGGCGGCCG CGGAGTATCC TGGAGCTGCA GACAGTGCGG GCCTGCGCCC AGTCCCGGCT    60
GTCCTCGCCG CGACCCCTCC TCAGCCCTGG GCGCGCGCAC GCTGGGGCCC CGCGGGGCTG   120
GCCGCCTAGC GAGCCTGCCG GTCGACCCCA GCCAGCGCAG CGACGGGGCG CTGCCTGGCC   180
CAGGCGCACA CGGAAGTGCG CTTCTCTGAA GTAGCTTTGG AAAGTAGAGA AGAAAATCCA   240
GTTTGCTTCT TGGAGAACAC TGGACAGCTG AATAAATGCA GTATCTAAAT ATAAAAGAGG   300
ACTGCAATGC CATGGCTTTC TGTGCTAAAA TGAGGAGCTC CAAGAAGACT GAGGTGAACC   360
TGGAGGCCCC TGAGCCAGGG GTGGAAGTGA TCTTCTATCT GTCGGACAGG GAGCCCCTCC   420
GGCTGGGCAG TGGAGAGTAC ACAGCAGAGG AACTGTGCAT CAGGGCTGCA CAGGCATGCC   480
GTATCTCTCC TCTTTGTCAC AACCTCTTTG CCCTGTATGA CGAGAACACC AAGCTCTGGT   540
ATGCTCCAAA TCGCACCATC ACCGTTGATG ACAAGATGTC CCTCCGGCTC CACTACCGGA   600
TGAGGTTCTA TTTCACCAAT TGGCATGGAA CCAACGACAA TGAGCAGTCA GTGTGGCGTC   660
ATTCTCCAAA GAAGCAGAAA AATGGCTACG AGAAAAAAAA GATTCCAGAT GCAACCCCTC   720
TCCTTGATGC CAGCTCACTG GAGTATCTGT TTGCTCAGGG ACAGTATGAT TTGGTGAAAT   780
GCCTGGCTCC TATTCGAGAC CCCAAGACCG AGCAGGATGG ACATGATATT GAGAACGAGT   840
GTCTAGGGAT GGCTGTCCTG GCCATCTCAC ACTATGCCAT GATGAAGAAG ATGCAGTTGC   900
CAGAACTGCC CAAGGACATC AGCTACAAGC GATATATTCC AGAAACATTG AATAAGTCCA   960
TCAGACAGAG GAACCTTCTC ACCAGGATGC GGATAAATAA TGTTTTCAAG GATTTCCTAA  1020
AGGAATTTAA CAACAAGACC ATTTGTGACA GCAGCGTGTC CACGCATGAC CTGAAGGTGA  1080
AATACTTGGC TACCTTGGAA ACTTTGACAA AACATTACGG TGCTGAAATA TTTGAGACTT  1140
CCATGTTACT GATTTCATCA GAAAATGAGA TGAATTGGTT TCATTCGAAT GACGGTGGAA  1200
ACGTTCTCTA CTACGAAGTG ATGGTGACTG GGAATCTTGG AATCCAGTGG AGGCATAAAC  1260
CAAATGTTGT TTCTGTTGAA AAGGAAAAAA ATAAACTGAA GCGGAAAAAA CTGGAAAATA  1320
AACACAAGAA GGATGAGGAG AAAAACAAGA TCCGGGAAGA GTGGAACAAT TTTTCTTACT  1380
TCCCTGAAAT CACTCACATT GTAATAAAGG AGTCTGTGGT CAGCATTAAC AAGCAGGACA  1440
ACAAGAAAAT GGAACTGAAG CTCTCTTCCC ACGAGGAGGC CTTGTCCTTT GTGTCCCTGG  1500
TAGATGGCTA CTTCCGGCTC ACAGCAGATG CCCATCATTA CCTCTGCACC GACGTGGCCC  1560
CCCCGTTGAT CGTCCACAAC ATACAGAATG GCTGTCATGG TCCAATCTGT ACAGAATACG  1620
CCATCAATAA ATTGCGGCAA GAAGGAAGCG AGGAGGGGAT GTACGTGCTG AGGTGGAGCT  1680
GCACCGACTT TGACAACATC CTCATGACCG TCACCTGCTT TGAGAAGTCT GAGCAGGTGC  1740
AGGGTGCCCA GAAGCAGTTC AAGAACTTTC AGATCGAGGT GCAGAAGGGC CGCTACAGTC  1800
TGCACGGTTC GGACCGCAGC TTCCCCAGCT TGGGAGACCT CATGAGCCAC CTCAAGAAGC  1860
AGATCCTGCG CACGGATAAC ATCAGCTTCA TGCTAAAACG CTGCTGCCAG CCCAAGCCCC  1920
GAGAAATCTC CAACCTGCTG GTGGCTACTA AGAAAGCCCA GGAGTGGCAG CCCGTCTACC  1980
CCATGAGCCA GCTGAGTTTC GATCGGATCC TCAAGAAGGA TCTGGTGCAG GGCGAGCACC  2040
TTGGGAGAGG CACGAGAACA CACATCTATT CTGGGACCCT GATGGATTAC AAGGATGACG  2100
AAGGAACTTC TGAAGAGAAG AAGATAAAAG TGATCCTCAA AGTCTTAGAC CCCAGCCACA  2160
GGGATATTTC CCTGGCCTTC TTCGAGGCAG CCAGCATGAT GAGACAGGTC TCCCACAAAC  2220
ACATCGTGTA CCTCTATGGC GTCTGTGTCC GCGACGTGGA GAATATCATG GTGGAAGAGT  2280
TTGTGGAAGG GGGTCCTCTG GATCTCTTCA TGCACCGGAA AAGCGATGTC CTTACCACAC  2340
CATGGAAATT CAAAGTTGCC AAACAGCTGG CCAGTGCCCT GAGCTACTTG GAGGATAAAG  2400
ACCTGGTCCA TGGAAATGTG TGTACTAAAA ACCTCCTCCT GGCCCGTGAG GGCATCGACA  2460
GTGAGTGTGG CCCATTCATC AAGCTCAGTG ACCCCGGCAT CCCCATTACG GTGCTGTCTA  2520
GGCAAGAATG CATTGAACGA ATCCCATGGA TTGCTCCTGA GTGTGTTGAG GACTCCAAGA  2580
ACCTGAGTGT GGCTGCTGAC AAGTGGAGCT TTGGAACCAC GCTCTGGGAA ATCTGCTACA  2640
ATGGCGAGAT CCCCTTGAAA GACAAGACGC TGATTGAGAA AGAGAGATTC TATGAAAGCC  2700
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GGTGCAGGCC AGTGACACCA TCATGTAAGG AGCTGGCTGA CCTCATGACC CGCTGCATGA  2760
ACTATGACCC CAATCAGAGG CCTTTCTTCC GAGCCATCAT GAGAGACATT AATAAGCTTG  2820
AAGAGCAGAA TCCAGATATT GTTTCAGAAA AAAAACCAGC AACTGAAGTG GACCCCACAC  2880
ATTTTGAAAA GCGCTTCCTA AAGAGGATCC GTGACTTGGG AGAGGGCCAC TTTGGGAAGG  2940
TTGAGCTCTG CAGGTATGAC CCCGAAGGGG ACAATACAGG GGAGCAGGTG GCTGTTAAAT  3000
CTCTGAAGCC TGAGAGTGGA GGTAACCACA TAGCTGATCT GAAAAAGGAA ATCGAGATCT  3060
TAAGGAACCT CTATCATGAG AACATTGTGA AGTACAAAGG AATCTGCACA GAAGACGGAG  3120
GAAATGGTAT TAAGCTCATC ATGGAATTTC TGCCTTCGGG AAGCCTTAAG GAATATCTTC  3180
CAAAGAATAA GAACAAAATA AACCTCAAAC AGCAGCTAAA ATATGCCGTT CAGATTTGTA  3240
AGGGGATGGA CTATTTGGGT TCTCGGCAAT ACGTTCACCG GGACTTGGCA GCAAGAAATG  3300
TCCTTGTTGA GAGTGAACAC CAAGTGAAAA TTGGAGACTT CGGTTTAACC AAAGCAATTG  3360
AAACCGATAA GGAGTATTAC ACCGTCAAGG ATGACCGGGA CAGCCCTGTG TTTTGGTATG  3420
CTCCAGAATG TTTAATGCAA TCTAAATTTT ATATTGCCTC TGACGTCTGG TCTTTTGGAG  3480
TCACTCTGCA TGAGCTGCTG ACTTACTGTG ATTCAGATTC TAGTCCCATG GCTTTGTTCC  3540
TGAAAATGAT AGGCCCAACC CATGGCCAGA TGACAGTCAC AAGACTTGTG AATACGTTAA  3600
AAGAAGGAAA ACGCCTGCCG TGCCCACCTA ACTGTCCAGA TGAGGTTTAT CAACTTATGA  3660
GGAAATGCTG GGAATTCCAA CCATCCAATC GGACAAGCTT TCAGAACCTT ATTGAAGGAT  3720
TTGAAGCACT TTTAAAATAA GAAGCATGAA TAACATTTAA ATTCCACAGA TTATCAAGTC  3780
CTTCTCCTGC AACAAATGCC CAAGTCATTT TTTAAAAATT TCTAATGAAA GAAGTTTGTG  3840
TTCTGTCCAA AAAGTCACTG AACTCATACT TCAGTACATA TACATGTATA AGGCACACTG  3900
TAGTGCTTAA TATGTGTAAG GACTTCCTCT TTAAATTTGG TACCAGTAAC TTAGTGACAC  3960
ATAATGACAA CCAAAATATT TGAAAGCACT TAAGCACTCC TCCTTGTGGA AAGAATATAC  4020
CACCATTTCA TCTGGCTAGT TCACCATCAC AACTGCATTA CCAAAAGGGG ATTTTTGAAA  4080
ACGAGGAGTT GACCAAAATA ATATCTGAAG ATGATTGCTT TTCCCTGCTG CCAGCTGATC  4140
TGAAATGTTT TGCTGGCACA TTAATCATAG ATAAAGAAAG ATTGATGGAC TTAGCCCTCA  4200
AATTTCAGTA TCTATACAGT ACTAGACCAT GCATTCTTAA AATATTAGAT ACCAGGTAGT  4260
ATATATTGTT TCTGTACAAA AATGACTGTA TTCTCTCACC AGTAGGACTT AAACTTTGTT  4320
TCTCCAGTGG CTTAGCTCCT GTTCCTTTGG GTGATCACTA GCACCCATTT TTGAGAAAGC  4380
TGGTTCTACA TGGGGGGATA GCTGTGGAAT AGATAATTTG CTGCATGTTA ATTCTCAAGA  4440
ACTAAGCCTG TGCCAGTGCT TTCCTAAGCA GTATACCTTT AATCAGAACT CATTCCCAGA  4500
ACCTGGATGC TATTACACAT GCTTTTAAGA AACGTCAATG TATATCCTTT TATAACTCTA  4560
CCACTTTGGG GCAAGCTATT CCAGCACTGG TTTTGAATGC TGTATGCAAC CAGTCTGAAT  4620
ACCACATACG CTGCACTGTT CTTAGAGGGT TTCCATACTT ACCACCGATC TACAAGGGTT  4680
GATCCCTGTT TTTACCATCA ATCATCACCC TGTGGTGCAA CACTTGAAAG ACCCGGCTAG  4740
AGGCACTATG GACTTCAGGA TCCACTAGAC AGTTTTCAGT TTGCTTGGAG GTAGCTGGGT  4800
AATCAAAAAT GTTTAGTCAT TGATTCAATG TGAACGATTA CGGTCTTTAT GACCAAGAGT  4860
CTGAAAATCT TTTTGTTATG CTGTTTAGTA TTCGTTTGAT ATTGTTACTT TTCACCTGTT  4920
GAGCCCAAAT TCAGGATTGG TTCAGTGGCA GCAATGAAGT TGCCATTTAA ATTTGTTCAT  4980
AGCCTACATC ACCAAGGTCT CTGTGTCAAA CCTGTGGCCA CTCTATATGC ACTTTGTTTA  5040
CTCTTTATAC AAATAAATAT ACTAAAGACT TT
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Seq ID NO: B64 Protein sequence
Protein Accession #: A39577

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1          11         21         31         41         51
|          |          |          |          |          |
MQYLNIKEDC NAMAFCAKMR SSKKTEVNLE APEPGVEVIF YLSDREPLRL GSGEYTAEEL    60
CIRAAQACRI SPLCHNLFAL YDENTKLWYA PNRTITVDDK MSLRLHYRMR FYFTNWHGTN   120
DNEQSVWRHS PKKQKNGYEK KKIPDATPLL DASSLEYLFA QGQYDLVKCL APIRDPKTEQ   180
DGHDIENECL GMAVLAISHY AMMKKMQLPE LPKDISYKRY IPETLNKSIR QRNLLTRMRI   240
NNVFKDFLKE FNNKTICDSS VSTHDLKVKY LATLETLTKH YGAEIFETSM LLISSENEMN   300
WFHSNDGGNV LYYEVMVTGN LGIQWRHKPN VVSVEKEKNK LKRKKLENKD KKDEEKNKIR   360
EEWNNFSFFP EITHIVIKES VVSINKQDNK KMELKLSSHE EALSFVSLVD GYFRLTADAH   420
HYLCTDVAPP LIVHNIQNGC HGPICTEYAI NKLRQEGSEE GMYVLRWSCT DFDNILMTVT   480
CFEKSEQVQG AQKQFKNFQI EVQKGRYSLH GSDRSFPSLG DLMSHLKKQI LRTDNISFML   540
KRCCQPKPRE ISNLLVATKK AQEWQPVYPM SQLSFDRILK KDLVQGEHLG RGTRTHIYSG   600
TLMDYKDDEG TSEEKKIKVI LKVLDPSHRD ISLAFFEAAS MMRQVSHKHI VYLYGVCVRD   660
VENIMVEEFV EGGPLDLFMH RKSDVLTTPW KFKVAKQLAS ALSYLEDKDL VHGNVCTKNL   720
LLAREGIDSE CGPFIKLSDP GIPITVLSRQ ECIERIPWIA PECVEDSKNL SVAADKWSFG   780
TTLWEICYNG EIPLKDKTLI EKERFYESRC RPVTPSCKEL ADLMTRCMNY DPNQRPFFRA   840
IMRDINKLEE QNPDIVSRKK NQPTEVDPTH FEKRFLKRIR DLGEGHFGKV ELCRYDPEDN   900
TGEQVAVKSL KPESGGNHIA DLKKEIEILR NLYHENIVKY KGICTEDGGN GIKLIMEFLP   960
SGSLKEYLPK NKNKINLKQQ LKYAVQICKG MDYLGSRQYV HRDLAARNVL VESEHQVKIG  1020
DFGLTKAIET DKEYYTVKDD RDSPVFWYAP ECLMQSKFYI ASDVWSFGVT LHELLTYCDS  1080
DSSPMALFLK MIGPTHGQMT VTRLVNTLKE GKRLPCPPNC PDEVYQLMRK CWEFQPSNRT  1140
SFQNLIEGFE ALLK
```

Seq ID NO: B65 DNA sequence
Nucleic Acid Accession #: NM_004867.1
Coding sequence: 140..931

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1          11         21         31         41         51
|          |          |          |          |          |
GATCCCAGAC CTCGGCTTGC AGTAGTGTTA GACTGAAGAT AAAGTAAGTG CTGTTTGGGC    60
TAACAGGATC TCCTCTTGCA GTCTGCAGCC CAGGACGCTG ATTCCAGCAG CGCCTTACCG   120
CGCAGCCCGA AGATTCACTA TGGTGAAAAT CGCCTTCAAT ACCCCTACCG CCGTGCAAAA   180
GGAGGAGGCG CGGCAAGACG TGGAGGCCCT CCTGAGCCGC ACGGTCAGAA CTCAGATACT   240
GACCGGCAAG GAGCTCCGAG TTGCCACCCA GGAAAAAGAG GGCTCCTCTG GGAGATGTAT   300
GCTTACTCTC TTAGGCCTTT CATTCATCTT GGCAGGACTT ATTGTTGGTG GAGCCTGCAT   360
TTACAAGTAC TTCATGCCCA AGAGCACCAT TTACCGTGGA GAGATGTGCT TTTTTGATTC   420
TGAGGATCCT GCAAATTCCC TTCGTGGAGG AGAGCCTAAC TTCCTGCCTG TGACTGAGGA   480
GGCTGACATT CGTGAGGATG ACAACATTGC AATCATTGAT GTGCCTGTCC CCAGTTTCTC   540
TGATAGTGAC CCTGCAGCAA TTATTCATGA CTTTGAAAAG GGAATGACTG CTTACCTGGA   600
CTTGTTGCTG GGGAACTGCT ATCTGATGCC CCTCAATACT TCTATTGTTA TGCCTCCAAA   660
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AAATCTGGTA GAGCTCTTTG GCAAACTGGC GAGTGGCAGA TATCTGCCTC AAACTTATGT   720
GGTTCGAGAA GACCTAGTTG CTGTGGAGGA AATTCGTGAT GTTAGTAACC TTGGCATCTT   780
TATTTACCAA CTTTGCAATA ACAGAAAGTC CTTCCGCCTT CGTCGCAGAG ACCTCTTGCT   840
GGGTTTCAAC AAACGTGCCA TTGATAAATG CTGGAAGATT AGACACTTCC CCAACGAATT   900
TATTGTTGAG ACCAAGATCT GTCAAGAGTA AGAGGCAACA GATAGAGTGT CCTTGGTAAT   960
AAGAAGTCAG AGATTTACAA TATGACTTTA ACATTAAGGT TTATGGGATA CTCAAGATAT  1020
TTACTCATGC ATTTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAAAAAA AAAAAAAAAA  1080
AA
```

Seq ID NO: B66 Protein sequence
Protein Accession #: NP_004858.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MVKIAFNTPT AVQKEEARQD VEALLSRTVR TQILTGKELR VATQEKEGSS GRCMLTLLGL    60
SFILAGLIVG GACIYKYFMP KSTIYRGEMC FFDSEDPANS LRGGEPNFLP VTEEADIRED   120
DNIAIIDVPV PSFSDSDPAA IIHDFEKGMT AYLDLLLGNC YLMPLNTSIV MPPKNLVELF   180
GKLASGRYLP QTYVVREDLV AVEEIRDVSN LGIFIYQLCN NRKSFRLRRR DLLLGFNKRA   240
IDKCWKIRHF PNEFIVETKI CQE
```

Seq ID NO: B67 DNA sequence
Nucleic Acid Accession #: XM_083862.1
Coding sequence: 121..813

```
1          11         21         31         41         51
|          |          |          |          |          |
ACGCGGGAGG TCTGAGCTGT GGGCTGAGGC AGCGCAGCCG CTGCGCCAGG GTGCGCGATG    60
CCTTGAACCT GGGAAACTAT GTGAAGCAAC ACTCTGGATT TTGAAAGACA TCTTTTCATC   120
ATGGGACAGC AAATTTCGGA TCAGACACAG TTGGTTATTA ACAAGTTACC AGAAAAAGTA   180
GCAAAACATG TTACGTTGGT TCGAGAGAGT GGCTCCTTAA CTTATGAAGA ATTTCTCGGG   240
AGAGTAGCTG AGCTTAATGA TGTAACGGCT AAAGTGGCTT CTGGCCAGGA AAAACATCTT   300
CTCTTTGAGG TACAACCTGG GTCTGATTCC TCTGCTTTTT GGAAAGTGGT TGTACGGGTG   360
GTCTGTACCA AGATTAACAA AAGCAGTGGC ATTGTGGAGG CATCACGGAT CATGAATTTA   420
TACCAGTTTA TTCAACTTTA TAAAGATATC ACAAGTCAAG CAGCAGGAGT ATCGGCACAG   480
AGCTCCACCT CTGAAGAACC TGATGAAAAC TCATCCTCTG TAACATCTTG TCAGGCTAGT   540
CTTTGGATGG GAAGGGTGAA GCAGCTGACC GATGAGGAGG AGTGTTGTAT CTGTATGGAT   600
GGGCGGGCTG ACCTCATCCT GCCTTGTGCT CACAGCTTTT GTCAGAAGTG TATTGATAAA   660
TGGAGTGATC GACACAGGAA TTGCCCTATT TGTCGCCTAC AGATGACTGG AGCAAATGAA   720
TCTTGGGTGG TATCAGATGC ACCCACTGAA GATGATATGG CTAACTATAT TCTTAACATG   780
GCTGATGAGG CAGGCCAGCC CCACAGGCCA TGACCTTGAA GTGAAAGTCT TCTGTTGCTA   840
TTGTGGGCTC AAATATTTGG TCATGGGGGA AGAATGTAGG GTTGTGGCAC TGGCACAGAC   900
ACAGGAAAAT CCATTTTCCC CACTCTTTTA TTTTTGCTAT TCTGATCATT TGTCCCCCTT   960
TTAAAAATAA ACTTCCCATG TCTTCCAAAA AAAAAAAAAA AAAAA
```

Seq ID NO: B68 Protein sequence
Protein Accession #: XP_083862.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGQQISDQTQ LVINKLPEKV AKHVTLVRES GSLTYEEFLG RVAELNDVTA KVASGQEKHL    60
LFEVQPGSDS SAFWKVVVRV VCTKINKSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ   120
SSTSEEPDEN SSSVTSCQAS LWMGRVKQLT DEEECCICMD GRADLILPCA HSFCQKCIDK   180
WSDRHRNCPI CRLQMTGANE SWVVSDAPTE DDMANYILNM ADEAGQPHRP
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Seq ID NO: B69 DNA sequence
Nucleic Acid Accession #: NM_002975.1
Coding sequence: 180..1151

```
1          11         21         31         41         51
|          |          |          |          |          |
CGACCAACGG ACCGGACAGA GACGAGGAGA GGAACAGGAA GAGAGAAGCT GGGAGAATCG    60
GGAACCTGGG GGCTAGTGAC CTGCACACAG GGCAGGGGCA CTCGGCAGTT CCCAGAGGCC   120
ACCCCTCCCA CCCCAGACAT CCAGACATCT GGAACTTTGG GTGCCAAGAG TCCAGCTTAA   180
TGCAGGCAGC CTGGCTTTTG GGGGCTTTGG TGGTCCCCCA GCTCTTGGGC TTTGGCCATG   240
GGGCTCGGGG AGCAGAGAGG GAGTGGGAGG GAGGCTGGGG AGGTGCCCAG GAGGAGGAGC   300
GGGAGAGGGA GGCCCTGATG CTGAAGCATC TGCAGGAAGC CCTAGGACTG CCTGCTGGGA   360
GGGGGGATGA GAATCCTGCC GGAACTGTTG AGGGAAAAGA GGACTGGGAG ATGGAGGAGG   420
ACCAGGGGGA GGAAGAGGAG GAGGAAGCAA CGCCAACCCC ATCCTCCGGC CCCAGCCCCT   480
CTCCCACCCC TGAGGACATC GTCACTTACA TCCTGGGCCG CCTGGCCGGC CTGGACGCAG   540
GCCTGCACCA GCTGCACGTC CGTCTGCACG CGTTGGACAC CCGCGTGGTC GAGCTGACCC   600
AGGGGCTGCG GCAGCTGCGG AACGCGGCAG GCGACACCCG CGATGCCGTG CAAGCCCTGC   660
AGGAGGCGCA GGGTCGCGCC GAGCGCGAGC ACGGCCGCTT GGAGGGCTGC CTGAAGGGGC   720
TGCGCCTGGG CCACAAGTGC TTCCTGCTCT CGCGCGACTT CGAAGCTCAG GCGGCGGCGC   780
AGGCGCGGTG CACGGCGCGG GGCGGGAGCC TGGCGCAGCC GGCAGACCGC CAGCAGATGG   840
AGGCGCTCAC TCGGTACCTG CGCGCGGCGC TCGCTCCCTA CAACTGGCCC GTGTGGCTGG   900
GCGTGCACGA TCGGCGCGCC GAGGGCCTCT ACCTCTTCGA AAACGGCCAG CGCGTGTCCT   960
TCTTCGCCTG GCATCGCTCA CCCCGCCCCG AGCTCGGCGC CCAGCCCAGC GCCTCGCCGC  1020
ATCCGCTCAG CCCGGACCAG CCCAACGGTG GCACGCTCGA GAACTGCGTG GCGCAGGCCT  1080
CTGACGACGG CTCCTGGTGG GACCACGACT GCCAGCGGCG TCTCTACTAC GTCTGCGAGT  1140
TCCCCTTCTA GCGGGGCCGG TACCCCGCCT CCTTGCCCAT CCCACCACCC GGCCTTTCCC  1200
TGCGCCGTGC CCACCCTCCT CCGGAATCGC CCTTCCCTTC CTGGCCACGA ATGGCAGCGT  1260
CCTCCCCGAC CCCCAGTCTG GGCGCTTCTG GGAGGGCTCT TGCGGTGCCG GCACTCCTCC  1320
TTGTTAGTGT CTTTCCTTGA AGGGGCGGGC ACCAGGCTAG GTCCGGTGCC AATAAATCCT  1380
TGTGGAATCT GAAAAAAAAA AAAAAAA
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Seq ID NO: B70 Protein sequence
Protein Accession #: NP_002966.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQAAWLLGAL VVPQLLGFGH GARGAEREWE GGWGGAQEEE RERFALMLKH LQEALGLPAG    60
RGDENPAGTV EGKEDWEMEE DQGEEEEEEA TPTPSSGPSP SPTPEDIVTY ILGRLAGLDA   120
GLHQLHVRLH ALDTRVVELT QGLRQLRNAA GDTRDAVQAL QEAQGRAERE HGRLEGCLKG   180
LRLGHKCFLL SRDFEAQAAA QARCTARGGS LAQPADRQQM EALTRYLRAA LAPYNWPVWL   240
GVHDRRAEGL YLFENGQRVS FFAWHRSPRP ELGAQPSASP HPLSPDQPNG GTLENCVAQA   300
SDDGSWWDHD CQRRLYYVCE FPF
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Seq ID NO: B71 DNA sequence
Nucleic Acid Accession #: BC000839.1

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1          11         21         31         41         51
|          |          |          |          |          |
CTGGCCAGGG CGACTGGCGG ATAAGGTCTT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG    60
TGGGGCTTTG TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGGTCCCCC TTCCTATGAT   120
GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AAGTAACTCT GAGGAGATGG   180
GCCCTGCAAG CCTCCTTCTT AGCCGTCTGT TCAGAAAATA GCGTTTTCGA AATGCCCTGA   240
GTTGACCTAA TGTCTTATTG GGCTCCTGTC TGCAGGATTT ACGCGCACGT TGGAACCGAA   300
GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAGG AATGGGACAA   360
GACCCATCTT TATGCAAAGC CAGCGTTACA GTAATGTTCC AGCATCTCAT AATCTATCCT   420
GGGGAATTCA GCTGCCTCCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCCTCTAT   480
CTTACAGAGC AGCTTGTTGC TATATACCAT TGAAAAGCCT TCAGAGCTGA GAGGTACTAC   540
TAACCAATAA CCTGCTTGGC TCAAAGGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT   600
TTGAGGAAAA CTAGGTGTCT GTGTTCACTC CAGGCTGAAG TTACAGGTCT GAGCAAATAA   660
GGTGTATAAA AAATGGAATC TGTCTTGGAG GACATCAGAA GGTGAATTTT CCAAGTTCTT   720
GGACAACCTA GCTGTTGAAA AGCTTTCTGG GTTTGGGGGG TATTTCAGAT GTACCTTAAA   780
GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT   840
GTGTATCACA TTTCTGTATT TTATCACCCC CTTCCTGCAA CATTATTTAT CTGGAATCTA   900
CCTGCCCTTT TGTTTTTTAG ATACAAGGGC TTGGTTTTGT TACCCAGGCT GGTTTCAAGG   960
CCATAGCTTT AAGAGATCCT CTCACCACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA  1020
TTCATGGCAC CCAGACTTTG CTGCCTTTCT TACATGATCC AGGCCCAGAA CCCAAACTCA  1080
GGCACTGTAT AGATGACCAC TTTCGTAAAC TACTGACCTA GCTTGTTGCC AATTGTTGAT  1140
TGAACTTCCC ATAACTCCAC TTCGTGTCTG TTCCTCTGTA TACAGCCACC TTCTGTTCCC  1200
GTCATGAGCC TTTAGGTCTC CATTTGCATA TTGCAAATAC TATGTTCCAT GTAGGTAGCT  1260
CATTCAGGGC CTTGCTCTTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCAATTTG  1320
TGTTGCTGTG TTGGTTGTTG ATGAAAATAA TAAAATGATT GATTACATAA AAAAAAAAAA  1380
AAAAAAA
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Seq ID NO: B72 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
TGCTAGTAGG GCCTGGGTTA ATCGGCCGAG GGTGGCTTCG TGGTCTTTAT AGCTGTTACT    60
CTTTGTACTT GTCTTTTTCT TTTATTTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA   120
CGCACTATGG CACGAGGCTC GTGCTGCCTG GCCAGGGCGA CTGGCGGATA AGGTCTTGTG   180
CGTGGCCTCG AGGCTTAAAA GTAGCAGTGG GGCTTTGTGA AGGACAAAAT GGCGATGGCG   240
GGCCGTGTAG GTCCCCCTTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG   300
TGAGGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTTGCTTAGC CGTCTGTTCA   360
GAAAATAGCG TTTTCGAAAT GCCCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC   420
AGGATTTACG CGCACGTTGG AACCGAAGAG AGCTCTGTTG TTGCAATGTT CAGCCCACAA   480
GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCATCTTTAT GCAAAGCCAG CGTTACAGTA   540
ATGTTCCAGC ATCTCATAAT CTATCCTGGG GAATTCAGCT GCCTCCCAGG GTGAATACAG   600
GTATTCCTGA TGACAGTCTG CCTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCATTGA   660
AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGGCCAGC   720
ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGTCTGTG TTCACTCCAG   780
GCTGAAGTTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAATCTGT CTTGGAGGAC   840
ATCAGAAGGT GAATTTTCCA AGTTCTTGGA CAACCTAGCT GTTGAAAAGC TTTCTGGGTT   900
TGGGGGGTAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAAGA CACTGGGAGC   960
CAATGAAACA GCAGTTGAGG GTTTGCTGTG TATCACATTT CTGTATTTTA TCACCCCCTT  1020
CCTGCAACAT TATTTATCTG GAATCTACCT GCCCTTTTGT TTTTTAGATA CAAGGGCTTG  1080
GTTTTGTTAC CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT  1140
TCCAAAGTGC TGGGATTGCA GGTGTGATTC ATGGCACCCA GACTTTGCTG CCTTTCTTAC  1200
ATGATCCAGG CCCAGAACCC AAACTCAGGC ACTGTATAGA TGACCACTTT CGTAAACTAC  1260
TGACCTAGCT TGTTGCCAAT TGTTGATTGA ACTTCCCATA ACTCCACTTC GTGTCTGTTC  1320
CTCTGTATAC AGCCACCTTC TGTTCCCGTC ATGAGCCTTT AGGTCTCCAT TTGCATATTG  1380
CAAATACTAT GTTCCATGTA GGTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG  1440
TTCCCTTGAG GACTGGCTGT CAATTTGTGT TGCTGTGTTG GTTGTTGATG AAAATAATAA  1500
AATGATTGAT TACATAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAACAAA CACAAAAAAC  1560
CGCCGCGCTT TTTCCCGGGC GCACAAAGTT ATAAAACGCC GTCCATC
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Seq ID NO: B73 sequence
Nucleic Acid Accession #: NM_000222.1
Coding sequence: 22..2952

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1          11         21         31         41         51
|          |          |          |          |          |
GATCCCATCG CAGCTACCGC GATGAGAGGC GCTCGCGGCG CCTGGGATTT TCTCTGCGTT    60
CTGCTCCTAC TGCTTCGCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA   120
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CCGTCTCCAC CATCCATCCA TCCAGGAAAA TCAGACTTAA TAGTCCGCGT GGGCGACGAG 180
ATTAGGCTGT TATGCACTGA TCCGGGCTTT GTCAAATGGA CTTTTGAGAT CCTGGATGAA 240
ACGAATGAGA ATAAGCAGAA TGAATGGATC ACGGAAAAGG CAGAAGCCAC CAACACCGGC 300
AAATACACGT GCACCAACAA ACACGGCTTA AGCAATTCCA TTTATGTGTT TGTTAGAGAT 360
CCTGCCAAGC TTTTCCTTGT TGACCGCTCC TTGTATGGGA AAGAAGACAA CGACACGCTG 420
GTCCGCTGTC CTCTCACAGA CCCAGAAGTG ACCAATTATT CCCTCAAGGG GTGCCAGGGG 480
AAGCCTCTTC CCAAGGACTT GAGGTTTATT CCTGACCCCA AGGCGGGCAT CATGATCAAA 540
AGTGTGAAAC GCGCCTACCA TCGGCTCTGT CTGCATTGTT CTGTGGACCA GGAGGGCAAG 600
TCAGTGCTGT CGGAAAAATT CATCCTGAAA GTGAGGCCAG CCTTCAAAGC TGTGCCTGTT 660
GTGTCTGTGT CCAAAGCAAG CTATCTTCTT AGGGAAGGGG AAGAATTCAC AGTGACGTGC 720
ACAATAAAAG ATGTGTCTAG TTCTGTGTAC TCAACGTGGA AAAGAGAAAA CAGTCAGACT 780
AAACTACAGG AGAAATATAA TAGCTGGCAT CACGGTGACT TCAATTATGA ACGTCAGGCA 840
ACGTTGACTA TCAGTTCAGC GAGAGTTAAT GATTCTGGAG TGTTCATGTG TTATGCCAAT 900
AATACTTTTG GATCAGCAAA TGTCACAACA ACCTTGGAAG TAGTAGATAA AGGATTCATT 960
AATATCTTCC CCATGATAAA CACTACAGTA TTTGTAAACG ATGGAGAAAA TGTAGATTTG 1020
ATTGTTGAAT ATGAAGCATT CCCCAAACCT GAACACCAGC AGTGGATCTA TATGAACAGA 1080
ACCTTCACTG ATAAATGGGA AGATTATCCC AAGTCTGAGA ATGAAAGTAA TATCAGATAC 1140
GTAAGTGAAC TTCATCTAAC GAGATTAAAA GGCACCGAAG GAGGCACTTA CACATTCCTA 1200
GTGTCCAATT CTGACGTCAA TGCTGCCATA GCATTTAATG TTTATGTGAA TACAAAACCA 1260
GAAATCCTGA CTTACGACAG GCTCGTGAAT GGCATGCTCC AATGTGTGGC AGCAGGATTC 1320
CCAGAGCCCA CAATAGATTG GTATTTTTGT CCAGGAACTG AGCAGAGATG CTCTGCTTCT 1380
GTACTGCCAG TGGATGTGCA GACACTAAAC TCATCTGGGC CACCGTTTGG AAAGCTAGTG 1440
GTTCAGAGTT CTATAGATTC TAGTGCATTC AAGCACAATG GCACGGTTGA ATGTAAGGCT 1500
TACAACGATG TGGGCAAGAC TTCTGCCTAT TTTAACTTTG CATTTAAAGG TAACAACAAA 1560
GAGCAAATCC ATCCCCACAC CCTGTTCACT CCTTTGCTGA TTGGTTTCGT AATCGTAGCT 1620
GGCATGATGT GCATTATTGT GATGATTCTG ACCTACAAAT ATTTACAGAA ACCCATGTAT 1680
GAAGTACAGT GGAAGGTTGT TGAGGAGATA AATGGAAACA ATTATGTTTA CATAGACCCA 1740
ACACAACTTC CTTATGATCA CAAATGGGAG TTTCCCAGAA ACAGGCTGAG TTTTGGGAAA 1800
ACCCTGGGTG CTGGAGCTTT CGGGAAGGTT GTTGAGGCAA CTGCTTATGG CTTAATTAAG 1860
TCAGATGCGG CCATGACTGT CGCTGTAAAG ATGCTCAAGC CGAGTGCCCA TTTGACAGAA 1920
CGGGAAGCCC TCATGTCTGA ACTCAAAGTC CTGAGTTACC TTGGTAATCA CATGAATATT 1980
GTGAATCTAC TTGGAGCCTG CACCATTGGA GGGCCCACCC TGGTCATTAC AGAATATTGT 2040
TGCTATGGTG ATCTTTTGAA TTTTTTGAGA AGAAAACGTG ATTCATTTAT TTGTTCAAAG 2100
CAGGAAGATC ATGCAGAAGC TGCACTTTAT AAGAATCTTC TGCATTCAAA GGAGTCTTCC 2160
TGCAGCGATA GTACTAATGA GTACATGGAC ATGAAACCTG GAGTTTCTTA TGTTGTCCCA 2220
ACCAAGGCCG ACAAAAGGAG ATCTGTGAGA ATAGGCTCAT ACATAGAAAG AGATGTGACT 2280
CCCGCCATCA TGGAGGATGA CGAGTTGGCC CTAGACTTAG AAGACTTGCT GAGCTTTTCT 2340
TACCAGGTGG CAAAGGGCAT GGCTTTCCTC GCCTCCAAGA ATTGTATTCA CAGAGACTTG 2400
GCAGCCAGAA ATATCCTCCT TACTCATGGT CGGATCACAA AGATTTGTGA TTTTGGTCTA 2460
GCCAGAGACA TCAAGAATGA TTCTAATTAT GTGGTTAAAG GAAACGCTCG ACTACCTGTG 2520
AAGTGGATGG CACCTGAAAG CATTTTCAAC TGTGTATACA CGTTTGAAAG TGACGTCTGG 2580
TCCTATGGGA TTTTTCTTTG GGAGCTGTTC TCTTTAGGAA GCAGCCCCTA TCCTGGAATG 2640
CCGGTCGATT CTAAGTTCTA CAAGATGATC AAGGAAGGCT TCCGGATGCT CAGCCCTGAA 2700
CACGCACCTG CTGAAATGTA TGACATAATG AAGACTTGCT GGGATGCAGA TCCCCTAAAA 2760
AGACCAACAT TCAAGCAAAT TGTTCAGCTA ATTGAGAAGC AGATTTCAGA GAGCACCAAT 2820
CATATTTACT CCAACTTAGC AAACTGCAGC CCCAACCGAC AGAAGCCCGT GGTAGACCAT 2880
TCTGTGCGGA TCAATTCTGT CGGCAGCACC GCTTCCTCCT CCCAGCCTCT GCTTGTGCAC 2940
GACGATGTCT GAGCAGAATC AGTGTTTGGG TCACCCCTCC AGGAATGATC TCTTCTTTTG 3000
GCTTCCATGA TGGTTATTTT CTTTTCTTTC AACTTGCATC CAACTCCAGG ATAGTGGGCA 3060
CCCCACTGCA ATCCTGTCTT TCTGAGCACA CTTTAGTGGC CGATGATTTT TGTCATCAGC 3120
CACCATCCTA TTGCAAAGGT TCCAACTGTA TATATTCCCA ATAGCAACGT AGCTTCTACC 3180
ATGAACAGAA AACATTCTGA TTTGGAAAAA GAGAGGGAGG TATGGACTGG GGGCCAGAGT 3240
CCTTTCCAAG GCTTCTCCAA TTCTGCCCAA AAATATGGTT GATAGTTTAC CTGAATAAAT 3300
GGTAGTAATC ACAGTTGGCC TTCAGAACCA TCCATAGTAG TATGATGATA CAAGATTAGA 3360
AGCTGAAAAC CTAAGTCCTT TATGTGGAAA ACAGAACATC ATTAGAACAA AGGACAGAGT 3420
ATGAACACCT GGGCTTAAGA AATCTAGTAT TTCATGCTGG GAATGAGACA TAGGCCATGA 3480
AAAAAATGAT CCCCAAGTGT GAACAAAAGA TGCTCTTCTG TGGACCACTG CATGAGCTTT 3540
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GCCTCCCTAG CCAGCACTTG TATATACGCA TCTATAAATT GTCCGTGTTC ATACATTTGA 3660
GGGGAAAACA CCATAAGGTT TCGTTTCTGT ATACAACCCT GGCATTATGT CCACTGTGTA 3720
TAGAAGTAGA TTAAGAGCCA TATAAGTTTG AAGGAAACAG TTAATACCAT TTTTTAAGGA 3780
AACAATATAA CCACAAAGCA CAGTTTGAAC AAAATCTCCT CTTTTAGCTG ATGAACTTAT 3840
TCTGTAGATT CTGTGGAACA AGCCTATCAG CTTCAGAATG GCATTGTACT CAATGGATTT 3900
GATGCTGTTT GACAAAGTTA CTGATTCACT GCATGGCTCC CACAGGAGTG GGAAAACACT 3960
GCCATCTTAG TTTGGATTCT TATGTAGCAG GAAATAAAGT ATAGGTTTAG CCTCCTTCGC 4020
AGGCATGTCC TGGACACCGG GCCAGTATCT ATATATGTGT ATGTACGTTT GTATGTGTGT 4080
AGACAAATAT TTGGAGGGGT ATTTTTGCCC TGAGTCCAAG AGGGTCCTTT AGTACCTGAA 4140
AAGTAACTTG GCTTTCATTA TTAGTACTGC TCTTGTTTCT TTTCACATAG CTGTCTAGAG 4200
TAGCTTACCA GAAGCTTCCA TAGTGGTGCA GAGGAAGTGG AAGGCATCAG TCCCTATGTA 4260
TTTGCAGTTC ACCTGCACTT AAGGCACTCT GTTATTTAGA CTCATCTTAC TGTACCTGTT 4320
CCTTAGACCT TCCATAATGC TACTGTCTCA CTGAAACATT TAAATTTTAC CCTTTAGACT 4380
GTAGCCTGGA TATTATTCTT GTAGTTTACC TCTTTAAAAA CAAAACAAAA CAAAACAAAA 4440
AACTCCCCTT CCTCACTGCC CAATATAAAA GGCAAATGTG TACATGGCAG AGTTTGTGTG 4500
TTGTCTTGAA AGATTCAGGT ATGTTGCCTT TATGGTTTCC CCCTTCTACA TTTCTTAGAC 4560
TACATTTAGA GAACTGTGGC CGTTATCTGG AAGTAACCAT TTGCACTGGA GTTCTATGCT 4620
CTCGCACCTT TCCAAAGTTA ACAGATTTTG GGGTTGTGTT GTCACCCAAG AGATTGTTGT 4680
TTGCCATACT TTGTCTGAAA AATTCCTTTG TGTTTCTATT GACTTCAATG ATAGTAAGAA 4740
AAGTGGTTGT TAGTTATAGA TGTCTAGGTA CTTCAGGGGC ACTTCATTGA GAGTTTTGTC 4800
TTGCCATACT TTGTCTGAAA AATTCCTTTG TGTTTCTATT GACTTCAATG ATAGTAAGAA 4860
AAGTGGTTGT TAGTTATAGA TGTCTAGGTA CTTCAGGGGC ACTTCATTGA GAGTTTTGTC 4920
AATGTCTTTT GAATATTCCC AAGCCCATGA GTCCTTGAAA ATATTTTTTA TATATACAGT 4980
AACTTTATGT GTAAATACAT AAGCGGCGTA AGTTTAAAGG ATGTTGGTGT TCCACGTGTT 5040
TTATTCCTGT ATGTTGTCCA ATTGTTGACA GTTCTGAAGA ATTC

Seq ID NO: B74 protein sequence
Protein Accession #: NP_000213.1

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1          11         21         31         41         51
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MRGARGAWDF LCVLLLLLRV QTGSSQPSVS PGEPSPPSIH PGKSDLIVRV GDEIRLLCTD    60
PGFVKWTFEI LDETNENKQN EWITEKAEAT NTGKYTCTNK HGLSNSIYVF VRDPAKLFLV   120
DRSLYGKEDN DTLVRCPLTD PEVTNYSLKG CQGKPLPKDL RFIPDPKAGI MIKSVKRAYH   180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAFKA VPVVSVSKAS YLLREGEEFT VTCTIKDVSS   240
SVYSTWKREN SQTKLQEKYN SWHHGDFNYE RQATLTISSA RVNDSGVFMC YANNTFGSAN   300
VTTTLEVVDK GFINIFPMIN TTVFVNDGEN VDLIVEYEAF PKPEHQQWIY MNRTFTDKWE   360
DYPKSENESN IRYVSELHLT RLKGTEGGTY TFLVSNSDVN AAIAFNVYVN TKPEILTYDR   420
LVNGMLQCVA AGFPEPTIDW YFCPGTEQRC SASVLPVDVQ TLNSSGPPFG KLVVQSSIDS   480
SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIHPHT LFTPLLIGFV IVAGMMCIIV   540
MILTYKYLQK PMYEVQWKVV EEINGNNYVY IDPTQLPYDH KWEFPRNRLS FGKTLGAGAF   600
GKVVEATAYG LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLSYLGNH MNIVNLLGAC   660
TIGGPTLVIT EYCCYGDLLN FLRRKRDSFI CSKQEDHAEA ALYKNLLHSK ESSCSDSTNE   720
YMDMKPGVSY VVPTKADKRR SVRIGSYIER DVTPAIMEDD ELALDLEDLL SFSYQVAKGM   780
AFLASKNCIH RDLAARNILL THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAPES   840
IFNCVYTFES DVWSYGIFLW ELFSLGSSPY PGMPVDSKFY KMIKEGFRML SPEHAPAEMY   900
DIMKTCWDAD PLKRPTFKQI VQLIEKQISE STNHIYSNLA NCSPNRQKPV VDHSVRINSV   960
GSTASSSQPL LVHDDV
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Seq ID NO: B75 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58..2298

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GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTTGTT GGCGGAAGCG TGTAAAATCA   120
GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG   180
TTTAGTTCCA ATCGTCAGAA AATTTTGGAA AGAACGGAAA TCTTAAACCA AGAATGGAAA   240
CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG   300
GAGTGTTCGG TGACCAGTGA CTTGGATTTT CCAACACAAG TCATCCCATT AAAGACTCTG   360
AATGCAGTTG CTTCAGTACC CATAATGTAT TCTTGGTCTC CCCTACAGCA GAATTTTATG   420
GTGGAAGATG AAACTGTTTT ACATAACATT CCTTATATGG GAGATGAAGT TTTAGATCAG   480
GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAAGTACA CGGGGATAGA   540
GAATGTGGGT TTATAAATGA TGAAATTTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT   600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA   660
GATCTGGAGG ATCACCGAGA TGATAAAGAA AGCCGCCCAC CTCGGAAATT TCCTTCTGAT   720
AAAATTTTGG AGGCCATTTC CTCAATGTTT CCAGATAAGG GCACAGCAGA AGAACTAAAG   780
GAAAAATATA AAGAACTCAC CGAACAGCAG CTCCCAGGCG CACTTCCTCC TGAATGTACC   840
CCCAACATAG ATGGACCAAA TGCTAAATCT GTTCAGAGAG AGCAAAGCTT ACACTCCTTT   900
CATACGCTTT TCTGTAGGCG ATGTTTTAAA TATGACTGCT TCCTACATCC TTTTCATGCA   960
ACACCCAACA CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTTGTGGA  1020
CCACAGTGTT ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG  1080
CGGATAAAGA CCCCACCAAA ACGTCCAGGA GGCCGCAGAA GAGGACGGCT TCCCAATAAC  1140
AGTAGCAGGC CCAGCACCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTGAT  1200
AGGGAAGCAG GGACTGAAAC GGGGGGAGAG AACAATGATA AAGAAGAAGA AGAGAAGAAA  1260
GATGAAACTT CGAGCTCCTC TGAAGCAAAT TCTCGGTGTC AAACACCAAT AAAGATGAAG  1320
CCAAATATTG AACCTCCTGA GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTAGA  1380
GTCCTCATTG GCACTTACTA TGACAATTTC TGTGCCATTG CTAGGTTAAT TGGGACCAAA  1440
ACATGTAGAC AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC  1500
GCTGAGGATG TGGATACTCC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA  1560
CACTGCAGAA AGATACAGCT GAAAAAGGAC GGCTCCTCTA ACCATGTTTA CAACTATCAA  1620
CCCTGTGATC ATCCACGCCA GCCTTGTGAC AGTTCGTGCC CTTGTGTGAT AGCACAAAAT  1680
TTTTGTGAAA AGTTTTGTCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCCGC  1740
TGCAAAGCAC AGTGCAACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC  1800
CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTGGG ACAGTAAAAA TGTGTCCTGC  1860
AAGAACTGCA GTATTCAGCG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG  1920
GCAGGCTGGG GGATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC  1980
TGTGGAGAGA TTATTTCTCA AGATGAAGCT GACAGAAGAG GGAAAGTGTA TGATAAATAC  2040
ATGTGCAGCT TTCTGTTCAA CTTGAACAAT GATTTTGTGG TGGATGCAAC CCGCAAGGGT  2100
AACAAAATTC GTTTTGCAAA TCATTCGGTA AATCCAAACT GCTATGCAAA AGTTATGATG  2160
GTTAACGGTG ATCACAGGAT AGGTATTTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG  2220
CTGTTTGTTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCGG CATCGAAAGA  2280
GAAATGGAAA TCCCTTGACA TCTGCTACCT CCTCCCCCTC CTCTGAAACA GCTGCCTTAG  2340
CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAAATTCTG  2400
AATTTGCAAA GTACTGTAAG AATAATTTAT AGTAATGAGT TTAAAAATCA ACTTTTTATT  2460
GCCTTCTCAC CAGCTGCAAA GTGTTTTGTA CCAGTGAATT TTTGCAATAA TGCAGTATGG  2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAACTTGAA AAAAAAAAAA AAAAAA
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Seq ID NO: B76 Protein sequence
Protein Accession #: NP_004447

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1          11         21         31         41         51
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MGQTGKKSEK GPVCWRKRVK SEYMRLRQLK RFRRADEVKS MFSSNRQKIL ERTEILNQEW    60
KQRRIQPVHI LTSVSSLRGT RECSVTSDLD FPTQVIPLKT LNAVASVPIM YSWSPLQQNF   120
MVEDETVLHN IPYMGDEVLD QDGTFIEELI KNYDGKVHGD RECGFINDEI FVELVNALGQ   180
YNDDDDDDDG DDPEEREEKQ KDLEDHRDDK ESRPPRKFPS DKILEAISSM FPDKGTAEEL   240
KEKYKELTEQ QLPGALPPEC TPNIDGPNAK SVQREQSLHS FHTLFCRRCF KYDCFLHPFH   300
ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GGRRRGRLPN   360
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NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEEK KDETSSSSEA NSRCQTPIKM   420
KPNIEPPENV EWSGAEASMF RVLIGTYYDN FCAIARLIGT KTCRQVYEFR VKESSIIAPA   480
PAEDVDTPPR KKKRKHRLWA AHCRKIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPCVIAQ   540
NFCEKFCQCS SECQNRFPGC RCKAQCNTKQ CPCYLAVREC DPDLCLTCGA ADHWDSKNVS   600
CKNCSIQRGS KKHLLLAPSD VAGWGIFIKD PVQKNEPISE YCGEIISQDE ADRRGKVYDK   660
YMCSFLFNLN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE   720
ELFVDYRYSQ ADALKYVGIE REMEIP
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Seq ID NO: B77 DNA sequence
Nucleic Acid Accession #: NM_007015
Coding sequence: 1..1005

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TGCAGCCCCC CGGCGTACGC TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC   120
AAGGTGGGAG CCGTGGTCCT CATTTCGGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG   180
GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT   240
ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC   300
TTTAAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCA GAATGGCATC   360
ACAGGAATTC GTTTTGCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT   420
ATTCCTGAGG TGGGCGCCGT GACCAAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC   480
ATGCCAGTCA AATATGAAGA AAATTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG   540
GACAACAGCT TCTTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTTCTGG   600
CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAAGAA GAGAAGTGGT AAGAAAAATT   660
GTTCCAACTA CCACAAAAAG ACCACACAGT GGACCACGGA GCAACCCAGG CGCTGGAAGA   720
CTGAATAATG AAACCAGACC CAGTGTTCAA GAGGACTCAC AAGCCTTCAA TCCTGATAAT   780
CCTTATCATC AGCAGGAAGG GGAAAGCATG ACATTCGACC CTAGACTGGA TCACGAAGGA   840
ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG   900
GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC   960
ATGCCATGTA GCTGGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTCATATAT  1020
CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTA AGGCAGGTTG  1080
ATGCTGATGG GACCATAAAA TATTTTTACA CGCAGCCTGA GCGGTTATTC TTGACACTCT  1140
TAACAGAATT TTTTTAATCG TTTTCCAGAA CTTTAGTATA TGCAAATGCA CTGAAAGGGT  1200
AGTTCAAGTC TAAAATGCCA TAACCCCGTT ATTTGTTATT TTTTATTTGC ATTGATTTGC  1260
CATAAGTCTT CCCTTGCTTG CATCTTCCAA AGCTATTTCG AAATAAACAC GAAAATTTAC  1320
AGTTTGCC
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Seq ID NO: B78 Protein sequence
Protein Accession #: NP_008946

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1          11         21         31         41         51
|          |          |          |          |          |
MTENSDKVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG    60
AFYFWKGSDS HIYNVHYTMS INGKLQDGSM EIDAGNNLET FKMGSGAEEA IAVNDFQNGI   120
TGIRFAGGEK CYIKAQVKAR IPEVGAVTKQ SISSKLEGKI MPVKYEENSL IWVAVDQPVK   180
DNSFLSSKVL ELCGDLPIFW LKPTYPKEIQ RERREVVRKI VPTTTKRPHS GPRSNPGAGR   240
LNNETRPSVQ EDSQAFNPDN PYHQQEGESM TFDPRLDHEG ICCIECRRSY THCQKICEPL   300
GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV
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Seq ID NO: B79 DNA sequence
Nucleic Acid Accession #: NM_012449.1
Coding sequence: 66..1085

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1          11         21         31         41         51
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CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG    60
AATTAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA   120
GGAGAAATTT AGAAGAAGAC GATTATTTGC ATAAGGACAC GGGAGAGACC AGCATGCTAA   180
AAAGACCTGT GCTTTTGCAT TTGCACCAAA CAGCCCATGC TGATGAATTT GACTGCCCTT   240
CAGAACTTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTTGCCAATT AAAATAGCTG   300
CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTTCTGAG GGAAGTAATT CACCCTTTAG   360
CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCATCAAC AAAGTCTTGC   420
CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG   480
TCCAACTTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT   540
TAACAAGAAA GCAGTTTGGG CTTCTCAGTT TCTTTTTTGC TGTACTGCAT GCAATTTATA   600
GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC   660
AGGTCCAACA AAATAAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT   720
ATGTGTCTCT GGGAATTGTG GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC   780
CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA   840
TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCCTGGAAT AAGTGGATAG   900
ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCCTTCCAA   960
TTGTTGTCCT GATATTTAAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA  1020
AGATTAGACA TGGTTGGGAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCCCAGT  1080
TGTAGAATTA CTGTTTACAC ACATTTTTGT TCAATATTGA TATATTTTAT CACCAACATT  1140
TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA
```

Seq ID NO: B80 Protein sequence
Protein Accession #: NP_036581.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE    60
LQHTQELFPQ WHLPIKIAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM   120
```

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VSITLLALVY LPGVIAAIVQ LHNGTKYKKF PHWLDKWMLT RKQFGLLSFF FAVLHAIYSL   180
SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS   240
VSDSLTWREF HYIQSKLGIV SLLLGTIHAL IFAWNKWIDI KQFVWYTPPT FMIAVFLPIV   300
VLIFKSILFL PCLRKKILKI RHGWEDVTKI NKTEICSQL
```

Seq ID NO: B81 DNA sequence
Nucleic Acid Accession #: NM_000684
Coding sequence: 87..1520

```
1          11         21         31         41         51
|          |          |          |          |          |
TGCTACCCGC GCCCGGGCTT CTGGGGTGTT CCCCAACCAC GGCCCAGCCC TGCCACACCC    60
CCCGCCCCCG GCCTCCGCAG CTCGGCATGG GCGCGGGGGT GCTCGTCCTG GGCGCCTCCG   120
AGCCCGGTAA CCTGTCGTCG GCCGCACCGC TCCCCGACGG CGCGGCCACC GCGGCGCGGC   180
TGCTGGTGCC CGCGTCGCCG CCCGCCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCCGAGC   240
CGCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGCTGAT GGCGCTCATC GTGCTGCTCA   300
TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCCGCGG CTGCAGACGC   360
TCACCAACCT CTTCATCATG TCCCTGGCCA GCGCCGACCT GGTCATGGGG CTGCTGGTGG   420
TGCCGTTCGG GGCCACCATC GTGGTGTGGG GCCGCTGGGA GTACGGCTCC TTCTTCTGCG   480
AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA   540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCAGAGC CTGCTGACGC   600
GCGCGCGGGC GCGGGGCCTC GTGTGCACCG TGTGGGCCAT CTCGGCCCTG GTGTCCTTCC   660
TGCCCATCCT CATGCACTGG TGGCGGGCGG AGAGCGACGA GGCGCGCCGC TGCTACAACG   720
ACCCCAAGTG CTGCGACTTC GTCACCAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT   780
CCTTCTACGT GCCCCTGTGC ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCGAGGCCC   840
AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCCGTTT CCTCGGCGGC CCAGCGCGGC   900
CGCCCTCGCC CTCGCCCTCG CCCGTCCCCG CGCCCGCGCC GCCGCCCGGA CCCCCGCGCC   960
CCGCCGCCGC CGCCGCCACC GCCCCGCTGG CCAACGGGCG TGCGGGTAAG CGGCGGCCCT  1020
CGCGCCTCGT GGCCCTACGC GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG  1080
TCTTCACGCT CTGCTGGCTG CCCTTCTTCC TGGCCAACGT GGTGAAGGCC TTCCACCGCG  1140
AGCTGGTGCC CGACCGCCTC TTCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCCT  1200
TCAACCCCAT CATCTACTGC CGCAGCCCCG ACTTCCGCAA GGCCTTCCAG GGACTGCTCT  1260
GCTGCGCGCG CAGGGCTGCC CGCCGGCGCC ACGCGACCCA CGGAGACCGG CCGCGCGCCT  1320
CGGGCTGTCT GGCCCGGCCC GGACCCCCGC CATCGCCCGG GGCCGCCTCG GACGACGACG  1380
ACGACGATGT CGTCGGGGCC ACGCCGCCCG CGCGCCTGCT GGAGCCCTGG GCCGGCTGCA  1440
ACGGCGGGGC GGCGGCGGAC AGCGACTCGA GCCTGGACGA GCCGTGCCGC CCCGGCTTCG  1500
CCTCGGAATC CAAGGTGTAG GGCCCGGCGC GGGGCGCGGA CTCCGGGCAC GGCTTCCCAG  1560
GGGAACGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAACTCGA AGCCCACAAT  1620
CCTCGTCTGA ATCATCCGAG GCAAAGAGAA AAGCCACGGA CCGTTGCACA AAAAGGAAAG  1680
TTTGGGAAGG GATGGGAGAG TGGCTTGCTG ATGTTCCTTG TTG
```

Seq ID NO: B82 Protein sequence
Protein Accession #: NP_000675.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGAGVLVLGA SEPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQWTAG    60
MGLLMALIVL LIVAGNVLVI VAIAKTPRLQ TLTNLFIMSL ASADLVMGLL VVPFGATIVV   120
WGRWEYGSFF CELWTSVDVL CVTASIETLC VIALDRYLAI TSPFRYQSLL TRARARGLVC   180
TVWAISALVS FLPILMHWWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM   240
AFVYLRVFRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAATAP   300
LANGRAGKRR PSRLVALREQ KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVPDRLFV   360
FFNWLGYANS AFNPIIYCRS PDFRKAFQGL LCCARRAARR RHATHGDRPR ASGCLARPGP   420
PPSPGAASDD DDDDVVGATP PARLLEPWAG CNGGAAADSD SSLDEPCRPG FASESKV
```

Seq ID NO: B83 DNA sequence
Nucleic Acid Accession #: NM_000729.2
Coding sequence: 2..421

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCTCAGCTG CCGGGCTGCT CCGGTTGGAA ACGCCAAGCC AGCTGCCGTC CTAATCCAAA    60
AGCCATGAAC AGCGGCGTGT GCCTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCCT   120
GACGCAGCCG GTGCCTCCCG CAGATCCCGC GGGCTCCGGG CTGCAGCGGG CAGAGGAGGC   180
GCCCCGTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG   240
CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT   300
CGTTAAGAAC CTGCAGAACC TGGACCCCAG CCACAGGATA AGTGACCGGG ACTACATGGG   360
CTGGATGGAT TTTGGCCGTC GCAGTGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA   420
GCCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACAA   480
TCACACTCAT AACTCATTGT CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC   540
TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACACGCT CACCAGAAGT   600
TGTGCAAACT GAAGACAAAA CTGTTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT   660
TATGCTATTA AAGTGATTTC ATTCTGCC
```

Seq ID NO: B84 Protein sequence
Protein Accession #: NP_000720.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MNSGVCLCVL MAVLAAGALT QPVPPADPAG SGLQRAEEAP RRQLRVSQRT DGESRAHLGA    60
LLARYIQQAR KAPSGRMSIV KNLQNLDPSH RISDRDYMGW MDFGRRSAEE YEYPS
```

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

A1 DNA SEQUENCE

Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
Unigene number:	Hs.154210
Probeset Accession #:	M31210
Nucleic Acid Accession #:	M31210
Coding sequence:	251-1396

```
TCTAAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG    60
AACGCAACTT CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAGGA   120
AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT   180
CTCGCCTCGC CCTCTAGCGT TCGTCTGGAG TAGCGCCACC CCGGCTTCCT GGGGACACAG   240
GGTTGGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCCACCGCA GCTCGGTCTC   300
TGACTACGTC AACTATGATA TCATCGTCCG GCATTACAAC TACACGGGAA AGCTGAATAT   360
CAGCGCGGAC AAGGAGAACA GCATTAAACT GACCTCGGTG GTGTTCATTC TCATCTGCTG   420
CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCCA   480
CCGACCCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTTGG CAGGAGTAGC   540
CTACACAGCT AACCTGCTCT TGTCTGGGGC CACCACCTAC AAGCTCACTC CCGCCCAGTG   600
GTTTCTGCGG GAAGGGAGTA TGTTTGTGGC CCTGTCAGCC TCCGTGTTCA GTCTCCTCGC   660
CATCGCCATT GAGCGCTATA TCACAATGCT GAAAATGAAA CTCCACAACG GGAGCAATAA   720
CTTCCGCCTC TTCCTGCTAA TCAGCGCCTG CTGGGTCATC TCCCTCATCC TGGGTGGCCT   780
GCCTATCATG GGCTGGAACT GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCCGCT   840
CTACCACAAG CACTATATCC TCTTCTGCAC CACGGTCTTC ACTCTGCTTC TGCTCTCCAT   900
CGTCATTCTG TACTGCAGAA TCTACTCCTT GGTCAGGACT CGGAGCCGCC GCCTGACGTT   960
CCGCAAGAAC ATTTCCAAGG CCAGCCGCAG CTCTGAGAAT GTGGCGCTGC TCAAGACCGT  1020
AATTATCGTC CTGAGCGTCT TCATCGCCTG CTGGGCACCG CTCTTCATCC TGCTCCTGCT  1080
GGATGTGGGC TGCAAGGTGA AGACCTGTGA CATCCTCTTC AGAGCGGAGT ACTTCCTGGT  1140
GTTAGCTGTG CTCAACTCCG GCACCAACCC CATCATTTAC ACTCTGACCA ACAAGGAGAT  1200
GCGTCGGGCC TTCATCCGGA TCATGTCCTG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG  1260
CAAATTCAAG CGACCCATCA TCGCCGGCAT GGAATTCAGC CGCAGCAAAT CGGACAATTC  1320
CTCCCACCCC CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTATGTCTT CTGGAAACGT  1380
CAACTCTTCT TCCTAGAACT GGAAGCTGTC CACCCACCGG AAGCGCTCTT TACTTGGTCG  1440
CTGGCCACCC CAGTGTTTGG AAAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT  1500
GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGGTGGTGT CGGGTGTTGG  1560
TGGGTAGAGT TAGTTCCTGT GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCCT  1620
GGAATATATA TTCTACCCCC CTGGAGCTTT GATTTTGCAC TGAGCCAAAG GTCTAGCATT  1680
GTCAAGCTCC TAAAGGGTTC ATTTGGCCCC TCCTCAAAGA CTAATGTCCC CATGTGAAAG  1740
CGTCTCTTTG TCTGGAGCTT TGAGGAGATG TTTTCCTTCA CTTTAGTTTC AAACCCAAGT  1800
GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCCCTGTACA TCCCACACCC CACCCTCCCT  1860
TCCCTTCATA CCCCTCCTCA ACGTTCTTTT ACTTTATACT TTAACTACCT GAGAGTTATC  1920
AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAAT AGGCTATGTT GAGTACGTAG  1980
GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAAACAAT GTCCTTCGCT GAGGCCAAAG  2040
TTTCCATGTA AGCGGGATCC GTTTTTTGGA ATTTGGTTGA AGTCACTTTG ATTTCTTTAA  2100
AAAACATCTT TTCAATGAAA TGTGTTACCA TTTCATATCC ATTGAAGCCG AAATCTGCAT  2160
AAGGAAGCCC ACTTTATCTA AATGATATTA GCCAGGATCC TTGGTGTCCT AGGAGAAACA  2220
GACAAGCAAA ACAAAGTGAA AACCGAATGG ATTAACTTTT GCAAACCAAG GGAGATTTCT  2280
TAGCAAATGA GTCTAACAAA TATGACATCC GTCTTTCCCA CTTTTGTTGA TGTTTATTTC  2340
AGAATCTTGT GTGATTCATT TCAAGCAACA ACATGTTGTA TTTTGTTGTG TTAAAAGTAC  2400
TTTTCTTGAT TTTTGAATGT ATTTGTTTCA GGAAGAAGTC ATTTTATGGA TTTTTCTAAC  2460
CCGTGTTAAC TTTTCTAGAA TCCACCCTCT TGTGCCCTTA AGCATTACTT TAACTGGTAG  2520
GGAACGCCAG AACTTTTAAG TCCAGCTATT CATTAGATAG TAATTGAAGA TATGTATAAA  2580
TATTACAAAG AATAAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAAAC  2640
CGAGAGATGT CTTGTTTTTT TAAAAAGAAT AGTATTTAAT AGGTTTCTGA CTTTTGTGGA  2700
TCATTTTGCA CATAGCTTTA TCAACTTTTA AACATTAATA AACTGATTTT TTTAAAG
```

A2 Protein sequence:

Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
Unigene number:	Hs.154210
Probeset Accession #:	M31210
Protein Accession #:	AAA52336
Signal sequence:	none found
Transmembrane domains:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSV VFILICCFII    60
LENIFVLLTI WKTKKFHRPM YYFIGNLALS DLLAGVAYTA NLLLSGATTY KLTPAQWFLR   120
EGSMFVALSA SVFSLLAIAI ERYITMLKMK LHNGSNNFRL FLLISACWVI SLILGGLPIM   180
GWNCISALSS CSTVLPLYHK HYILFCTTVF TLLLLSIVIL YCRIYSLVRT RSRRLTFRKN   240
ISKASRSSEN VALLKTVIIV LSVFIACWAP LFILLLLDVG CKVKTCDILF RAEYFLVLAV   300
LNSGTNPIIY TLTNKEMRRA FIRIMSCCKC PSGDSAGKFK RPIIAGMEFS RSKSDNSSHP   360
QKDEGDNPET IMSSGNVNSS S
```

A3 DNA SEQUENCE

Gene name:	G protein-coupled receptor 51
Unigene number:	Hs.198612
Probeset Accession #:	AA452928
Nucleic Acid Accession #:	NM_004624.1

Coding sequence: 1-2826 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCTTCCC CGCGGAGGTC CGGGCAGCCA GGGCGGCCGC CGCCGCCGCC ACCGCCGCCC    60
GCGCGCCTGC TACTGCTACT GCTGCTGCCG CTGCTGCTGC CTCTGGCGCC CGGGGCCTGG   120
GGCTGGGCGC GGGGCGCCCC CCGGCCGCCG CCCAGCAGCC CGCCGCTCTC CATCATGGGC   180
CTCATGCCGC TCACCAAGGA GGTGGCCAAG GGCAGCATCG GGCGCGGTGT GCTCCCCGCC   240
GTGGAACTGG CCATCGAGCA GATCCGCAAC GAGTCACTCC TGCGCCCCTA CTTCCTCGAC   300
CTGCGGCTCT ATGACACGGA GTGCGACAAC GCAAAAGGGT TGAAAGCCTT CTACGATGCA   360
ATAAAATACG GGCCGAACCA CTTGATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC   420
ATCATTGCAG AGTCCCTCCA AGGCTGGAAT CTGGTGCAGC TTTCTTTTGC TGCAACCACG   480
CCTGTTCTAG CCGATAAGAA AAAATACCCT TATTTCTTTC GGACCGTCCC ATCAGACAAT   540
GCGGTGAATC CAGCCATTCT GAAGTTGCTC AAGCACTACC AGTGGAAGCG CGTGGGCACG   600
CTGACGCAAG ACGTTCAGAG GTTCTCTGAG GTGCGGAATG ACCTGACTGG AGTTCTGTAT   660
GGCGAGGACA TTGAGATTTC AGACACCGAG AGCTTCTCCA ACGATCCCTG TACCAGTGTC   720
AAAAAGCTGA AGGGGAATGA TGTGCGGATC ATCCTTGGCC AGTTTGACCA GAATATGGCA   780
GCAAAAGTGT TCTGTTGTGC ATACGAGGAG AACATGTATG GTAGTAAATA TCAGTGGATC   840
ATTCCGGGCT GGTACGAGCC TTCTTGGTGG GAGCAGGTGC ACACGGAAGC CAACTCATCC   900
CGCTGCCTCC GGAAGAATCT GCTTGCTGCC ATGGAGGGCT ACATTGGCGT GGATTTCGAG   960
CCCCTGAGCT CCAAGCAGAT CAAGACCATC TCAGGAAAGA CTCCACAGCA GTATGAGAGA  1020
GAGTACAACA ACAAGCGGTC AGGCGTGGGG CCCAGCAAGT TCCACGGGTA CGCCTACGAT  1080
GGCATCTGGG TCATCGCCAA GACACTGCAG AGGGCCATGG AGACACTGCA TGCCAGCAGC  1140
CGGCACCAGC GGATCCAGGA CTTCAACTAC ACGGACCACA CGCTGGGCAG GATCATCCTC  1200
AATGCCATGA ACGAGACCAA CTTCTTCGGG GTCACGGGTC AAGTTGTATT CCGGAATGGG  1260
GAGAGAATGG GGACCATTAA ATTTACTCAA TTTCAAGACA GCAGGGAGGT GAAGGTGGGA  1320
GAGTACAACG CTGTGGCCGA CACACTGGAG ATCATCAATG ACACCATCAG GTTCCAAGGA  1380
TCCGAACCAC CAAAAGACAA GACCATCATC CTGGAGCAGC TGCGGAAGAT CTCCCTACCT  1440
CTCTACAGCA TCCTCTCTGC CCTCACCATC CTCGGGATGA TCATGGCCAG TGCTTTTCTC  1500
TTCTTCAACA TCAAGAACCG GAATCAGAAG CTCATAAAGA TGTCGAGTCC ATACATGAAC  1560
AACCTTATCA TCCTTGGAGG GATGCTCTCC TATGCTTCCA TATTTCTCTT TGGCCTTGAT  1620
GGATCCTTTG TCTCTGAAAA GACCTTTGAA ACACTTTGCA CCGTCAGGAC CTGGATTCTC  1680
ACCGTGGGCT ACACGACCGC TTTTGGGGCC ATGTTTGCAA AGACCTGGAG AGTCCACGCC  1740
ATCTTCAAAA ATGTGAAAAT GAAGAAGAAG ATCATCAAGG ACCAGAAACT GCTTGTGATC  1800
GTGGGGGGCA TGCTGCTGAT CGACCTGTGT ATCCTGATCT GCTGGCAGCC TGTGGACCCC  1860
CTGCGAAGGA CAGTGGAGAA GTACAGCATG GAGCCGGACC CAGCAGGACG GGATATCTCC  1920
ATCCGCCCTC TCCTGGAGCA CTGTGAGAAC ACCCATATGA CCATCTGGCT TGGCATCGTC  1980
TATGCCTACA AGGGACTTCT CATGTTGTTC GGTTGTTTCT TAGCTTGGGA GACCCGCAAC  2040
GTCAGCATCC CCGCACTCAA CGACAGCAAG TACATCGGGA TGAGTGTCTA CAACGTGGGG  2100
ATCATGTGCA TCATCGGGGC CGCTGTCTCC TTCCTGACCC GGGACCAGCC CAATGTGCAG  2160
TTCTGCATCG TGGCTCTGGT CATCATCTTC TGCAGCACCA TCACCCTCTG CCTGGTATTC  2220
GTGCCGAAGC TCATCACCCT GAGAACAAAC CCAGATGCAG CAACGCAGAA CAGGCGATTC  2280
CAGTTCACTC AGAATCAGAA GAAAGAAGAT TCTAAAACGT CCACCTCGGT CACCAGTGTG  2340
AACCAAGCCA GCACATCCCG CCTGGAGGGC CTACAGTCAG AAAACCATCG CCTGCGAATG  2400
AAGATCACAG AGCTGGATAA AGACTTGGAA GAGGTCACCA TGCAGCTGCA GGACACACCA  2460
GAAAAGACCA CCTACATTAA ACAGAACCAC TACCAAGAGC TCAATGACAT CCTCAACCTG  2520
GGAAACTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATTT TAAAAAATCA CCTCGATCAA  2580
AATCCCCAGC TACAGTGGAA CACAACAGAG CCCTCTCGAA CATGCAAAGA TCCTATAGAA  2640
GATATAAACT CTCCAGAACA CATCCAGCGT CGGCTGTCCC TCCAGCTCCC CATCCTCCAC  2700
CACGCCTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTCAGCCC CTGCGTCAGC  2760
CCCACCGCCA GCCCCCGCCA CAGACATGTG CCACCCTCCT TCCGAGTCAT GGTCTCGGGC  2820
CTGTAA
```

A4 Protein sequence:

Gene name:	G protein-coupled receptor 51
Unigene number:	Hs.198612
Probeset Accession #:	AA452928
Protein Accession #:	NP_005449.1
Signal sequence:	1-42
Pfam domains:	7tm_3 [481-754], ANF_receptor [130-204]
Transmembrane domains:	22-44, 477-499, 517-539, 552-574, 595-617, 653-675, 692-713, 722-744
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MASPRRSGQP GRPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP PSSPPLSIMG.   60
LMPLTKEVAK GSIGRGVLPA VELAIEQIRN ESLLRPYFLD LRLYDTECDN AKGLKAFYDA   120
IKYGPNHLMV FGGVCPSVTS IIAESLQGWN LVQLSFAATT PVLADKKKYP YFFRTVPSDN   180
AVNPAILKLL KHYQWKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV   240
KKLKGNDVRI ILGQFDQNMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS   300
RCLRKNLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQQYER EYNNKRSGVG PSKFHGYAYD   360
GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIIL NAMNETNFFG VTGQVVFRNG   420
ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP   480
LYSILSALTI LGMIMASAFL FFNIKNRNQK LIKMSSPYMN NLIILGGMLS YASIFLFGLD   540
GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKMKKK IIKDQKLLVI   600
VGGMLLIDLC ILICWQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLGIV   660
YAYKGLLMLF GCFLAWETRN VSIPALNDSK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ   720
FCIVALVIIF CSTITLCLVF VPKLITLRTN PDAATQNRRF QFTQNQKKED SKTSTSVTSV   780
NQASTSRLEG LQSENHRLRM KITELDKDLE EVTMQLQDTP EKTTYIKQNH YQELNDILNL   840
GNFTESTDGG KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPILH   900
HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L
```

A5 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.293616
Probeset Accession #: AW043782
Nucleic Acid Accession #: none found
Coding sequence: 38-1075(underlined sequence corresponds to start and stop codon)

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG    60
CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAACAACT TCACCAATGA   120
GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA   180
GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA   240
GTCGAAATGT GGCCCAACCT TCTTCCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG   300
CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC   360
AAACCCTCTG CTTTGCTCCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA   420
GAGCTTCATC TGCGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA   480
AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA   540
TTACCCCAGC ATCACCTATG CCATCATCGG CAGCTCCGTC ATTTTTGTGC TGGTGGTGGC   600
CCTGCTGGCA CTGGTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT   660
GCACCGGCTG CAGCACCCTG TGCTGCTGTC CCGCCTGGTG GTCCTGGACC ACCCCCACCA   720
CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA   780
GAATGCGTCG GAAGTAGGCT CCCCACCCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC   840
TGCGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC   900
CGACCTGCCC CCCTACCGCT CCCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC   960
CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCCAGGA  1020
GGGCACTGCT GAGCCCAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC  1080
AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTTG  1140
TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT  1200
AACTATCTCT GCATTCCCCT CCTCCCCCAG ACTTCAGAGA TGTTTTTCTG GCGTCTCAGT  1260
TGACATGATC TGTTGTGCGT CTTTTCTGTC AGGTCACTCT TCCCTTGGGA CCCGAGATCA  1320
CACCCTCATT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG  1380
AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA  1440
CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG  1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAAATT CCATTTGAGC  1560
ATCAAAACCT GCTTTGCACA ATCCTATTTG ATGCCCCCAG TTCAGCAGAG TCAGTGGCCA  1620
AAGAAAACTT TGGACGTGAG TAACACCCTT CAGCAGTCGC AACGTTATTT TGGTTTTGTG  1680
AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTTG CCCAAGAATG  1740
CTCATTCTGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCCTAA AATAGGCAGG  1800
GAGCCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC  1860
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCACC CTCCCAGCTG  1920
ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT  1980
GTATGTCCCT GTGGCCCACA CCCAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC  2040
CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTTGG ACTTGAGGAC  2100
ACTGGTTTCT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC  2160
CTGCACTGTG CACGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG  2220
GGTCAGGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG  2280
AGACAATTTG GAGTCAAGAT TTTCCATTTG GATCTATTTT AAATCTTTTA GAAATGCATT  2340
TGAAACAGTG TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA  2400
AGCTGTCTCT TTTTTTGTTT TTCCTTTAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC  2460
ACACCCTTGC CCCGCTGAGC CCCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG  2520
ACATTTGTGC ATTGTTGCAC TTTGAGGTTA TTATTTATCA AGTTCTTGAA GGAAGCAGAA  2580
AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT  2640
TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT  2700
AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAAATGGAA CCAGGTAGAG  2760
CCACTCCGGG CAGCTGTCAC CCATTCAGAA CTTCTTTCCG CAGCTGAAGA AATGTTCAGT  2820
AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTCAG  2880
TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA  2940
AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA  3000
AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTTAA AATAGCACTT GAGTTATTTT  3060
CTGAGTAATC CAATAAAGAA CTTTTGATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA  3120
CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC  3180
TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT  3240
GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT  3300
AGATAAGGGA TGCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTTT ATTATAGATT  3360
TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT  3420
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TTTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG  3540
AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT  3600
AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA  3660
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GAAAGGTTGT GTGTCGTTGC TTTTTGTGTT TTGGTTAGGC TTGGTTTTGT TTTTTAATTT  3780
TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAWG GWMCTAMARM  3840
AAMMAAAAAC AWYWTTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTTAACA CCACTTCGGG  3900
TGGGGCGGCG GGGCCCACGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG  3960
GAAACCCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAAA ACGCGCCGGG  4020
GGAAACCGCA GAGTGTTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG  4080
GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G
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A6 Protein sequence:
Gene name: ESTs

Unigene number: Hs.293616
Probeset Accession #: AW043782
Protein Accession #: none found
Signal sequence: 1-17
Transmembrane domains: 169-191
LDLa domains: 28-66, 70-108, 112-149
Cellular Localization: plasma membrane

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MWLLGPLCLL LSSAAESQLL PGNNPTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD    60
EKECPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC   120
KNGLCIDKSF ICDGQNNCQD NSDEESCESS QEPGSGQVFV TSENQLVYYP SITYAIIGSS   180
VIFVLVVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ   240
YVASQAEQNA SEVGSPPSYS EALLDQRPAW YDLPPPPYSS DTESLNQADL PPYRSRSGSA   300
NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV
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A7 DNA SEQUENCE
Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)

Unigene number: Hs.149609
Probeset Accession #: X06256
Nucleic Acid Accession #: NM_002205
Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

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ATGGGGAGCC GGACGCCAGA GTCCCCTCTC CACGCCGTGC AGCTGCGCTG GGGCCCCCGG    60
CGCCGACCCC CGCTSSTGCC GCTGCTGTTG CTGCTSSTGC CGCCGCCACC CAGGGTCGGG   120
GGCTTCAACT TAGACGCGGA GGCCCCAGCA GTACTCTCGG GGCCCCCGGG CTCCTTCTTC   180
GGATTCTCAG TGGAGTTTTA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA   240
CCCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCCT   300
TGGGGTGCCA GCCCCACACA GTGCACCCCC ATTGAATTTG ACAGCAAAGG CTCTCGGCTC   360
CTGGAGTCCT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCCTTGCAG   420
TGGTTCGGGG CAACAGTTCG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC   480
AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA   540
GATAACTTCA CCCGAATTCT GGAGTATGCA CCCTGCCGCT CAGATTTCAG CTGGGCAGCA   600
GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT   660
TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG   720
ATTGCAGAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT   780
CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTTGGTGAA   840
TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAAGGGAA CCTCACTTAC   900
GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACTT CTCAGGGGAA   960
CAGATGGCCT CCTACTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GGACGGGCTG  1020
GATGACTTGC TGGTGGGGGC ACCCCTGCTC ATGGATCGGA CCCCTGACGG GCGGCCTCAG  1080
GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCCACC  1140
CTTACCCTCA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCCTGGGG  1200
GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC  1260
CAGCAGGGAG TAGTGTTTGT ATTTCCTGGG GGCCCAGGAG GGCTGGGCTC TAAGCCTTCC  1320
CAGGTTCTGC AGCCCCTGTG GGCAGCCAGC CACACCCCAG ACTTCTTTGG CTCTGCCCTT  1380
CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCTTTGGT  1440
GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CCGCTAGTGC CTCCCTCACC  1500
ATCTTCCCCG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCCTGTG  1560
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GGTTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA  1680
CTGTTCCTGG CCTCCAGGCA GGCAACCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT  1740
CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA  1800
CTCTCGCCGA TTCACATCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC  1860
CACGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG  1920
ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCCTG ACCTGCAGCT GGAAGTGTTT  1980
GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCCATGCC  2040
CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG  2100
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TTTGCCGTGA ACCAGAGCCG CCTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA  2220
GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC  2280
ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGTT  2340
TCCTTTCGGC TCTCCGTGGA GGCTCAGGCC CAGGTCACCC TGAACGGTGT CTCCAAGCCT  2400
GAGGCAGTGC TATTCCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG  2460
GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT  2520
AGCCAGGGTG TGCTGGAACT CAGCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCCTATAT  2580
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GAGTTGGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAAC GGGAAGCTCC AAGCCGCAGC  2700
TCTGCTTCCT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTTT CAGGCTGCGC  2760
TGTGAGCTCG GGCCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAGTTGCA TTTCCGAGTC  2820
TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG  2880
TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCCTCGGC AGCTGCCCCA AAAAGAGCGT  2940
CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTGG  3000
ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC  3060
TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG  3120
CTCAAGCCTC CAGCCACCTC TGATGCCTGA
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A8 Protein sequence:

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
Unigene number: Hs.149609
Probeset Accession #: X06256
Protein Accession #: NP_002196
Signal sequence: 1-42
Transmembrane domains: 998-1020
Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036
Cellular Localization: plasma membrane

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MGSRTPESPL HAVQLRWGPR RRPPLLPLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF    60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL   120
LESSLSSSEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCYLST   180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ   240
IAESYYPEYL INLVQGQLQT RQASSIYDDS YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY   300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ   360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET   420
QQGVVFVFPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRDLDGNG YPDLIVGSFG   480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI   540
GFTVELQLDW QKQKGGVRRA LFLASRQATL TQTLLIQNGA REDCREMKIY LRNESEFRDK   600
LSPIHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF   660
GEQNHVYLGD KNALNLTFHA QNVGEGGAYE AELRVTAPPE AEYSGLVRHP GNFSSLSCDY   720
FAVNQSRLLV CDLGNPMKAG ASLWGGLRFT VPHLRDTKKT IQFDFQILSK NLNNSQSDVV   780
SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPQKEE DLGPAVHHVY ELINQGPSSI   840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLHH QQKREAPSRS   900
SASSGPQILK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV   960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IIILAILFGL LLLGLLIYIL  1020
YKLGFFKRSL PYGTAMEKAQ LKPPATSDA
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A9 DNA SEQUENCE

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
Unigene number: Hs.287797
Probeset Accession #: X07979
Nucleic Acid Accession #: NM_002211.1
Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

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CAAACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA   120
GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT   180
TCTGCACGAT GTGATGATTT AGAAGCCTTA AAAAAGAAGG GTTGCCCTCC AGATGACATA   240
GAAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAACCAA CCGTAGCAAA   300
GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCACA GCAGTTGGTT   360
TTGCGATTAA GATCAGGGGA GCCACAGACA TTTACATTAA AATTCAAGAG AGCTGAAGAC   420
TATCCCATTG ACCTCTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTTGGAG   480
AATGTAAAAA GTCTTGGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCGGACTTC   540
AGAATTGGAT TTGGCTCATT TGTGGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA   600
GCTAAGCTCA GGAACCCTTG CACAAGTGAA CAGAACTGCA CCAGCCCATT TAGCTACAAA   660
AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTTGG AAAACAGCGC   720
ATATCTGGAA ATTTGGATTC TCCAGAAGGT GGTTTCGATG CCATCATGCA AGTTGCAGTT   780
TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTTTC CACAGATGCC   840
GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAAA TGATGGACAA   900
TGTCACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT   960
CACCTTGTCC AGAAACTGAG TGAAAATAAT ATTCAGACAA TTTTTGCAGT TACTGAAGAA  1020
TTTCAGCCTG TTTACAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA  1080
TCTGCAAATT CTAGCAATGT AATTCAGTTG ATCATTGATG CATACAATTC CCTTTCCTCA  1140
GAAGTCATTT TGGAAAACGG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC  1200
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GACAGCTTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC  1380
ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA  1440
AATGGGACAT TTGAGTGTGG CGCGTGCAGG TGCAATGAAG GGCGTGTGG TAGACATTGT  1500
GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC  1560
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GATAGATCCA ATGGCTTAAT TTGTGGAGGA AATGGTGTTT GCAAGTGTCG TGTGTGTGAG  1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTTCTT TGGATACTAG TACTTGTGAA  1800
GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT  1860
ACAGATCCGA AGTTTCAAGG GCAAACGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT  1920
GCTGAGCATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA  1980
TGCACACAGG AATGTTCCTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC  2040
CAGCCGGTCC AACCTGATCC TGTGTCCCAT TGTAAGGAGA AGGATGTTGA CGACTGTTGG  2100
TTCTATTTTA CGTATTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT  2160
CCAGAGTGTC CCACTGGTCC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAATT  2220
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GTTCTTATTG GCCTTGCATT ACTGCTGATA TGGAAGCTTT TAATGATAAT TCATGACAGA 2280
AGGGAGTTTG CTAAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAT 2340
CCTATTTATA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGGG AAAATGA

A10 Protein sequence:

Gene name:	Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
Unigene number:	Hs.287797
Probeset Accession #:	X07979
Protein Accession #:	NP_002202.1
Signal sequence:	1-21
Transmembrane domains:	732-754
INB domain:	34-464
PSI domain:	26-76
Cellular Localization:	plasma membrane

1 11 21 31 41 51

MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
SARCDDLEAL KKKGCPPDDI ENPRGSKDIK KNKNVTNRSK GTAEKLKPED ITQIQPQQLV 120
LRLRSGEPQT FTLKFKRAED YPIDLYYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180
RIGFGSFVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKGE VFNELVGKQR 240
ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFSTDA GFHFAGDGKL GGIVLPNDGQ 300
CHLENNMYTM SHYYDYPSIA HLVQKLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGTL 360
SANSSNVIQL IIDAYNSLSS EVILENGKLS EGVTISYKSY CKNGVNGTGE NGRKCSNISI 420
GDEVQFEISI TSNKCPKKDS DSFKIRPLGF TEEVEVILQY ICECECQSEG IPESPKCHEG 480
NGTFECGACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVCRK 540
RDNTNEIYSG KFCECDNFNC DRSNGLICGG NGVCKCRVCE CNPNYTGSAC DCSLDTSTCE 600
ASNGQICNGR GICECGVCKC TDPKFQGQTC EMCQTCLGVC AEHKECVQCR AFNKGEKKDT 660
CTQECSYFNI TKVESRDKLP QPVQPDPVSH CKEKDVDDCW FYFTYSVNGN NEVMVHVVEN 720
PECPTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIIHDR REFAKFEKEK MNAKWDTGEN 780
PIYKSAVTTV VNPKYEGK

A11 DNA SEQUENCE

Gene name:	selectin E (endothelial adhesion molecule 1)
Unigene number:	Hs.89546
Probeset Accession #:	M24736
Nucleic Acid Accession #:	NM_000450
Coding sequence:	1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60
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CAGCAAAGGT ACACACACCT GGTTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
TCCATATTGA GCTATTCACC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360
GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
GCTGCCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAT TGTGAACTGT 540
ACAGCCCTGG AATCCCCTGA GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAAACTTC 600
AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
ACCATGCAGT GTATGTCCTC TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCCTGGA 780
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GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
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GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
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GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC 1260
GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCTTCAGC 1380
TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA 1440
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CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
CTTTCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
TGCTTACGGA AAGCAAAGAA ATTTGTTCCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A12 Protein sequence:

Gene name:	Selectin E (endothelial adhesion molecule 1)
Unigene number:	Hs.89546
Probeset Accession #:	M24736
Protein Accession #:	NP_000441
Signal sequence:	1-22
Transmembrane domains:	555-573
C-lectin domain:	23-139

Cellular Localization: plasma membrane

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|          |          |          |          |          |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRYTHLVAI QNKEEIEYLN    60
SILSYSPSYY WIGIRKVNNV WVWVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK   120
DVGMWNDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC   180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV   240
ECDAVTNPAN GFVECFQNPG SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK   300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPAQVECT TQGQWTQQIP   360
VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN   420
EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ   480
WTEEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW   540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRK CLRKAKKFVP ASSCQSLESD   600
GSYQKPSYIL
```

A13 DNA SEQUENCE

Gene name: G protein-coupled receptor 39
Unigene number: Hs.85339
Probeset Accession #: AA349893
Nucleic Acid Accession #: NM_001508
Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC    60
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC   120
TTCGTGATGG GCCTTCTGGG GAACAGCGCC ACCATTCGGG TCACCCAGGT GCTGCAGAAG   180
AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC   240
TTGGTGTTCC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC   300
ACGTCCAGCT ACACCCTGTC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC   360
GCTACGCTGC TGCACGTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC   420
TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG   480
GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCCTG   540
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG   600
CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC   660
CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC   720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC   780
ACGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG   840
ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG   900
ATTCGGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG   960
GCGTACATGA TCCTCCTCCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCATCAAC  1020
CCGCTCCTGT ACACGGTGTC CTCGCAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC  1080
TGCCGCCTGT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC  1140
ACCACCGACA GCGCCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC  1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG  1260
TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC  1320
AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA
```

A14 Protein sequence:

Gene name: G protein-coupled receptor 39
Unigene number: Hs.85339
Probeset Accession #: AA349893
Protein Accession #: NM_001508, NP_001409
Signal sequence: none found
Pfam domains: 7tm_1 [72-172, 224-344]
Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK    60
KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY   120
ATLLHVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL   180
VNVPSHRGLT CNRSSTRHHE QPETSNMSIC TNLSSRWTVF QSSIFGAFVV YLVVLLSVAF   240
MCWNMMQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ   300
IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC   360
CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPQ   420
SKSQSLSLES LEPNSGAKPA NSAAENGFQE HEV
```

AI Prostate

A15 DNA sequence

Gene name: CEGP1
Unigene number: Hs.222399
Probeset Accession #: AA256485
Nucleic Acid Accession #: AJ400877
Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
```

```
GGCGTCCGCG CACACCTCCC CGCGCCGCCG CCGCCACCGC CCGCACTCCG CCGCCTCTGC    60
CCGCAACCGC TGAGCCATCC ATGGGGGTCG CGGGCCGCAA CCGTCCCGGG GCGGCCTGGG   120
CGGTGCTGCT GCTGCTGCTG CTGCTGCCGC CACTGCTGCT GCTGGCGGGG GCCGTCCCGC   180
CGGGTCGGGG CCGTGCCGCG GGGCCGCAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG   240
ATGACTGCCA TGCCGACGCC CTGTGTCAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA   300
AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC   360
TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT   420
TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG   480
AGAACAATGG CGGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGCTGCT   540
GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG   600
GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCCAAGGG   660
GCAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA   720
TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG   780
GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG   840
AGCGAGAGGA CACTGTCCTG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG   900
ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG   960
ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCCTGTT GGATTCACTC  1020
TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT  1080
GTGATCATTT CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAAGGATTTA  1140
AATTATTAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT  1200
GTGACCACAG CTGCATCAAC CACCCTGGCA CATTTGCTTG TGCTTGCAAC CGAGGGTACA  1260
CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT  1320
GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA  1380
AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT  1440
CACCCCGTGT GTCCCTGCAC TGCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT  1500
GTCACTCTGG CATTCACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA  1560
AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTTCCCGAG GGTCTGCGAC  1620
CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT  1680
GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT  1740
TTATCACTGT TGAGTTTGAG CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTTGTGACC  1800
TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA  1860
AGGCCGTCCA CAGCGAGCAG TTTCACCTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA  1920
AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCTG TGGAGTGGGC CAGGGTCATG  1980
CAGAAAACCA ATGTGTCAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT  2040
GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT  2100
GCCCAAGACC AGGAAATTCT GGGGCCCTGA AGACCCCAGA AGCTTGGAAT ATGTCTGAAT  2160
GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGCACCT TGCCAGCTCT  2220
GTGCCCTGGG CACGTTCCAG CCTGAAGCTG GTCGAACTTC CTGCTTCCCC TGTGGAGGAG  2280
GCCTTGCCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT  2340
GTTCACCTGG ACATTTCTAC AACACCACCA CTCACCGATG TATTCGTTGC CCAGTGGGAA  2400
CATACCAGCC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG  2460
ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG  2520
GAGATTTCAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG  2580
AGTGTACGTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATCGTG GTCCCTGAGA  2640
TCTTCCTGCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT  2700
CCAATTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT  2760
CCAGGTCAAA GAAGCTGTGG ATTCAGTTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT  2820
TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCAGGA ACTCATTGAA GACATAGTTC  2880
GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAAACTTA  2940
TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCCAGG  3000
AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT  3060
TTTTGAGACC TTACAAATGA CTCAGCCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG  3120
GGTTGGTGGG ACAGAGCTGT CTTCCTTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCCTC  3180
CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGGTAAATT  3240
GAACTTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT  3300
CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGGACT  3360
TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCCTCC TCAAGGAGTC  3420
TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACTTCAGC TTCCTCTAGC  3480
CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG  3540
CAAGAGGGGA GGGAAGGAGA CCCCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG  3600
ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACTTG  3660
AGTTCTAAGC AGTGCTCGTG AAAAAAAAAA GCAGAAAGAA TTAGAAATAA ATAAAAACTA  3720
AGCACTTCTG GAGACAT
```

A16 Protein sequence

Gene name:	CEGP1
Unigene number:	Hs.222399
Probeset Accession #:	AA256485
Protein Accession #:	CAB92285
Signal sequence:	1-31
Transmembrane domains:	none
PFAM domains:	EGF-like_domains [49-84,132-167,177-213,286-321,407-442] CUB_domain [809-918]
Cellular Localization:	may be secreted

```
1          11         21         31         41         51
MGVAGRNRPG AAWAVLLLLL LLPPLLLLAG AVPPGRGRAA GPQEDVDECA QGLDDCHADA    60
LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNYR CTCFDGFMLA   120
HDGHNCLDVD ECLENNGGCQ HTCVNVMGSY ECCCKEGFFL SDNQHTCIHR SEEGLSCMNK   180
DHGCSHICKE APRGSVACEC RPGFELAKNQ RDCILTCNHG NGGCQHSCDD TADGPECSCH   240
PQYKMHTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCDRTCKDT   300
```

```
STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK   360
SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQQVCVN   420
TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL   480
SSDVTTIRTS VTFKLNEGKC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGKQV   540
PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ   600
FHLQLSGMNL DVAKKPPRTS ERQAESCGVG QGHAENQCVS CRAGTYYDGA RERCILCPNG   660
TFQNEEGQMT CEPCPRPGNS GALKTPEAWN MSECGGLCQP GEYSADGFAP CQLCALGTFQ   720
PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYQPEFG   780
KNNCVSCPGN TTTDFDGSTN ITQCKNRRCG GELGDFTGYI ESPNYPGNYP ANTECTWTIN   840
PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSSNSVTTY ETCQTYERPI AFTSRSKKLW   900
IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLIKALFDV   960
LAHPQNYFKY TAQESREMFP RSFIRLLRSK VSRFLRPYK
```

A17 DNA sequence

Gene name:	ESTs
Unigene number:	Hs.293102
Probeset Accession #:	AI951118, AW170035, AL044891, AI908272
Nucleic Acid Accession #:	none found
Coding sequence:	1-489 (entire sequence is an open-reading-frame)

```
1          11         21         31         41         51
|          |          |          |          |          |
CAAAAAGAAA TAGATAAAAT AAATGGAAAA TTAGAAGAGT CTCCTGATAA TGATGGTTTT    60
CTGAAGGCTC CCTGCAGAAT GAAAGTTTCT ATTCCAACTA AAGCCTTAGA ATTGATGGAC   120
ATGCAAACTT TCAAAGCAGA GCCTCCCCAG AAGCCATCTG CCTTCGAGCC TGCCATTGAA   180
ATGCAAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA   240
GATCAGATGT TCCCTTCAGA ATCAAAACAA AAGAASGTTG AAGAAAATTC TTGGGATTCT   300
GAGAGTCTCC GTGAGACTGT TTCACAGAAG GATGTGTGTG TACCCAAGGC TACACATCAA   360
AAAGAAATGG ATAAAATAAG TGGAAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG   420
GATACAGTTC ATTCTTGTGA AAGAACAAGG GAACTTCAAA AAGACCCCTG TGACCCACGT   480
TCAGGAAAA
```

A18 Protein sequence

Gene name:	ESTs
Unigene number:	Hs.293102
Probeset Accession #:	AI951118, AW170035, AL044891, AI908272
Protein Accession #:	none found
Signal sequence:	none
Transmembrane domains:	none
Cellular Localization:	nuclear

```
1          11         21         31         41         51
|          |          |          |          |          |
QKEIDKINGK LEESPDNDGF LKAPCRMKVS IPTKALELMD MQTFKAEPPE KPSAFEPAIE    60
MQKSVPNKAL ELKNEQTLRA DQMFPSESKQ KXVEENSWDS ESLRETVSQK DVCVPKATHQ   120
KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDPCDPR SGK
```

Breast

A19 DNA SEQUENCE

Gene name:	TMPRSS3a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Nucleic Acid Accession #:	AB038157
Coding sequence:	202-1566 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTCATGCCC GTGTGAGCCA    60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG   120
CCATCTACAT TTTTGGGACT CGGGAATTAT GACGTAGAGG TGGAGGCGGA GCCGGATGTC   180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC   240
TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA   300
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC   360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC   420
TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC   480
GGAGTCTCGG ATTGCAAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG   540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCATGTGCTC CGATGACTGG   600
AAGGGTCACT ACGCAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA   660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT   720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA   780
TGTGCCTCTG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC   840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC   900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCT GTGGATCATC   960
ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT  1020
CTAGTTTCCC TGTTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC  1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA  1140
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC  1200
GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC  1260
TCCCCTGTCC TGAACCACGC GGCCGTCCCT TTGATTTCCA ACAAGATCTG CAACCACAGG  1320
GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC  1380
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GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG  1440
AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG  1500
TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA  1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA  1620
TCCTCCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCTTG GAGCTCTGAG  1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT  1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG  1800
AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC  1860
TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT  1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA  1980
CCTCAAATGA TGTGCCTGCT TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC  2040
ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA  2100
AGGGCGGCCT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG  2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC  2220
GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCAGAA  2280
CCAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA  2340
ATGACTCGTT TAAGGCCTAT TTTCATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA  2400
TTGTCCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA  2460
AAAAAAAA
```

A20 Protein sequence:

Gene name:	TMPRSS3a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Protein Accession #:	BAB20077
Signal sequence:	none found
Transmembrane domains:	43-65, 239-261
Tryp_SPc domain:	216-444
Cellular Localization:	not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI    60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF   120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK   180
VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH   240
LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR   300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVLNHA   360
AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSCQGD SGGPLVCQER RLWKLVGATS   420
FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT
```

A21 DNA SEQUENCE

Gene name:	ESTs; opposite strand to TRPS1
Unigene number:	none
Probeset Accession #:	AA428090
Nucleic Acid Accession #:	AA428090

Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAAT AGACCAAAGG    60
CAAGTTGTTG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC   120
TTTTCAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAACCGT   180
GATTCTGTTG GGCTTCCTGG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA   240
GGAAAAACAA CTAACCTCAG CCATTTGCCC AATTTCCACC TTGCTAGTTA TCAGAGTTCA   300
CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGGAATT TATTCTGAGC   360
AAGTGTTTTG TTCAGCTTGC AGTATTAAAA CAAAAAAAAC ATTGCCTCCA GCTGCAAAGC   420
AAGGGCATTG CCATTATGAA AGCCCCTCAA AGACTCTCTG CTATTTTCAA AACATGGAAA   480
GAAAAAGGGA AAAAAGAAAA AAAAATAATA ATTAGAAGGA TTTGTTCCTT AATTTGGGCT   540
CCCAAAAATG AGAAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAAACTCTC   600
CAAGCAAATC TTCTGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTTGTATT   660
TTTCCTTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCTTTCCT ATCTGGATCT   720
GTTCTGCCTC ATTTCTCTTT CAAAGTCATC TTTCAGGGAA CTTGCCCTGA TTAATTTGAT   780
TTTAACCAAA CAAATAAGAT ATTTGATATA TTAATTTAAA CTTTTTGAGA TGATTGATTA   840
GGAATTGCAT CATGTTCACA TGAGTATACC GAATTCAAAG TTAAACTTCA TAAGCAGGAG   900
TTTTTACACA TCGTAACATA ATCATTACCC AATACTCGAC ACTCAATATT TGATACTCAA   960
CTGAATGTTT TTGAAATAAA CACATTTTTA TGTTATCTCT CTGGAGAAAG TAGTATATAT  1020
CTTTTTACAC AAAATATATC AGTGAGAGAG TGTTTGTTTA AGAAAAAAAA TCAAAGCACA  1080
ACAAGTTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTTTAGA ATGGTGATTT  1140
GATTTCACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA  1200
TATATATATA TATATATATA TATATTACAA TGATCTGTAT TTCCTATTGC TAGAAGGATG  1260
AAAGTGAATC CATATAAACC ATACCAACGC CGTTATGTGT AACTGGTGGT AAAACTTTAT  1320
TATTCAAGTT TAGATGTAAC AGACATCTTT GCTGCCTGAA GATTGTTTGC ATAAGAAATA  1380
CACCAAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAAAACAAA ATAAAATAAA  1440
ACGAAAAAAT TTCATGTGTT GTAAGAACAG AACTATTATA GCCAACATTC TAGTATTCAA  1500
ATCAGGACTA CAAATTGAAT TCTTTTTCTT AGCAACATGA AATCATTCCA TATGAAAGAC  1560
ATTTTCTGCT GGTGAATATT GCTGTAAGTT AAATTTTACA TTGGCATTTT GAGATGTTCC  1620
CCCCTCATGC CTCCCCCAAA GTTTTCCATG TGGTTGTCAA ATAGTCCGC
```

A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1
Unigene number: none
Probeset Accession #: AA428090
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 113-129
Cellular Localization: not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MKPSLKHWAD IKMFSEIDQR QVVGEEIHLQ VVSVSYLVEN FSDTDDLMSI VEESDSCYNR    60
DSVGLPGRAG DRLQPKTKPR GKTTNLSHLP NFHLASYQSS LLFKLQGSYY GNLLVEFILS   120
KCFVQLAVLK QKKHCLQLQS KGIAIMKAPQ RLSAIFKTWK EKGKKEKKII IRRICSLIWA   180
PKNEK
```

A23 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.29383
Probeset Accession #: AW207206
Nucleic Acid Accession #: AL133619
Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCCA GCTCGCCGAC CCCGGGCTCT    60
CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG   120
CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG   180
CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG   240
GAAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCTCCCCA GGCACACTCA   300
ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA   360
GGGGGAACAC AGGACGGGGA GCCCCTCCAG ACTGTCCTTG CCCACCTGGC TGCACTGGCC   420
CCTGTATGCC AACCCAGTGG GTACAGGTTC TGGGGGACCT GGACAGATGC CGCTACCTCT   480
AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCACG TGCTGCTCTC GGGAAGCCCA   540
GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT   600
CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG   660
CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCCTCAC   720
ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG   780
GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCCTGT TTCCTTGCCA CTTGTCCAAG   840
GCACTTCCCC ATCCTGACAG CGGCCCCCAC CCAGCCCAGG ATCCTGGGCT GTGGTCTCAA   900
GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA   960
TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCCAGGGA  1020
GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG  1080
CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCAGTGC TGGGGACGCT  1140
GACAGGACAC GGGAAGAGGC CATGCTTTCC CTCGGGACCT GCTGTTCCAT GTGTCCCAAG  1200
CCCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG  1260
GGCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC  1320
AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGCG  1380
GGCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG  1440
TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC  1500
TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCCAGA AGGCGGACCT GGAAGAGGAG  1560
CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCCTGGGG TACAAGGGCA GGCCAGAAAG  1620
GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC  1680
AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCCTGC CCCTTCCCCT GCGAAAGCCC  1740
ACCACACTTA GGCAGTGCGA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCAG  1800
ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC  1860
CCGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCCAA GGTCTCCACC  1920
AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA  1980
CTGAAGCAGA CCCCGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG  2040
AAACGGCGCC TGCATCGCTC AGTGCTTTGA
```

A24 Protein sequence:

Gene name: ESTs
Unigene number: Hs.29383
Probeset Accession #: AW207206
Protein Accession #: T43457
Signal sequence: none found
Transmembrane domains: 303-322
Cellular Localization: not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL    60
QQQHSEMLAK LHEEIEHLKR ENKGEPARGP RPALPPQAHS TLPLPQHRNT AINSSTRLGS   120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAATS SRGWTMLCSQ AQHVLLSGSP   180
GPEVIAGRQV ATGCSPDLPP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH   240
MLGAQGIWTH SIQGSLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSGPH PAQDPGLWSQ   300
AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVEGGP FPSRCGNSSE   360
LFWAKCGPSR QPQPCSAGDA DRTREEAMLS LGTCCSMCPK PSCFPDGPSG NHLSRASAPL   420
GARWVCINGV WVEPGGPSPA RLKEGSSRTH RPGGKRGRLA GGSADTVRSP ADSLSMSSFQ   480
SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGQARK   540
```

```
EKAEASNAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ   600
TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA   660
LKQTPKNNFA ERQKRLQAMQ KRRLHRSVL
```

A25 DNA SEQUENCE

Gene name: ESTs; prolactin receptor
Unigene number: Hs.25252
Probeset Accession #: AA057193
Nucleic Acid Accession #: NM_000949
Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GGAGGCTGAA ATCCCCAGAC GCCGGTTTTC TGGGCTGGGC TTTCTGCTTA CTCACTCCTT    60
CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTTCCACACA ATGGAGCTTC   120
ATGTCCTCGT GCAGGAAGTA CTCATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC   180
TAAAGAACTC TCCTATTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCCTGAA   240
GTGAACTTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG   300
CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT   360
TACCTCCTGG AAAACCTGAG ATCTTTAAAT GTCGTTCTCC CAATAAGGAA ACATTCACCT   420
GCTGGTGGAG GCCTGGGACA GATGGAGGAC TTCCTACCAA TTATTCACTG ACTTACCACA   480
GGGAAGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCAACTCCT   540
GCCACTTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA   600
CTAACCAGAT GGGAAGCAGT TTCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC   660
AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAAACA GCCAGAAGAC AGAAAACCCT   720
ACCTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAACTGGT TGGTTCACGC   780
TCCTGTATGA AATTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG   840
GGCAGCAAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG   900
TTCGCTGCAA ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTCAGA   960
TACCTAGTGA CTTCACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCTTTCTG  1020
CTGTCATCTG TTTGATTATT GTCTGGGCAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT  1080
GCATCTTTCC GCCAGTTCCT GGGCCAAAAA TAAAAGGATT TGATGCTCAT CTGTTGGAGA  1140
AGGGCAAGTC TGAAGAACTA CTGAGTGCCT TGGGATGCCA AGACTTTCCT CCCACTTCTG  1200
ACTATGAGGA CTTGCTGGTG GAGTATTTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA  1260
TGTCAGTCCA TTCAAAAGAA CACCCAAGTC AAGGTATGAA ACCCACATAC CTGGATCCTG  1320
ACACTGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCCT TTTGTCTGAA AAGTGTGAGG  1380
AACCCCAGGC CAATCCCTCC ACATTCTATG ATCCTGAGGT CATTGAGAAG CCAGAGAATC  1440
CTGAAACAAC CCACACCTGG GACCCCCAGT GCATAAGCAT GGAAGGCAAA ATCCCCTATT  1500
TTCATGCTGG TGGATCCAAA TGTTCAACAT GGCCCTTACC ACAGCCCAGC CAGCACAACC  1560
CCAGATCCTC TTACCACAAT ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG  1620
CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA  1680
AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTCTGAGA  1740
CTGACCAGGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC  1800
CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAAGATGG TGCATTATCA TTGCTACCAA  1860
AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT  1920
ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGGTGCCA GATCCACATG  1980
CTAAAAACGT GGCTTGCTTT GAAGAATCAG CCAAAGAGGC CCCACCATCA CTTGAACAGA  2040
ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC  2100
TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCCTTTCAC TGATAGCTTG  2160
ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTACGTGA  2220
AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGCTCCA  2280
TTTTTAACCA CTTGCCTCTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCCT  2340
AACTGTGATT TGTAGATTTA CTTTTTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT  2400
AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAG  2460
GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATTGT TTACCATAGA  2520
AAGATGACAA AAGAAAATTT TCCACATAGG AAAATGCCAT GAAAATTGCT TTTGAAAAAC  2580
AACTGCATAA CCTTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT  2640
AAAGAAAGAA TGCATTCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA  2700
TTGCTGATAT GCAAGTAAGA AAT
```

A26 Protein sequence:

Gene name: ESTs; prolactin receptor
Unigene number: Hs.25252
Probeset Accession #: AA057193
Protein Accession #: NP_000940
Signal sequence: 1-23
Transmembrane domains: 237-253
FN3 domains: 28-112, 127-215
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MKENVASATV FTLLLFLNTC LLNGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGGLPTNY    60
SLTYHREGET LMHECPDYIT GGPNSCHFGK QYTSMWRTYI MMVNATNQMG SSFSDELYVD   120
VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW   180
EIHFAGQQTE FKILSLHPGQ KYLVQVRCKP DHGYWSAWSP ATFIQIPSDF TMNDTTVWIS   240
VAVLSAVICL IIVWAVALKG YSMVTCIFPP VPGPKIKGFD AHLLEKGKSE ELLSALGCQD   300
FPPTSDYEDL LVEYLEVDDS EDQHLMSVHS KEHPSQGMKP TYLDPDTDSG RGSCDSPSLL   360
SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDPQCISME GKIPYFHAGG SKCSIWPLPQ   420
```

```
PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQREVE   480
SFHSETDQDT PWLLPQEKTP FGSAKPLDYV EIHKVNKDGA LSLLPKQREN SGKPKKPGTP   540
ENNKEYAKVS GVMDNNILVL VPDPHAKNVA CFEESAKEAP PSLEQNQAEK ALANFTATSS   600
KCRLQLGGLD YLDPACFTHS FH
```

A27 DNA SEQUENCE

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)
Unigene number: Hs.169266
Probeset Accession #: L07615
Nucleic Acid Accession #: NM_000909.1
Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT    60
GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATTC CAATATCGGG   120
AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTTGTCTAAA   180
ATAATCTATA ACAACCAAAC CAATCAAAAT GAATTCAACA TTATTTTCCC AGGTTGAAAA   240
TCATTCAGTC CACTCTAATT TCTCAGAGAA GAATGCCCAG CTTCTGGCTT TTGAAAATGA   300
TGATTGTCAT CTGCCCTTGG CCATGATATT TACCTTAGCT CTTGCTTATG GAGCTGTGAT   360
CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAAC AAAAGGAGAT   420
GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT   480
CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC   540
GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTTCAATC ACTGTGTCCA TTTTCTCTCT   600
GGTTCTCATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA   660
TAATAGACAT GCTTATGTAG GTATTGCTGT GATTTGGGTC CTTGCTGTGG CTTCTTCTTT   720
GCCTTTCCTG ATCTACCAAG TAATGACTGA TGAGCCGTTC CAAAATGTAA CACTTGATGC   780
GTACAAAGAC AAATACGTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTTGTCTTA   840
TACCACTCTC CTCTTGGTGC TGCAGTATTT TGGTCCACTT TGTTTTATAT TTATTTGCTA   900
CTTCAAGATA TATATACGCC TAAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA   960
TAAGTACAGG TCCAGTGAAA CCAAAAGAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC  1020
ATTTGCAGTC TGCTGGCTCC CTCTTACCAT CTTTAACACT GTGTTTGATT GGAATCATCA  1080
GATCATTGCT ACCTGCAACC ACAATCTGTT ATTCCTGCTC TGCCACCTCA CAGCAATGAT  1140
ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCCTGAAC AAAAACTTCC AGAGAGACTT  1200
GCAGTTCTTC TTCAACTTTT GTGATTTCCG GTCTCGGGAT GATGATTATG AAACAATAGC  1260
CATGTCCACG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC  1320
ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT  1380
GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT  1440
TCTCCCAAGG AATGGGGTTG AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT  1500
TTACTGCTTT TGTTGTAGTT GTCATAATTA CATTTGGAAC AAAAGGTGTG GGCTTTGGGG  1560
TCTTCTGGAA ATAGTTTTGA CCAGACATCT TTGAAGTGCT TTTTGTGAAT TTATGCATAT  1620
AATATAAAGA CTTTTATACT GTACTTATTG GAATGAAATT TCTTTAAAGT ATTACGATGC  1680
GCTGACTTCA GAAGTACCTG CCATCCAATA CGGTCATTAG ATTGGGTCAT CTTGATTAGA  1740
TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT  1800
TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT  1860
GAAGTCATTC AGAAGTGGTT TGAGGTTTCT GTTTTTTGGT GGTTTTTGTT TGTTTTTTTT  1920
TTTTTTCACC TTAAGGGAGG CTTTCATTTC CTCCCGACTG ATTGTCACTT AAATCAAAAT  1980
TTAAAAATGA ATAAAAAGAC ATACTTCTCA GCTGCAAATA TTATGGAGAA TTGGGCACCC  2040
ACAGGAATGA AGAGAGAAAG CAGCTCCCCA ACTTCAAAAC CATTTTGGTA CCTGACAACA  2100
AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT  2160
TATATTTATT TGAATTGATG GTCAAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAGTGT  2220
TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC  2280
ACAAATATCG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAAC TTTCAATGTC  2340
CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTCAC TTTACCTAGC  2400
AGGGAAAAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAACT  2460
GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TTACTGAATA GTTGTGTCAT  2520
GTTAATGTGC CTAATTTCAT GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTTGGAG  2580
AAACTATATT TTAAAGAACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG  2640
TGTTTGATTT TAAAAGGGCG GACATTTTAT TAAAATCAAT ATTGTTTTTG CTTTTTCTGA  2700
GGAGTCTCTT TCAGTTTCAT TTTTTCTCAT CCCATGACTT CCCTCCGATG GT
```

A28 Protein sequence:

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds
Unigene number: Hs.169266
Probeset Accession #: L07615
Protein Accession #: NP_000900.1
Signal sequence: none found
Pfam domains: 7tm_1 [57-91]
Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286, 300-322
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MNSTLFSQVE NHSVHSNFSE KNAQLLAFEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA    60
LIIIILKQKE MRNVTNILIV NLSFSDLLVA IMCLPFTFVY TLMDHWVFGE AMCKLNPFVQ   120
CVSITVSIFS LVLIAVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT   180
DEPFQNVTLD AYKDKYVCFD QFPSDSHRLS YTTLLLVLQY FGPLCFIFIC YFKIYIRLKR   240
RNNMMDKMRD NKYRSSETKR INIMLLSIVV AFAVCWLPLT IFNTVFDWNH QIIATCNHNL   300
LFLLCHLTAM ISTCVNPIFY GFLNKNFQRD LQFFFNFCDP RSRDDDYETI AMSTMHTDVS   360
```

KTSLKQASPV AFKKINNNDD NEKI

A29 DNA SEQUENCE
Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)
Unigene number: Hs.208229
Probeset Accession #: AI819198
Nucleic Acid Accession #: NM_032551.1
Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCGGC CAACGCCTCC    60
GGCTGCCCGG GCTGTGGCGC CAACGCCTCG GACGGCCCAG TCCCTTCGCC GCGGGCCGTG   120
GACGCCTGGC TCGTGCCGCT CTTCTTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC   180
TCGCTGGTCA TCTACGTCAT CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC   240
ATCGCCAACC TGGCGGCCAC GGACGTGACC TTCCTCCTGT GCTGCGTCCC CTTCACGGCC   300
CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GGCGACTTCA TGTGCAAGTT CGTCAACTAC   360
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC   420
TGGTACGTGA CGGTGTTCCC GTTGCGCGCC CTGCACCGCC GCACGCCCCG CCTGGCGCTG   480
GCTGTCAGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTCGCCCTG   540
CACCGCCTGT CACCCGGGCC GCGCGCCTAC TGCAGTGAGG CCTTCCCCAG CCGCGCCCTG   600
GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC   660
TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCCGGG TCGCCGTGCG CCCCGCGCCC   720
GCCGATAGCG CCCTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAAG   780
GTCTCGCGGC TGGTGGCGGC CGTGGTCCTG CTCTTCGCCG CCTGCTGGGG CCCCATCCAG   840
CTGTTCCTGG TGCTGCAGGC GCTGGGCCCC GCGGGCTCCT GGCACCCACG CAGCTACGCC   900
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCCTACA GCAACTCCGC GCTGAACCCG   960
CTGCTCTACG CCTTCCTGGG CTCGCACTTC CGACAGGCCT TCCGCCGCGT CTGCCCCTGC  1020
GCGCCGCGCC GCCCCCGCCG CCCCCGCCGG CCCGGACCCT CGGACCCCGC AGCCCCACAC  1080
GCGGAGCTGC ACCGCCTGGG GTCCCACCCG GCCCCCGCCA GGGCGCAGAA GCCAGGGAGC  1140
AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA
```

A30 Protein sequence
Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA
Unigene number: Hs.208229
Protein Accession #: AI819198
Signal sequence: none found
Pfam domains: 7tm_1 [59-323]
Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSPRAV DAWLVPLFFA ALMLLGLVGN    60
SLVIYVICRH KPMRTVTNFY IANLAATDVT FLLCCVPFTA LLYPLPGWVL GDFMCKFVNY   120
IQQVSVQATC ATLTAMSVDR WYVTVFPLRA LHRRTPRLAL AVSLSIWVGS AAVSAPVLAL   180
HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP   240
ADSALQGQVL AERAGAVRAK VSRLVAAVVL LFAACWGPIQ LFLVLQALGP AGSWHPRSYA   300
AYALKTWAHC MSYSNSALNP LLYAFLGSHF RQAFRRVCPC APRRPRRPRR PGPSDPAAPH   360
AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL
```

A31 DNA SEQUENCE
Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)
Unigene number: Hs.252387
Probeset Accession #: NM_014246
Nucleic Acid Accession #: NM_014246
Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCGCCGC CGCCGCCGCC CGTGCTGCCC GTGCTGCTGC TCCTGGCCGC CGCCGCCGCC    60
CTGCCGGCGA TGGGGCTGCG AGCGGCCGCC TGGGAGCCGC GCGTACCCGG CGGGACCCGC   120
GCCTTCGCCC TCCGGCCCGG CTGTACCTAC GCGGTGGGCG CCGCTTGCAC GCCCCGGGCG   180
CCGCGGGAGC TGCTGGACGT GGGCCGCGAT GGGCGGCTGG CAGGACGTCG GCGCGTCTCG   240
GGCGCGGGGC GCCCGCTGCC GCTGCAAGTC CGCTTGGTGG CCCGCAGTGC CCCGACGGCG   300
CTGAGCCGCC GCCTGCGGGC GCGCACGCAC CTTCCCGGCT GCGGAGCCCG TGCCCGGCTC   360
TGCGGAACCG GTGCCCGGCT CTGCGGGGCG CTCTGCTTCC CCGTCCCCGG CGGCTGCGCG   420
GCCGCGCAGC ATTCGGCGCT CGCAGCTCCG ACCACCTTAC CCGCCTGCCG CTGCCCGCCG   480
CGCCCCAGGC CCCGCTGTCC CGGCCGTCCC ATCTGCCTGC CGCCGGGCGG CTCGGTCCGC   540
CTGCGTCTGC TGTGCGCCCT GCGGCGCGCG GCTGGCGCCG TCCGGGTGGG ACTGGCGCTG   600
GAGGCCGCCA CCGCGGGGAC GCCCTCCGCG TCGCCATCCC CATCGCCGCC CCTGCCGCCG   660
AACTTGCCCG AAGCCCGGGC GGGGCCGGCG CGACGGGCCC GGCGGGGCAC GAGCGGCAGA   720
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A32 Protein Sequence

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1),
Unigene number: Hs.252387
Protein Accession #: NP_055061
Signal sequence: 1-20
Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092, 1110-1199
Pfam domains: Laminin_EGF [2003-2048], 7tm_2 [2465-2708]
Latrophilin/GPS domains: 2407-2460
Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704
Cellular Localization: plasma membrane

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ASSHSSDSED DGVGAEEKWD PARGAVHSTP KGDAVANHVP AGWPDQSLAE SDSEDPSGKP  2880
RLKVETKVSV ELHREEQGSH RGEYPPDQES GGAARLASSQ PPEQRKGILK NKVTYPPPLT  2940
LTEQTLKGRL REKLADCEQS PTSSRTSSLG SGGPDCAITV KSPGREPGRD HLNGVAMNVR  3000
TGSAQADGSD SEKP
```

A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
Unigene number: Hs.198252
Probeset Accession #: X95876
Nucleic Acid Accession #: X95876
Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CCAACCACAA GCACCAAAGC AGAGGGGCAG GCAGCACACC ACCCAGCAGC CAGAGCACCA    60
GCCCAGCCAT GGTCCTTGAG GTGAGTGACC ACCAAGTGCT AAATGACGCC GAGGTTGCCG   120
```

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CCCTCCTGGA GAACTTCAGC TCTTCCTATG ACTATGGAGA AAACGAGAGT GACTCGTGCT   180
GTACCTCCCC GCCCTGCCCA CAGGACTTCA GCCTGAACTT CGACCGGGCC TTCCTGCCAG   240
CCCTCTACAG CCTCCTCTTT CTGCTGGGGC TGCTGGGCAA CGGCGCGGTG GCAGCCGTGC   300
TGCTGAGCCG GCGGACAGCC CTGAGCAGCA CCGACACCTT CCTGCTCCAC CTAGCTGTAG   360
CAGACACGCT GCTGGTGCTG ACACTGCCGC TCTGGGCAGT GGACGCTGCC GTCCAGTGGG   420
TCTTTGGCTC TGGCCTCTGC AAAGTGGCAG GTGCCCTCTT CAACATCAAC TTCTACGCAG   480
GAGCCCTCCT GCTGGCCTGC ATCAGCTTTG ACCGCTACCT GAACATAGTT CATGCCACCC   540
AGCTCTACCG CCGGGGGCCC CCGGCCCGCG TGACCCTCAC CTGCCTGGCT GTCTGGGGGC   600
TCTGCCTGCT TTTCGCCCTC CCAGACTTCA TCTTCCTGTC GGCCCACCAC GACGAGCGCC   660
TCAACGCCAC CCACTGCCAA TACAACTTCC CACAGGTGGG CCGCACGGCT CTGCGGGTGC   720
TGCAGCTGGT GGCTGGCTTT CTGCTGCCCC TGCTGGTCAT GGCCTACTGC TATGCCCACA   780
TCCTGGCCGT GCTGCTGGTT TCCAGGGGCC AGCGGCGCCT GCGGGCCATG CGGCTGGTGG   840
TGGTGGTCGT GGTGGCCTTT GCCCTCTGCT GGACCCCCTA TCACCTGGTG GTGCTGGTGG   900
ACATCCTCAT GGACCTGGGC GCTTTGGCCC GCAACTGTGG CCGAGAAAGC AGGGTAGACG   960
TGGCCAAGTC GGTCACCTCA GGCCTGGGCT ACATGCACTG CTGCCTCAAC CCGCTGCTCT  1020
ATGCCTTTGT AGGGGTCAAG TTCCGGGAGC GGATGTGGAT GCTGCTCTTG CGCCTGGGCT  1080
GCCCCAACCA GAGAGGGCTC CAGAGGCAGC CATCGTCTTC CCGCCGGGAT TCATCCTGGT  1140
CTGAGACCTC AGAGGCCTCC TACTCGGGCT TGTGAGGCCG GAATCCGGGC TCCCCTTTCG  1200
CCCACAGTCT GACTTCCCCG CATTCCAGGC TCCTCCCTCC CTCTGCCGGC TCTGGCTCTC  1260
CCCAATATCC TCGCTCCCGG GACTCACTGG CAGCCCCAGC ACCACCAGGT CTCCCGGGAA  1320
GCCACCCTCC CAGCTCTGAG GACTGCACCA TTGCTGCTCC TTAGCTGCCA AGCCCCATCC  1380
TGCCGCCCGA GGTGGCTGCC TGGAGCCCCA CTGCCCTTCT CATTTGGAAA CTAAAACTTC  1440
ATCTTCCCCA AGTGCGGGGA GTACAAGGCA TGGCGTAGAG GGTGCTGCCC CATGAAGCCA  1500
CAGCCCAGGC CTCCAGCTCA GCAGTGACTG TGGCCATGGT CCCCAAGACC TCTATATTTG  1560
CTCTTTTATT TTTATGTCTA AAATCCTGCT TAAAACTTTT CAATAAACAA GATCGTCAGG  1620
ACCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA BHCLITERAT  1680
UREBHCBLAS TPBHCORTHO LOGUESMOUS ECXCRMYLEV SERQVLDASD FAFLLENSTS  1740
PYDYGENESD FSDSPPCPQD FSLNFDRTFL PALYSLLFLL GLLGNGAVAA VLLSQRTALS  1800
STDTFLLHLA VADVLLVLTL PLWAVDAAVQ WVFGPGLCKV AGALFNINFY AGAFLLACIS  1860
FDRYLSIVHA TQIYRRDPRV RVALTCIVVW GLCLLFALPD FIYLSANYDQ RLNATHCQYN  1920
FPQVGRTALR VLQLVAGFLL PLLVMAYCYA HILAVLLVSR GQRRFRAMRL VVVVVAAFAV  1980
CWTPYHLVVL VDILMDVGVL ARNCGRESHV DVAKSVTSGM GYMHCCLNPL LYAFVGVKFR  2040
EQMWMLFTRL GRSDQRGPQR QPSSSRRESS WSETTEASYL GL
```

A34 Protein sequence

Gene name:	CXCR3(G protein-coupled receptor 9);chemokine(C-X-C) receptor 3
Unigene number:	Hs.198252
Protein Accession #:	P49682
Signal sequence:	none found
Pfam domains:	7tm_1 [70-318]
Transmembrane domains:	57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323
DRY box:	148-149
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MVLEVSDHQV LNDAEVAALL ENFSSSYDYG ENESDSCCTS PPCPQDFSLN FDRAFLPALY    60
SLLFLLGLLG NGAVAAVLLS RRTALSSTDT FLLHLAVADT LLVLTLPLWA VDAAVQWVFG   120
SGLCKVAGAL FNINFYAGAL LLACISFDRY LNIVHATQLY RRGPPARVTL TCLAVWGLCL   180
LFALPDFIFL SAHHDERLNA THCQYNFPQV GRTALRVLQL VAGFLLPLLV MAYCYAHILA   240
VLLVSRGQRR LRAMRLVVVV VVAFALCWTP YHLVVLVDIL MDLGALARNC GRESRVDVAK   300
SVTSGLGYMH CCLNPLLYAF VGVKFRERMW MLLLRLGCPN QRGLQRQPSS SRRDSSWSET   360
SEASYSGL
```

A35 DNA SEQUENCE

Gene name:	Differentially expressed CO16 gene (clone MGC:5257)
Unigene number:	Hs.69517
Probeset Accession #:	AA447522
Nucleic Acid Accession #:	BC001291
Coding sequence:	44-541 (start and stop codons are underlined)

```
1          11         21         31         41         51
|          |          |          |          |          |
GGGGGCGCCG CGCGCTGACC CTCCCTGGGC ACCGCTGGGG ACGATGGCGC TGCTCGCCTT    60
GCTGCTGGTC GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG   120
AGATCCAGAG GACTCCCAGC GAACGGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG   180
TGAGAGAGAA AACACTTTCG AGTGCCAGAA CCCAAGGAGG TGCAAATGGA CAGAGCCATA   240
CTGCGTTATA GCGGCCGTGA AAATATTTCC ACGTTTTTTC ATGGTTGCGA AGCAGTGCTC   300
CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA   360
GCCCATGCCC TTCTTTTACC TCAAGTGTTG TAAAATTCGC TACTGCAATT TAGAGGGGCC   420
ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG   480
GCTGTGGCTG GCCATCCTCC TGCTGCTGGC CTCCATTGCA GCCGGCCTCA GCCTGTCTTG   540
AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC   600
ACCTGTTGCA TTAAACTTGT TTTCTGTTGA TTACCTCTTG GTTTGACTTC CCAGGGTCTT   660
GGGATGGGAG AGTGGGGATC AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC   720
ACATTCAGAG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTTG   780
AAATCAAACC TTGTAACTCA TTTATTGCTG ATGGCCACTC TTTTCCTTGA CTCCCCTCTG   840
CCTCTGAGGG CTTCAGTATT GATGGGGAGG GAGGCCTAAG TACCACTCAT GGAGAGTATG   900
TGCTGAGATG CTTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG   960
GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCAGTGG GGCACACGTT  1020
AGGGCTGCCC CCATTCCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTC  1080
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CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAAACTTA GACTTCACCC  1140
ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCCACAC GTGTGTGTTC AACATCTGAA  1200
ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC  1260
CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAACAAAT ACAAGGGGAC  1320
TTCAAAAGTT CACGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA
```

A36 Protein sequence:

Gene name: Differentially expressed CO16 gene (clone MGC:5257)
Unigene number: Hs.69517
Probeset Accession #: AA447522
Protein Accession #: AAH01291
Signal sequence: 1-17 (first underlined sequence)
Transmembrane domain: 146 - 162
Cellular localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MALLALLLVV ALPRVWTDAN LTARQRDPED SQRTDEGDNR VWCHVCEREN TFECQNPRRC    60
KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKPEEK RFLLEEPMPF FYLKCCKIRY   120
CNLEGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSLS
```

A37 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.293616
Probeset Accession #: AW043782
Nucleic Acid Accession #: none found
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG    60
CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAACAACT TCACCAATGA   120
GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA   180
GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA   240
GTCGAAATGT GGCCCAACCT TCTTCCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG   300
CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC   360
AAACCCTCTG CTTTGCTCCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA   420
GAGCTTCATC TGCGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA   480
AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA   540
TTACCCCAGC ATCACCTATG CCATCATCGG CAGCTCCGTC ATTTTTGTGC TGGTGGTGGC   600
CCTGCTGGCA CTGGTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT   660
GCACCGGCTG CAGCACCCTG TGCTGCTGTC CCGCCTGGTG GTCCTGGACC ACCCCCACCA   720
CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA   780
GAATGCGTCG GAAGTAGGCT CCCCACCCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC   840
TGCGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC   900
CGACCTGCCC CCCTACCGCT CCCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC   960
CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCCAGGA  1020
GGGCACTGCT GAGCCCAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC  1080
AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTTG  1140
TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT  1200
AACTATCTCT GCATTCCCCT CCTCCCCCAG ACTTCAGAGA TGTTTTTCTG GCGTCTCAGT  1260
TGACATGATC TGTTGTGCGT CTTTTCTGTC AGGTCACTCT TCCCTTGGGA CCCGAGATCA  1320
CACCCTCATT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG  1380
AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA  1440
CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG  1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAAATT CCATTTGAGC  1560
ATCAAAACCT GCTTTGCACA ATCCTATTTG ATGCCCCCAG TTCAGCAGAG TCAGTGGCCA  1620
AAGAAAACTT TGGACGTGAG TAACACCCTT CAGCAGTCGC AACGTTATTT TGGTTTTGTG  1680
AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTTG CCCAAGAATG  1740
CTCATTCTGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCCTAA AATAGGCAGG  1800
GAGCCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC  1860
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCACC CTCCCAGCTG  1920
ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT  1980
GTATGTCCCT GTGGCCCACA CCCAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC  2040
CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTTGG ACTTGAGGAC  2100
ACTGGTTTCT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC  2160
CTGCACTGTG CACGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG  2220
GGTCAGGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG  2280
AGACAATTTG GAGTCAAGAT TTTCCATTTG GATCTATTTT AAATCTTTTA GAAATGCATT  2340
TGAAACAGTG TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA  2400
AGCTGTCTCT TTTTTTGTTT TTCCTTTAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC  2460
ACACCCTTGC CCCGCTGAGC CCCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG  2520
ACATTTGTGC ATTGTTGCAC TTTGAGGTTA TTATTTATCA AGTTCTTGAA GGAAGCAGAA  2580
AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT  2640
TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT  2700
AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAAATGGAA CCAGGTAGAG  2760
CCACTCCGGG CAGCTGTCAC CCATTCAGAA CTTCTTTCCG CAGCTGAAGA AATGTTCAGT  2820
AACCTGTTTG ACGCTAATTA AAACAGACCC TGCAGGAAGT GGGGCTAAAG TGGCATTCAG  2880
TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA  2940
AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA  3000
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AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTTAA AATAGCACTT GAGTTATTTT  3060
CTGAGTAATC CAATAAAGAA CTTTTGATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA  3120
CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC  3180
TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT  3240
GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT  3300
AGATAAGGGA TGCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTTT ATTATAGATT  3360
TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT  3420
TTTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT  3480
TTTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG  3540
AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT  3600
AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA  3660
TTTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG  3720
GAAAGGTTGT GTGTCGTTGC TTTTTGTGTT TTGGTTAGGC TTGGTTTTGT TTTTTAATTT  3780
TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAWG GWMCTAMARM  3840
AAMMAAAAAC AWYWTTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTTAACA CCACTTCGGG  3900
TGGGGCGGCG GGGCCCACGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG  3960
GAAACCCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAAA ACGCGCCGGG  4020
GGAAACCGCA GAGTGTTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG  4080
GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G
```

A38 Protein sequence:

Gene name:	ESTs
Unigene number:	Hs.293616
Probeset Accession #:	AW043782
Protein Accession #:	none found
Signal sequence:	1-17
Transmembrane domains:	169-191
LDLa domains:	28-66, 70-108, 112-149
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD    60
EKECPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC   120
KNGLCIDKSF ICDGQNNCQD NSDEESCESS QEPGSGQVFV TSENQLVYYP SITYAIIGSS   180
VIFVLVVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ   240
YVASQAEQNA SEVGSPPSYS EALLDQRPAW YDLPPPPYSS DTESLNQADL PPYRSRSGSA   300
NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV
```

A39 DNA sequence

Gene name:	ESTs
Unigene number:	Hs.128899
Probeset Accession #:	AA983251
Nucleic Acid Accession #:	AA983251

Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA    60
GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC   120
GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC   180
GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG   240
CCGCGGCCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCCT   300
CGCCTGCGTC CTGGACGTTC CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT   360
TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCCATC AGCGAGTGCA   420
ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA   480
GCTCCTGGAC CTAGGGCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC   540
CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCC GGGGGTCGCC GGGGCCACGA   600
CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCCAG GGTGGTGCCA   660
TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCCTGGAA CGCCGCTTCG CTCCTGCAGC   720
TGCTGCTGGC TGCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC   780
TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC   840
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG   900
GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC   960
CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA  1020
GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC  1080
TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC  1140
CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCCTCTCCCC TGCAGCGGCC CGCCTTGCCC  1200
ATCTACGTGC CGTTCCTCAT TGTTGGCTCC GTGTTTGTCG CCTTTATCAT CTTGGGGTCC  1260
CTGGTGGCAG CCTGTTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA  1320
GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC  1380
CGGGGGTCGT CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC  1440
GGGGCCCGGG CGCCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG  1500
AACAACGTGT ATGTCAACAT GCCCACGAAT TTCTCTGTGC TGAACTGTCA GCAGGCCACC  1560
CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG  1620
CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCCTGCA GCCTGGCTAC  1680
AGGCAGATTC AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG  1740
ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG  1800
GATTCTCGAG GTGGAAGTCC GCACATGTCG GTGGTATTTA TGGCACGATT CCTTTGGATG  1860
GCTTCATTTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT  1920
CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCCTC AGCTGGAGAT GACTGTGATG  1980
TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TCGTTGACGA  2040
AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT  2100
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TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTTATCTCC CTTTTACTGG GACTTTTTTT  2160
TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGCAG  2220
TGGTGCGATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC  2280
AGCCTCCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT  2340
TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA  2400
TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC  2460
TGAGCCTTTT TTTTTTTCTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT  2520
ATTCTAAAAG GAAACCTGTT TGAACTCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA  2580
GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG  2640
GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA  2700
TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC  2760
TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAAACCATT CATCCCCTTC  2820
TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTTT  2880
TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG  2940
TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT  3000
GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA  3060
AAAAATTTTC TTGTCTTAGT TATAAAAATT CAAAGAAATG TGTTACAAAG ATACTTAGTA  3120
TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTTACTTT  3180
GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG  3240
GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCCAC ACTGTTCTTG  3300
ATTTCCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT  3360
CAAATTCAAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAAGAT AACTTTAAGG  3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT  3480
GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATTC  3540
TGTTTCATGA CTGAATAATG TAAAACCAGT GTTGGCAATT GGTATCATCA ATGATACTCA  3600
TTTTTTAATA ACCAAAGGCA GGGGAAAATC ATTTTACTTA TTAATAAATA TTTTATGATG  3660
TGAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

A40 Protein sequence

Gene name:	ESTs
Unigene number:	Hs.128899
Protein Accession #:	none found
Signal sequence:	1-11
Transmembrane domains:	402-424
Cellular localization:	not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MLSGFLMSPS TQHRAQYTPG GKKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA    60
GEAEKGNRGE PPAWIRAQQQ PRPPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA   120
SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG   180
PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAPRVVP CGALAARPSP HPGTPLRSCS   240
CCWLRCWRRG RGPSGEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE   300
ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPPPV RAWQRCSPEG   360
SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPFLIVGS VFVAFIILGS   420
LVAACCRCL RPKQDPQQSR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS   480
GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGQYL HPPYVGYTVQ   540
HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQKMYPAV TV
```

A41 DNA SEQUENCE:

Gene name:	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number:	Hs.100686
Probeset Accession #:	AA487468
Nucleic Acid Accession #:	AA487468
Coding sequence:	55-555 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG    60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT   120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC   180
ACTTGGGTAC AAACTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA   240
ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC   300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT   360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA   420
GACCCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA   480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT   540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT   600
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAATA   660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAAATAAAT GTTTTTTAAA   720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAA
```

A42 Protein sequence:

Gene name:	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number:	Hs.100686
Probeset Accession #:	AA487468
Protein Accession #:	none found
Signal sequence:	1-23
Transmembrane domains:	none found
Cellular Localization:	secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK    60
PLMVIHHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM   120
FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL
```

A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Nucleic Acid Accession #: AF189723
Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC    60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC   120
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT   180
TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTTTTA   240
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTACAGTT   300
GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA   360
CCAGAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT   420
CCAGGTGATA CAGTTTGCCT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTT   480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTCT   540
AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT   600
GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCAT TGGAACAGGA   660
GAAAATTCTG AATTTGGGGA GGTTTTTAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC   720
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACTTT CCTTTTACTC CTTTGGTATA   780
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT   840
ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTCACAGTG   900
ACGCTAGCTC TTGGTGTTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT   960
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTCAG ATAAAACTGG AACACTGACG  1020
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT  1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTC  1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT  1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGCCCT TAATTGCTCT TGCAATGAAG  1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT  1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT  1380
TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA  1440
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC  1500
ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCCTGAACT GGGACAGCTG  1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT  1620
ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTC ACAGGAGACT  1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCCAAAA CTTCCCAGTC AGTCTCAGGA  1740
GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTGCAGTA  1800
TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT  1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC  1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC  1980
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT  2040
AATAACATTA AAAATTTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACTTTA  2100
ATCTCATTGG CTACATTAAT GAACTTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG  2160
ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA  2220
GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACTTGATA  2280
CTTAAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTTTGT CTTCTGGCGT  2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG  2400
TTTTTTGACA TGTTCAATGC ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT  2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA  2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG  2580
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG  2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT  2700
CTTGAAGTAT GA
```

A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI    60
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP   120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS   180
KVTAPQPAAT NGDLASRSNI AFMGTLVRCG KAKGVVIGTG ENSEFGEVFK MMQAEEAPKT   240
PLQKSMDLLG KQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPIVVTV   300
```

```
TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT   360
GVGYNQFGEV IVDGDVVHGF YNPAVSRIVE AGCVCNDAVI RNNTLMGKPT EGALIALAMK   420
MGLDGLQQDY IRKAEYPFSS EQKWMAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK   480
GQTLTLTQQQ RDVYQQEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTGVKEAV   540
TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV   600
FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEAADMI   660
LVDDDFQTIM SAIEEGKGIY NNIKNFVRFQ LSTSIAALTL ISLATLMNFP NPLNAMQILW   720
INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR   780
ELRDNVITPR DTTMTFTCFV FFDMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL   840
LVIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIIK KVERSREKIQ KHVSSTSSSF   900
LEV
```

A45 DNA sequence

Gene name: ESTs
Unigene number: Hs.157601
Probeset Accession #: W07459
Nucleic Acid Accession #: AC005383
Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT    60
TTTTATTTGC AGACCTGGGC CGATGCCGCT TTAAAAAACG CGAGGGGCTC TATGCACCTC   120
CCTGGCGGTA GTTCCTCCGA CCTCAGCCGG GTCGGGTCGT GCCGCCCTCT CCCAGGAGAG   180
ACAAACAGGT GTCCCACGTG GCAGCCGCGC CCCGGGCGCC CCTCCTGTGA TCCCGTAGCG   240
CCCCCTGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG   300
TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCCTTTCC TGTTGCTGGA GGCCGTCTGT   360
GTTTTCCTGT TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA   420
GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC   480
ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCGGGAAAG GGAGCTTTGA AAGGTCCAAG   540
CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA   600
GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCCCT TGGATTCATT TTCAACCCAA   660
CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA   720
CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC   780
CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG   840
CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG   900
GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCACG TGCTGTTGGC TGAGCAGGTG   960
GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC  1020
ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG  1080
GAGTTCGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCCTTGC GGTGCTGGCT  1140
GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCCTAA CCCACCCTGC CACCTGCTAC  1200
AGGACCACCT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT  1260
CCAGAAGGAC TGGACGGCTA CCAGTGCCTC TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC  1320
TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCCTGCT GGACAGCTCT  1380
GCGGGCACCA CTCTGGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG  1440
GCCGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG  1500
CTGGTGGCGG TGCCTGTGGG GGAGTACCAG GATGTGCCTG ACCTGGTCTG GAGCCTCGAT  1560
GGCATTCCCT TCCGTGGTGG CCCCACCCTG ACGGGCAGTG CCTTGCGGCA GGCGGCAGAG  1620
CGTGGCTTCG GGAGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTTTTG  1680
CTCACTGAGT CACACTCCGA GGATGAGGTT GCGGGCCCAG CGCGTCACGC AAGGGCGCGA  1740
GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCCGTGCGGG CAGAGCTGGA GGAGATCACA  1800
GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAAATCCCT  1860
GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG CGGCCAGGGT GCCGGACACA AGCCCTGGAC  1920
CTCGTCTTCA TGTTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG  1980
AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCGGC  2040
CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCCACCCGG  2100
GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCCTACCTAG GTGGGGTGGG CTCAGCCGGC  2160
ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCCTGGT  2220
GTCCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT  2280
GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA  2340
AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CGGGATTCCC TGATCCACGT GGCAGCTTAC  2400
GCCGACCTGC GGTACCACCA GGACGTGCTC ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG  2460
CCAGTCAACC TCTGCAAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAAT  2520
GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG  2580
TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATTC TTGAGACGCC CCTGAGGCAC  2640
ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCCTCCCA GCAACTACAG ACAAGGCCTG  2700
GGCACTGAAA TGGTGCCTAC CTTCTGGAAT GTCTGTGCCC CAGGTCCTTA GAATGTCTGC  2760
TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC  2820
ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTGAAAAGTT  2880
TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CCTTGTTGAG GCTATGTCAT  2940
CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCCTGAAG ACTTAAATTT AGCGGCCTGA  3000
CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCCAGCAG  3060
AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAAGCA  3120
GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAAGGGGG  3180
CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAAGA GACTTGGAAA  3240
GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT  3300
TGTGCATGGG CCCAGGTCTG GAGGGCCACG TAAAATCGTT CTGAGTCGTG AGCAGTGTCC  3360
ACCTTGAAGG TCTTC
```

A46 Protein sequence

Gene name: ESTs

Unigene number: Hs.157601
Protein Accession #: none found
Signal sequence: 1-17
Transmembrane domains: none found
VGW domains: 49-223; 341-518; 529-706
EGF domains: 298-333; 715-748
Cellular Localization: secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN    60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGPL   360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS   780
RTPPSNYREG LGTEMVPTFW NVCAPGP
```

COLON

A47 DNA SEQUENCE:
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG    60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT   120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC   180
ACTTGGGTAC AAACTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA   240
ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC   300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT   360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA   420
GACCCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA   480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT   540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT   600
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAATA   660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAAATAAAT GTTTTTTAAA   720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAA
```

A48 Protein sequence:
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK    60
PLMVIHHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM   120
FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL
```

A49 DNA SEQUENCE
Gene name: G protein-coupled receptor 56
Unigene number: Hs.6527
Probeset Accession #: AA478599
Nucleic Acid Accession #: NM_005682
Coding sequence: 163-2244(underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCAGCAGG GTCTCGCTCT GTCACACAGG CTGGAGTGCA GTGGTGTGAT CTTGGCTCAT    60
CGTAACCTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG   120
ATTACAGGTG GTGACTTCCA AGAGTGACTC CGTCGGAGGA AAATGACTCC CCAGTCGCTG   180
```

```
CTGCAGACGA CACTGTTCCT GCTGAGTCTG CTCTTCCTGG TCCAAGGTGC CCACGGCAGG   240
GGCCACAGGG AAGACTTTCG CTTCTGCAGC CAGCGGAACC AGACACACAG GAGCAGCCTC   300
CACTACAAAC CCACACCAGA CCTGCGCATC TCCATCGAGA ACTCCGAAGA GGCCCTCACA   360
GTCCATGCCC CTTTCCCTGC AGCCCACCCT GCTTCCCGAT CCTTCCCTGA CCCCAGGGGC   420
CTCTACCACT TCTGCCTCTA CTGGAACCGA CATGCTGGGA GATTACATCT TCTCTATGGC   480
AAGCGTGACT TCTTGCTGAG TGACAAAGCC TCTAGCCTCC TCTGCTTCCA GCACCAGGAG   540
GAGAGCCTGG CTCAGGGCCC CCCGCTGTTA GCCACTTCTG TCACCTCCTG GTGGAGCCCT   600
CAGAACATCA GCCTGCCCAG TGCCGCCAGC TTCACCTTCT CCTTCCACAG TCCTCCCCAC   660
ACGGCCGCTC ACAATGCCTC GGTGGACATG TGCGAGCTCA AAAGGGACCT CCAGCTGCTC   720
AGCCAGTTCC TGAAGCATCC CCAGAAGGCC TCAAGGAGGC CCTCGGCTGC CCCCGCCAGC   780
CAGCAGTTGC AGAGCCTGGA GTCGAAACTG ACCTCTGTGA GATTCATGGG GGACATGGTG   840
TCCTTCGAGG AGGACCGGAT CAACGCCACG GTATGGAAGC TCCAGCCCAC AGCCGGCCTC   900
CAGGACCTGC ACATCCACTC CCGGCAGGAG GAGGAGCAGA GCGAGATCAT GGAGTACTCG   960
GTGCTGCTGC CTCGAACACT CTTCCAGAGG ACGAAAGGCC GGAGCGGGGA GGCTGAGAAG  1020
AGACTCCTCC TGGTGGACTT CAGCAGCCAA GCCCTGTTCC AGGACAAGAA TTCCAGCCAA  1080
GTCCTGGGTG AGAAGGTCTT GGGGATTGTG GTACAGAACA CCAAAGTAGC CAACCTCACG  1140
GAGCCCGTGG TGCTCACTTT CCAGCACCAG CTACAGCCGA AGAATGTGAC TCTGCAATGT  1200
GTGTTCTGGG TTGAAGACCC CACATTGAGC AGCCCGGGGC ATTGGAGCAG TGCTGGGTGT  1260
GAGACCGTCA GGAGAGAAAC CCAAACATCC TGCTTCTGCA ACCACTTGAC CTACTTTGCA  1320
GTGCTGATGG TCTCCTCGGT GGAGGTGGAC GCCGTGCACA AGCACTACCT GAGCCTCCTC  1380
TCCTACGTGG GCTGTGTCGT CTCTGCCCTG GCCTGCCTTG TCACCATTGC CGCCTACCTC  1440
TGCTCCAGGG TGCCCCTGCC GTGCAGGAGG AAACCTCGGG ACTACACCAT CAAGGTGCAC  1500
ATGAACCTGC TGCTGGCCGT CTTCCTGCTG GACACGAGCT TCCTGCTCAG CGAGCCGGTG  1560
GCCCTGACAG GCTCTGAGGC TGGCTGCCGA GCCAGTGCCA TCTTCCTGCA CTTCTCCCTG  1620
CTCACCTGCC TTTCCTGGAT GGGCCTCGAG GGGTACAACC TCTACCGACT CGTGGTGGAG  1680
GTCTTTGGCA CCTATGTCCC TGGCTACCTA CTCAAGCTGA GCGCCATGGG CTGGGGCTTC  1740
CCCATCTTTC TGGTGACGCT GGTGGCCCTG GTGGATGTGG ACAACTATGG CCCCATCATC  1800
TTGGCTGTGC ATAGGACTCC AGAGGGCGTC ATCTACCCTT CCATGTGCTG GATCCGGGAC  1860
TCCCTGGTCA GCTACATCAC CAACCTGGGC CTCTTCAGCC TGGTGTTTCT GTTCAACATG  1920
GCCATGCTAG CCACCATGGT GGTGCAGATC CTGCCGCTGC GCCCCCACAC CCAAAAGTGG  1980
TCACATGTGC TGACACTGCT GGGCCTCAGC CTGGTCCTTG GCCTGCCCTG GGCCTTGATC  2040
TTCTTCTCCT TTGCTTCTGG CACCTTCCAG CTTGTCGTCC TCTACCTTTT CAGCATCATC  2100
ACCTCCTTCC AAGGCTTCCT CATCTTCATC TGGTACTGGT CCATGCGGCT GCAGGCCCGG  2160
GGTGGCCCCT CCCCTCTGAA GAGCAACTCA GACTGCGCCA GGCTCCCCAT CAGCTCGGGC  2220
AGCACCTCGT CCAGCCGCAT CTAGGCCTCC AGCCCACCTG CCCATGTGAT GAAGCAGAGA  2280
TGCGGCCTCG TCGCACACTG CCTGTGGCCC CCGAGCCAGG CCCAGCCCCA GGCCAGTCAG  2340
CCGCAGACTT TGGAAAGCCC AACGACCATG GAGAGATGGG CCGTTGCCAT GGTGGACGGA  2400
CTCCCGGGGC TGGGGCTTTT GAATTGGCCT TGGGGACTAC TCGGCTCTCA CTCAGCTCCC  2460
ACGGGACTCA GAAGTGCGCC GCCATGCTGC CTAGGGTACT GTCCCCACAT CTGTCCCAAC  2520
CCAGCTGGAG GCCTGGTCTC TCCTTACAAC CCCTGGGCCC AGCCTCATTG CTGGGGGCCA  2580
GGCCTTGGAT CTTGAGGGTC TGGCACATCC TTAATCCTGT GCCCCTGCCT GGGACAGAAA  2640
TGTGGCTCCA GTTGCTCTGT CTCTCGTGGT CACCCTGAGG GCACTCTGCA TCCTCTGTCA  2700
TTTTAACCTC AGGTGGCACC CAGGGCGAAT GGGGCCCAGG GCAGACCTTC AGGGCCAGAG  2760
CCCTGGCGGA GGAGAGGCCC TTTGCCAGGA GCACAGCAGC AGCTCGCCTA CCTCTGAGCC  2820
G
```

A50 Protein sequence

Gene name:	G protein-coupled receptor 56
Unigene number:	Hs.6527
Protein Accession #:	NM_005682.1
Signal sequence:	1-26
GPS domain:	342-394
Pfam domain:	7tm_2[400-665]
Transmembrane domains:	410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
Cellular Localization:	plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MTPQSLLQTT LFLLSLLFLV QGAHGRGHRE DFRFCSQRNQ THRSSLHYKP TPDLRISIEN    60
SEEALTVHAP FPAAHPASRS FPDPRGLYHF CLYWNRHAGR LHLLYGKRDF LLSDKASSLL   120
CFQHQEESLA QGPPLLATSV TSWWSPQNIS LPSAASFTFS FHSPPHTAAH NASVDMCELK   180
RDLQLLSQFL KHPQKASRRP SAAPASQQLQ SLESKLISVR FMGDMVSFEE DRINATVWKL   240
QPTAGLQDLH IHSRQEEEQS EIMEYSVLLP RTLFQRTKGR SGEAEKRLLL VDFSSQALFQ   300
DKNSSQVLGE KVLGIVVQNT KVANLTEPVV LTFQHQLQPK NVTLQCVFWV EDPTLSSPGH   360
WSSAGCETVR RETQTSCFCN HLTYFAVLMV SSVEVDAVHK HYLSLLSYVG CVVSALACLV   420
TIAAYLCSRV PLPCRRKPRD YTIKVHMNLL LAVFLLDTSF LLSEPVALTG SEAGCRASAI   480
FLHFSLLTCL SWMGLEGYNL YRLVVEVFGT YVPGYLLKLS AMGWGFPIFL VTLVALVDVD   540
NYGPIILAVH RTPEGVIYPS MCWIRDSLVS YITNLGLFSL VFLFNMAMLA TMVVQILRLR   600
PHTQKWSHVL TLLGLSLVLG LPWALIFFSF ASGTFQLVVL YLFSIITSFQ GFLIFIWYWS   660
MRLQARGGPS PLKSNSDCAR LPISSGSTSS SRI
```

A51 DNA SEQUENCE

Gene name:	Hypothetical protein FLJ20063
Unigene number:	Hs.5940
Probeset Accession #:	AA053660
Nucleic Acid Accession #:	AA053660
Coding sequence:	218-1360 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
CCCCCATGAC TTTGTACAGC TACTTCACTG CTTCCCCCCA ATTAGTACAC ATAGTTCCTC    60
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CACAATTCCT ACACCTGCTC CCCCCATAAT CAGTACACAT AGTTCCTCCA CAATTCCTAT   120
ACCTACTGCT GCAGACAGTG AGTCAACCAC AAATGTAAAT TCATTAGCTA CCTCTGACAT   180
AATCACCGCT TCATCTCCAA ATGATGGATT AATCACAATG GTTCCTTCTG AAACACAAAG   240
TAACAATGAA ATGTCCCCCA CCACAGAAGA CAATCAATCA TCAGGGCCTC CCACTGGCAC   300
CGCTTTATTG GAGACCAGCA CCCTAAACAG CACAGGTCCC AGCAATCCTT GCCAAGATGA   360
TCCCTGTGCA GATAATTCGT TATGTGTTAA GCTGCATAAT ACAAGTTTTT GCCTGTGTTT   420
AGAAGGGTAT TACTACAACT CTTCTACATG TAAGAAAGGA AAGGTATTCC CTGGGAAGAT   480
TTCAGTGACA GTATCAGAAA CATTTGACCC AGAAGAGAAA CATTCCATGG CCTATCAAGA   540
CTTGCATAGT GAAATTACTA GCTTGTTTAA AGATGTATTT GGCACATCTG TTTATGGACA   600
GACTGTAATT CTTACTGTAA GCACATCTCT GTCACCAAGA TCTGAAATGC GTGCTGATGA   660
CAAGTTTGTT GATGTAACAA TAGTAACAAT TTTGGCAGAA ACCACAAGTG ACAATGAGAA   720
GACTGTGACT GAGAAAATTA ATAAAGCAAT TAGAAGTAGC TCAAGCAACT TTCTAAACTA   780
TGATTTGACC CTTCGGTGTG ATTATTATGG CTGTAACCAG ACTGCGGATG ACTGCCTCAA   840
TGGTTTAGCA TGCGATTGCA AATCTGACCT GCAAAGGCCT AACCCACAGA GCCCTTTCTG   900
CGTTGCTTCC AGTCTCAAGT GTCCTGATGC CTGCAACGCA CAGCACAAGC AATGCTTAAT   960
AAAGAAGAGT GGTGGGGCCC CTGAGTGTGC GTGCGTGCCC GGCTACCAGG AAGATGCTAA  1020
TGGGAACTGC CAAAAGTGTG CATTTGGCTA CAGTGGACTC GACTGTAAGG ACAAATTTCA  1080
GCTGATCCTC ACTATTGTGG GCACCATCGC TGGCATTGTC ATTCTCAGCA TGATAATTGC  1140
ATTGATTGTC ACAGCAAGAT CAAATAACAA AACGAAGCAT ATTGAAGAAG AGAACTTGAT  1200
TGACGAAGAC TTTCAAAATC TAAAACTGCG GTCGACAGGC TTCACCAATC TTGGAGCAGA  1260
AGGGAGCGTC TTTCCTAAGG TCAGGATAAC GGCCTCCAGA GACAGCCAGA TGCAAAATCC  1320
CTATTCAAGA CACAGCAGCA TGCCCCGCCC TGACTATTAG AATCATAAGA ATGTGGAACC  1380
CGCCATGGCC CCCAACCAAT GTACAAGCTA TTATTTAGAG TGTTTAGAAA GACTGATGGA  1440
GAAGTGAGCA CCAGTAAAGA TCTGGCCTCC GGGGTTTTTC TTCCATCTGA CATCTGCCAG  1500
CCTCTCTGAA TGGAAGTTGT GAATGTTTGC AACGAATCCA GCTCACTTGC TAAATAAGAA  1560
TCTATGACAT TAAATGTAGT AGATGCTATT AGCGCTTGTC AGAGAGGTGG TTTTCTTCAA  1620
TCAGTACAAA GTACTGAGAC AATGGTTAGG GTTGTTTTCT TAATTCTTTT CCTGGTAGGG  1680
CAACAAGAAC CATTTCCAAT CTAGAGGAAA GCTCCCCAGC ATTGCTTGCT CCTGGGCAAA  1740
CATTGCTCTT GAGTTAAGTG ACCTAATTCC CCTGGGAGAC ATACGCATCA ACTGTGGAGG  1800
TCCGAGGGGA TGAGAAGGGA TACCCACCAT CTTTCAAGGG TCACAAGCTC ACTCTCTGAC  1860
AAGTCAGAAT AGGGACACTG CTTCTATCCC TCCAATGGAG AGATTCTGGC AACCTTTGAA  1920
CAGCCCAGAG CTTGCAACCT AGCCTCACCC AAGAAGACTG GAAAGAGACA TATCTCTCAG  1980
CTTTTTCAGG AGGCGTGCCT GGGAATCCAG GAACTTTTTG ATGCTAATTA GAAGGCCTGG  2040
ACTAAAAATG TCCACTATGG GGTGCACTCT ACAGTTTTTG AAATGCTAGG AGGCAGAAGG  2100
GGCAGAGAGT AAAAAACATG ACCTGGTAGA AGGAAGAGAG GCAAAGGAAA CTGGGTGGGG  2160
AGGATCAATT AGAGAGGAGG CACCTGGGAT CCACCTTCTT CCTTAGGTCC CCTCCTCCAT  2220
CAGCAAAGGA GCACTTCTCT AATCATGCCC TCCCGAAGAC TGGCTGGGAG AAGGTTTAAA  2280
AACAAAAAAT CCAGGAGTAA GAGCCTTAGG TCAGTTTGAA ATTGGAGACA AACTGTCTGG  2340
CAAAGGGTGC GAGAGGGAGC TTGTGCTCAG GAGTCCAGCC GTCCAGCCTC GGGGTGTAGG  2400
TTTCTGAGGT GTGCCATTGG GGCCTCAGCC TTCTCTGGTG ACAGAGGCTC AGCTGTGGCC  2460
ACCAACACAC AACCACACAC ACACAACCAC ACACACAAAT GGGGGCAACC ACATCCAGTA  2520
CAAGCTTTTA CAAATGTTAT TAGTGTCCTT TTTTATTTCT AATGCCTTGT CCTCTTAAAA  2580
GTTATTTTAT TTGTTATTAT TATTTGTTCT TGACTGTTAA TTGTGAATGG TAATGCAATA  2640
AAGTGCCTTT GTTAGATGGT GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A
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A52 Protein sequence:

Gene name:	Hypothetical protein FLJ20063
Unigene number:	Hs.5940
Probeset Accession #:	AA053660
Protein Accession #:	none found
Signal sequence:	none found
Transmembrane domains:	289-311
EGF domain:	45-74
SEA domain:	80-196
Cellular Localization:	plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MVPSETQSNN EMSPTTEDNQ SSGPPTGTAL LETSTLNSTG PSNPCQDDPC ADNSLCVKLH    60
NTSFCLCLEG YYYNSSTCKK GKVFPGKISV TVSETFDPEE KHSMAYQDLH SEITSLFKDV   120
FGTSVYGQTV ILTVSTSLSP RSEMRADDKF VDVTIVTILA ETTSDNEKTV TEKINKAIRS   180
SSSNFLNYDL TLRCDYYGCN QTADDCLNGL ACDCKSDLQR PNPQSPFCVA SSLKCPDACN   240
AQHKQCLIKK SGGAPECACV PGYQEDANGN CQKCAFGYSG LDCKDKFQLI LTIVGTIAGI   300
VILSMIIALI VTARSNNKTK HIEEENLIDE DFQNLKLRST GFTNLGAEGS VFPKVRITAS   360
RDSQMQNPYS RHSSMPRPDY
```

A53 DNA SEQUENCE

Gene name:	TMPRSS3a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Nucleic Acid Accession #:	AB038157
Coding sequence:	202-1566 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTCATGCCC GTGTGAGCCA    60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG   120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC   180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC   240
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TCATTCCGAT CGCTTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA   300
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC   360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC   420
TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC   480
GGAGTCTCGG ATTGCAAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG   540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCATGTGCTC CGATGACTGG   600
AAGGGTCACT ACGCAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA   660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT   720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA   780
TGTGCCTCTG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC   840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC   900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCT GTGGATCATC   960
ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT  1020
CTAGTTTCCC TGTTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC  1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA  1140
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC  1200
GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC  1260
TCCCCTGTCC TGAACCACGC GGCCGTCCCT TTGATTTCCA ACAAGATCTG CAACCACAGG  1320
GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC  1380
GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG  1440
AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG  1500
TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA  1560
ACCTGAAGAG GAAGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA  1620
TCCTCCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCTTG GAGCTCTGAG  1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT  1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG  1800
AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC  1860
TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT  1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA  1980
CCTCAAATGA TGTGCCTGCT TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC  2040
ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA  2100
AGGGCGGCCT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG  2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC  2220
GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCAGAA  2280
CCAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA  2340
ATGACTCGTT TAAGGCCTAT TTTCATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA  2400
TTGTCCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA  2460
AAAAAAAA
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A54 Protein sequence:

Gene name:	TMPRSS3a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Protein Accession #:	BAB20077
Signal sequence:	none found
Transmembrane domains:	43-65, 239-261
Tryp_SPc domain:	216-444
Cellular Localization:	plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI    60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF   120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK   180
VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH   240
LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR   300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVLNHA   360
AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSCQGD SGGPLVCQER RLWKLVGATS   420
FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT
```

A55 DNA SEQUENCE

Gene name:	Putative G protein-coupled receptor GPCR150
Unigene number:	Hs.97101
Probeset Accession #:	AA215333
Nucleic Acid Accession #:	NM_014373
Coding sequence:	322-1338(underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
GTGGCCTCGA GGTGGTGGCA GGGCCGCCCC CTGCAGTCCG GAGACGAACG CACGGACCGG    60
GCCTCCGGAG GCAGGTTCGG CTGGAAGGAA CCGCTCTCGC TTCGTCCTAC ACTTGCGCAA   120
ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA   180
AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA   240
GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATTT CAGCAGGTCT   300
TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAACTGCTC TTTTCAGTAC   360
CAGTTACGTC AAACAAACCA GCCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT   420
GGGAAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAAACAC CTGTCAAAAT   480
TTTATGGAAT ATTTTTGCAT TTCACTAGCA TTCGTTGATC TTTTACTTTT GGTAAACATT   540
TCCATTATAT TGTATTTCAG GGATTTTGTA CTTTTAAGCA TTAGGTTCAC TAAATACCAC   600
ATCTGCCTAT TTACTCAAAT TATTTCCTTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC   660
CTGACAGCTT GTATAGATTA TTGCCTGAAT TTCTCTAAAA CAACCAAGCT TTCATTTAAG   720
TGTCAAAAAT TATTTTATTT CTTTACAGTA ATTTTAATTT GGATTTCAGT CCTTGCTTAT   780
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GTTTTGGGAG ACCCAGCCAT CTACCAAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC   840
TGTCCTTTCT ATGTCAGCAT TCAGAGTTAC TGGCTGTCAT TTTTCATGGT GATGATTTTA   900
TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA   960
ACTTCCTATA TGAATGAAAC TATCTTATAT TTTCCTTTTT CATCCCACTC CAGTTATACT  1020
GTGAGATCTA AAAAAATATT CTTATCCAAG CTCATTGTCT GTTTTCTCAG TACCTGGTTA  1080
CCATTTGTAC TACTTCAGGT AATCATTGTT TTACTTAAAG TTCAGATTCC AGCATATATT  1140
GAGATGAATA TTCCCTGGTT ATACTTTGTC AATAGTTTTC TCATTGCTAC AGTGTATTGG  1200
TTTAATTGTC ACAAGCTTAA TTTAAAAGAC ATTGGATTAC CTTTGGATCC ATTTGTCAAC  1260
TGGAAGTGCT GCTTCATTCC ACTTACAATT CCTAATCTTG AGCAAATTGA AAAGCCTATA  1320
TCAATAATGA TTTGTTAATA TTATTAATTA AAAGTTACAG CTGTCATAAG ATCATAATTT  1380
TATGAACAGA AAGAACTCAG GACATATTAA AAAATAAACT GAACTAAAAC AACTTTTGCC  1440
CCCTGACTGA TAGCATTTCA GAATGTGTCT TTTGAAGGGC TATACCAGTT ATTAAATAGT  1500
GTTTTATTTT AAAAACAAAA TAATTCCAAG AAGTTTTTAT AGTTATTCAG GGACACTATA  1560
TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACATT TGGCTATACT  1620
GATGTTTGTG TTACTCAAAA AAACTACTGG ATGCAAACTG TTATGTAAAT CTGAGATTTC  1680
ACTGACAACT TTAAGATATC AACCTAAACA TTTTTATTAA ATGTTCAAAT GTAAGCAAGA  1740
AAAAAAAAA
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A56 Protein sequence

Gene name: Putative G protein-coupled receptor GPCR150
Unigene number: Hs.97101
Protein Accession #: NP_055188
Signal sequence: none found
Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297
Cellular Localization: plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MTALSSENCS FQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT CQNFMEYFCI    60
SLAFVDLLLL VNISIILYFR DFVLLSIRFT KYHICLFTQI ISFTYGFLHY PVFLTACIDY   120
CLNFSKTTKL SFKCQKLFYF FTVILIWISV LAYVLGDPAI YQSLKAQNAY SRHCPFYVSI   180
QSYWLSFFMV MILFVAFITC WEEVTTLVQA IRITSYMNET ILYFPFSSHS SYTVRSKKIF   240
LSKLIVCFLS TWLPFVLLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN   300
LKDIGLPLDP FVNWKCCFIP LTIPNLEQIE KPISIMIC
```

A57 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
Unigene number: Hs.19322
Probeset Accession #: AA088458
Nucleic Acid Accession #: AA088458
Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA    60
CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG   120
GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC   180
CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GCGGCTGCAG GGAGCCCCCG CCCACTGGGG   240
CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC   300
TGTGCCAGCC GGGCCCTGCC CCCGTCCTCC TCCGGGCCCC CCTGCCCTGC CCTGACGTCC   360
ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC   420
CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG   480
GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG   540
GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC   600
AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCCTCTC TGGCTGGAGA CCCCCGGCAG   660
GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCCGCCC TTGCCAGATG GGCTCCCCAG   720
GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG   780
ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCAG CTACTACTGG CCGCTGTCAG   840
TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCCG TTTCCAGCGG TGCCGCCCTG   900
GGTCCCATCT TCAGGGAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC   960
AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC  1020
CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT  1080
GTAAGCGGGG GGTGCCTGCC TGGCTGGGGA GCCCCAGGGA TAGCGGTCGG ACTTCAGGTT  1140
CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT  1200
GGCCTGCATG TGCCTCCCAC AGACCCTGGG GTGATGGCCT TCCCCCTCTT GGCCGGGACG  1260
TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA  1320
GACAGCTCCC AGGCACGTCA TAGGCAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC  1380
CTGGGGTCCT GCTCACCCCC CTTTGCTCTC ACGCCCAGCC TGTCCCCAGG TTTCAGCTGG  1440
GAGAGGCCAC CTCCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG  1500
GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT  1560
GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTCACCA  1620
GAACCAGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG  1680
TCAGTGTGTG TGGGGCGCAG GGCCTCCGAT GCGGGGTCAG TGCGTGGGGG GCGCAGGGCC  1740
CCCGATGCGG GGTCAGTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT  1800
ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC  1860
CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC  1920
TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT  1980
GCCCTCCTAC CCTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG  2040
ACCTCCTGGG CAGGAAAGGG TGCAGGTCCT GAGGGCCTGT GCCCCACAGC CCCAGCACCC  2100
AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCCGTCAGCA  2160
GGCTGGGGTC TGCCCACCAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC  2220
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TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340
GAGACAGGCT GGCACCTCCG GAAAAACTGC CTTTCAGCCT TGGTGTTCCG TGCAAGGTGA 2400
AAAGAAATAG GTCCTCCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2460
CACGAGGGGA GAATTTAAAG GCCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
GCAGACCCTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
GAGCAGCGTC CCTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT 2640
GCGTGCACAC TGTGATGACA CCCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700
CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760
TTTTGTGTTG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTCACGC 2820
CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
CCCCATCTCT ACAARAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940
TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA 3060
AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A58 DNA sequence

Gene name: ESTs
Unigene number: Hs.157601
Probeset Accession #: W07459
Nucleic Acid Accession #: AC005383
Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
TTTTATTTGC AGACCTGGGC CGATGCCGCT TTAAAAAACG CGAGGGGCTC TATGCACCTC 120
CCTGGCGGTA GTTCCTCCGA CCTCAGCCGG GTCGGGTCGT GCCGCCCTCT CCCAGGAGAG 180
ACAAACAGGT GTCCCACGTG GCAGCCGCGC CCCGGGCGCC CCTCCTGTGA TCCCGTAGCG 240
CCCCCTGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300
TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCCTTTCC TGTTGCTGGA GGCCGTCTGT 360
GTTTTCCTGT TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA 420
GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCGGGAAAG GGAGCTTTGA AAGGTCCAAG 540
CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCCCT TGGATTCATT TTCAACCCAA 660
CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC 780
CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG 840
CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900
GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCACG TGCTGTTGGC TGAGCAGGTG 960
GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080
GAGTTCGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCCTTGC GGTGCTGGCT 1140
GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCCTAA CCCACCCTGC CACCTGCTAC 1200
AGGACCACCT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
CCAGAAGGAC TGGACGGCTA CCAGTGCCTC TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCCTGCT GGACAGCTCT 1380
GCGGGCACCA CTCTGGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
GCCGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
CTGGTGGCGG TGCCTGTGGG GGAGTACCAG GATGTGCCTG ACCTGGTCTG GAGCCTCGAT 1560
GGCATTCCCT TCCGTGGTGG CCCCACCCTG ACGGGCAGTG CCTTGCGGCA GGCGGCAGAG 1620
CGTGGCTTCG GGAGCGCCAC CAGGACAGGC CAGGACCCGC CACGTAGAGT GGTGGTTTTG 1680
CTCACTGAGT CACACTCCGA GGATGAGGTT GCGGGCCCAG CGCGTCACGC AAGGGCGCGA 1740
GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCCGTGCGGG CAGAGCTGGA GGAGATCACA 1800
GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAAATCCCT 1860
GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG CGGCCAGGGT GCCGGACACA AGCCCTGGAC 1920
CTCGTCTTCA TGTTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCGGC 2040
CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCCACCCGG 2100
GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160
ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCCTGGT 2220
GTCCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT 2280
GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA 2340
AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CGGGATTCCC TGATCCACGT GGCAGCTTAC 2400
GCCGACCTGC GGTACCACCA GGACGTGCTC ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG 2460
CCAGTCAACC TCTGCAAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAAT 2520
GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580
TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATTC TTGAGACCCC CCTGAGGCAC 2640
ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCCTCCCA GCAACTACAG AGAAGGCCTG 2700
GGCACTGAAA TGGTGCCTAC CTTCTGGAAT GTCTGTGCCC CAGGTCCTTA GAATGTCTGC 2760
TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTGAAAAGTT 2880
TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CCTTGTTGAG GCTATGTCAT 2940
CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCCTGAAG ACTTAAATTT AGCGGCCTGA 3000
CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCCAGCAG 3060
AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAAGCA 3120
GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAAGGGGG 3180
CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAAGA GACTTGGAAA 3240
GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300
TGTGCATGGG CCCAGGTCTG GAGGGCCACG TAAAATCGTT CTGAGTCGTG AGCAGTGTCC 3360
ACCTTGAAGG TCTTC

A59 Protein sequence

Gene name: ESTs
Unigene number: Hs.157601
Protein Accession #: none found
Signal sequence: 1-17
Transmembrane domains: none found
VGW domains: 49-223; 341-518; 529-706
EGF domains: 298-333; 715-748
Cellular Localization: secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN    60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS   780
RTPPSNYREG LGTEMVPTFW NVCAPGP
```

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
Unigene number: Hs.63325
Probeset Accession #: AA411502
Nucleic Acid Accession #: NM_016425
Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC    60
AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA   120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC   180
TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG   240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT   300
GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA   360
GGGAACTGGT TCTCTGCCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT   420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG   480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT   540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG   600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC   660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC   720
CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA   780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA   840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC   900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA   960
GCCACCCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT  1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT  1080
GCGTACCAGG GGGAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG  1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG  1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCCAGG AGTATACACC  1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
```

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
Unigene number: Hs.63325
Probeset Accession #: AA411502
Protein Accession #: NP_057509
Signal sequence: none found
Transmembrane domains: 31-53
LDLa domain: 54-94
Tryp_SPc domain: 204-429
Cellular Localization: plasma membrane/ER

```
1          11         21         31         41         51
|          |          |          |          |          |
MLQDPDSDQP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY    60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT   120
GNWFSACFDN FTEALAETAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELRMRNSS   180
GPCLSGSLVS LHCLACGKSL KTPRVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV   240
LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIIE FNPMYPKDND IALMKLQFPL   300
TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD   360
AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT   420
KVSAYLNWIY NVWKAEL
```

A62 DNA SEQUENCE
Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
Unigene number: Hs.105484
Probeset Accession #: AA314779
Nucleic Acid Accession #: none found
Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT    60
CTGAGATCCT TGCACTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG   120
CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG   180
AGACCCAGCT GTGCTCCTGG ATGGTTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG   240
AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCAGT CTTACGGAAA CGGAGCCCAC   300
CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT   360
CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG   420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC   480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC   540
AACAAGCGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT   600
AACTCCTGCA CCAGCCCCGT CCTCTTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT   660
TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA   720
GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG   780
CCCCGCCATC CCTTTCCACA GTATCCTTCT TCCCTCCTCC CCTGTCTCTG GCTGTCTCGA   840
GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT   900
AAAGATTTGA AGACAGAAGG AAGAAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT   960
ACACCCTTCT GCCCTCTCTC CATTGCCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG  1020
TTTTTCCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA  1080
TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA
```

A63 Protein sequence:
Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
Unigene number: Hs.105484
Probeset Accession #: AA314779
Protein Accession #: none found
Signal sequence: 1-22
Transmembrane domains: none found
C-type lectin domain: 47-156
Cellular Localization: secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSN CYGYFRKLRN WSDAELECQS    60
YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG   120
KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP
```

A64 DNA SEQUENCE
Gene name: Cadherin 3, P-cadherin (placental)
Unigene number: Hs.2877
Probeset Accession #: X63629
Nucleic Acid Accession #: X63629
Coding sequence: 54-2543 (start and stop codons are underlined)

```
1          11         21         31         41         51
|          |          |          |          |          |
GCGGAACACC GGCCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC    60
TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCGCGG   120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG   180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC   240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG   300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC   360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC   420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT   480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG   540
AGACAGGCTG GTTGTTGTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC   600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA   660
TCATCGTGAC CGACCAGAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA   720
GTGTCTTAGA GGGAGTCCTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG   780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA   840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT   900
CCAGTGGCCT GGACCGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA   960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG  1020
ACAATGCTCC CATGTTTGAC CCCCAGAAGT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG  1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC  1140
GTGCCACCTA CCTTATCATG GGCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC  1200
CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC  1260
AGCACACCCT GTACGTTGAA GTGACCAACG AGGCCCCTTT TGTGCTGAAG CTCCCAACCT  1320
CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAC  1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA  1440
CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG  1500
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CAGGGTGGCT AGCCATCGAC CCAGACAGTG GCCAGGTCAC AGCTGTGGGC ACCCTCGACC  1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA  1620
ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG  1680
ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC  1740
ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCTTTC CAGGCCCAGC  1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG  1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG  1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC  1980
ATGTCGAAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG  2040
TCCTGGCTCT GCTGTTCCTC CTGCTGGTGC TGCTTTTGTT GGTGAGAAAG AAGCGGAAGA  2100
TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG  2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG  2220
AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA  2280
TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA  2340
AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG  2400
AGGGCAGCGG CTCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCCTCCGCC TCCGACCAAG  2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT  2520
ACGGTGGCGG GGAGGACGAC TAGGCGGCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC  2580
CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA  2640
GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT  2700
TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC  2760
CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCCAGAA GCCTCTTACC TGCCGTAAAA  2820
TGCTCAACCC TGTGTCCTGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT  2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT  2940
TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG  3000
TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT  3060
ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTTGCGT TGCTATAGAT  3120
GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTTT TATTAAAGAA A
```

A65 Protein sequence:

Gene name:	Cadherin 3, P-cadherin (placental)
Unigene number:	Hs.2877
Probeset Accession #:	X63629
Protein Accession #:	CAA45177
Signal sequence:	1-24
Transmembrane domain:	659-675 (second underlined sequence)
Cellular localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG    60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG   120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK   180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT   240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA   300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP   360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL   420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR   480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID   540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD   600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL   660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR   720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF   780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD
```

A66 DNA SEQUENCE

Gene name:	ATPase, Ca++ transporting, type 2C, member 1
Unigene number:	Hs.106778
Probeset Accession #:	N51919
Nucleic Acid Accession #:	AF189723
Coding sequence:	1-2712 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC    60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC   120
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT   180
TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTTTTA   240
ATGCATCAGT TTGATGATGC CGTCAGIATC ACTGTGGCAA TACTTATCGT TGTTACAGTT   300
GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA   360
CCAGAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT   420
CCAGGTGATA CAGTTTGCCT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTT   480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTCT   540
AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT   600
GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCAT TGGAACAGGA   660
GAAAATTCTG AATTTGGGGA GGTTTTTAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC   720
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACTTT CCTTTTACTC CTTTGGTATA   780
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT   840
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ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTCACAGTG   900
ACGCTAGCTC TTGGTGTTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT   960
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTCAG ATAAAACTGG AACACTGACG  1020
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT  1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTC  1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT  1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCCT TAATTGCTCT TGCAATGAAG  1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT  1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT  1380
TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA  1440
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC  1500
ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCCTGAACT GGGACAGCTG  1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT  1620
ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTC ACAGGAGACT  1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCCAAAA CTTCCCAGTC AGTCTCAGGA  1740
GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTGCAGTA  1800
TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT  1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC  1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC  1980
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT  2040
AATAACATTA AAAATTTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACTTTA  2100
ATCTCATTGG CTACATTAAT GAACTTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG  2160
ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA  2220
GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACTTGATA  2280
CTTAAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTTTGT CTTCTGGCGT  2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG  2400
TTTTTTGACA TGTTCAATGC ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT  2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA  2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG  2580
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG  2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT  2700
CTTGAAGTAT GA
```

A67 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined

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1          11         21         31         41         51
|          |          |          |          |          |
MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI    60
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP   120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS   180
KVTAPQPAAT NGDLASRSNI AFMGTLVRCG KAKGVVIGTG ENSEFGEVFK MMQAEEAPKT   240
PLQKSMDLLG KQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPIVVTV   300
TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT   360
GVGYNQFGEV IVDGDVVHGF YNPAVSRIVE AGCVCNDAVI RNNTLMGKPT EGALIALAMK   420
MGLDGLQQDY IRKAEYPFSS EQKWMAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK   480
GQTLTLTQQQ RDVYQQEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTGVKEAV   540
TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV   600
FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEAADMI   660
LVDDDFQTIM SAIEEGKGIY NNIKNFVRFQ LSTSIAALTL ISLATLMNFP NPLNAMQILW   720
INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR   780
ELRDNVITPR DTTMTFTCFV FFDMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL   840
LVIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIIK KVERSREKIQ KHVSSTSSSF   900
LEV
```

A68 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
Unigene number: Hs.170195
Probeset Accession #: BE616633
Nucleic Acid Accession #: NM_001719
Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT    60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG   120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC   180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA   240
GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT   300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC   360
CCATGTTCAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG   420
GCCAGGGCTT CTCCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA   480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG   540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC   600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT   660
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ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG   720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG   780
AGGAGGGCTG GCTGGTGTTT GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC   840
GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA   900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT   960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA  1020
GCCAGAACCG CTCCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG  1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC  1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG  1200
AGGGGGAGTG TGCCTTCCCT CTGAACTCCT ACATGAACGC CACCAACCAC GCCATCGTGC  1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCACGC  1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT  1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT  1440
TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA  1500
CTGCCTTTTG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG  1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA  1620
TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAAAA ACAACGCATA AAGAAAAATG  1680
GCCGGGCCAG GTCATTGGCT GGGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA  1740
TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT  1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA  1860
CAATAAAACG AATGAATG
```

A69 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number:	Hs.170195
Probeset Accession #:	BE616633
Protein Accession #:	NP_001710.1
Signal sequence:	1-30
Pfam domains:	TGFb_propeptide [37-281]
Transmembrane domains:	none found
Cellular Localization:	secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MHVRSLRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRLRSQE RREMQREILS    60
ILGLPHRPRP HLQGKHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS   120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY   180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVVNPR   240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS   300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE   360
GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY   420
RNMVVRACGC H
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Cervical

A70 DNA sequence

Gene name:	bone morphogenetic protein receptor IB (ALK-6)
Unigene number:	Hs.87223
Probeset Accession #:	AA250737
Nucleic Acid Accession #:	NM_001203
Coding sequence:	274-1782 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGCGGAGA CCGCGGCGCT    60
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT   120
GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTTGATAAA GGTTCAGACT TCTGCTGATT   180
CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC   240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA   300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC   360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA   420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTGCCTGT GGTCACTTCT   480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTCGGG ACACTCCCAT TCCTCATCAA   540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCTACA   600
CTGCCTCCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCTTTACTT   660
ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG   720
TATAAAAGAC AAGAAACCAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC   780
ATTCCTCCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA   840
TCAGGCCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAAACAG   900
ATTGGAAAAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT   960
GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG  1020
ACAGTGTTGA TGAGGCATGA AAACATTTTG GGTTTCATTG CTGCAGATAT CAAAGGGACA  1080
GGGTCCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT  1140
TATCTGAAGT CCACCACCCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC  1200
AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAACC AGCAATTGCC  1260
CATCGAGATC TGAAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACTTG CTGTATTGCT  1320
GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC  1380
ACTCGAGTTG GCACCAAACG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA  1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG  1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC  1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA  1620
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CGCCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACTC  1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA  1740
ACACTTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG  1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA  1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC  1920
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG  1980
TCTGTTTGTA GGCGGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT
```

A71 Protein sequence

Gene name:	bone morphogenetic protein receptor IB (ALK-6)
Unigene number:	Hs.72472 / Hs.87223
Probeset Accession #:	AA250737 / U89326
Protein Accession #:	NP_001194
Signal sequence:	1-13
Transmembrane domains:	128-144
PFAM domains:	activin_receptor [30-111], protein kinase [204-491]
Cellular Localization:	plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED    60
DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD   120
GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPRYS IGLEQDETYI PPGESLRDLI   180
EQSQSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTEEAS   240
WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS   300
MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILV KKNGTCCIAD LGLAVKFISD   360
TNEVDIPPNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFGLILWEV ARRCVSGGIV   420
EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS   480
RLTALRVKKT LAKMSESQDI KL
```

Bladder

A72 DNA SEQUENCE

Gene name:	Homo sapiens type II membrane serine protease mRNA
Unigene number:	Hs.63325
Probeset Accession #:	AA411502
Nucleic Acid Accession #:	NM_016425
Coding sequence:	1-1314 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC    60
AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA   120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC   180
TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG   240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT   300
GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA   360
GGGAACTGGT TCTCTGCCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT   420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG   480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT   540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG   600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC   660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC   720
CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA   780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA   840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC   900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA   960
GCCACCCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT  1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT  1080
GCGTACCAGG GGGAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG  1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG  1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCCAGG AGTATACACC  1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
```

A73 Protein sequence:

Gene name:	Homo sapiens type II membrane serine protease mRNA
Unigene number:	Hs.63325
Probeset Accession #:	AA411502
Protein Accession #:	NP_057509
Signal sequence:	none found
Transmembrane domains:	31-53
LDLa domain:	54-94
Tryp_SPc domain:	204-429
Cellular Localization:	plasma membrane/ER

```
1          11         21         31         41         51
|          |          |          |          |          |
MLQDPDSDQP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY    60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT   120
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GNWFSACFDN FTEALAETAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELRMRNSS   180
GPCLSGSLVS LHCLACGKSL KTPRVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV   240
LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIIE FNPMYPKDND IALMKLQFPL   300
TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD   360
AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT   420
KVSAYLNWIY NVWKAEL
```

A74 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
Unigene number: Hs.19322
Probeset Accession #: AA088458
Nucleic Acid Accession #: AA088458
Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA    60
CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG   120
GCGCCGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC   180
CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG   240
CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC   300
TGTGCCAGCC GGGCCCTGCC CCCGTCCTCC TCCGGGCCCC CCTGCCCTGC CCTGACGTCC   360
ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC   420
CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG   480
GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG   540
GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC   600
AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCCTCTC TGGCTGGAGA CCCCCGGCAG   660
GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCCGCCC TTGCCAGATG GGCTCCCCAG   720
GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG   780
ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCAG CTACTACTGG CCGCTGTCAG   840
TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCCG TTTCCAGCGG TGCCGCCCTG   900
GGTCCCATCT TCAGGGAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC   960
AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC  1020
CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT  1080
GTAAGCGGGG GGTGCCTGCC TGGCTGGGGA GCCCCAGGGA TAGCGGTCGG ACTTCAGGTT  1140
CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT  1200
GGCCTGCATG TGCCTCCCAC AGACCCTGGG GTGATGGCCT TCCCCCTCTT GGCCGGGACG  1260
TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA  1320
GACAGCTCCC AGGCACGTCA TAGGCAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC  1380
CTGGGGTCCT GCTCACCCCC CTTTGCTCTC ACGCCCAGCC TGTCCCCAGG TTTCAGCTGG  1440
GAGAGGCCAC CTCCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG  1500
GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT  1560
GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTCACCA  1620
GAACCAGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG  1680
TCAGTGTGTG TGGGGCGCAG GGCCTCCGAT GCGGGGTCAG TGCGTGGGGG GCGCAGGGCC  1740
CCCGATGCGG GGTCAGTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT  1800
ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC  1860
CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC  1920
TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT  1980
GCCCTCCTAC CCTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG  2040
ACCTCCTGGG CAGGAAAGGG TGCAGGTCCT GAGGGCCTGT GCCCCACAGC CCCAGCACCC  2100
AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCCGTCAGCA  2160
GGCTGGGGTC TGCCCACCAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC  2220
TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG  2280
GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT  2340
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A75 DNA SEQUENCE

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
Unigene number: Hs.227948
Probeset Accession #: AB035089
Nucleic Acid Accession #: AB035089
Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

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A76 Protein sequence:

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
Unigene number: Hs.227948
Probeset Accession #: AB035089
Protein Accession #: BAB21525
Signal sequence: none found
Transmembrane domains: none found
Serine Proteinase Inhibitor domain: 13-390
Cellular Localization: secreted

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A77 DNA SEQUENCE

Gene name: hypothetical protein FLJ13459
Unigene number: none found
Probeset Accession #: XM_047266
Nucleic Acid Accession #: XM_047266
Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

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GGAGGCTCAG GCTGGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCCAGAAGA  1140
CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCCTC ACGGGCAAGG TGGAGGCAGA  1200
GTTTGAGCTG CTGACTGTGG AGGAGGCCGA GAAACGGCCA GTGGGGAAGG GGCGGAAGCA  1260
GCCAGAGCCT CTGGAGAAAC CCAGCCGCCC CAAAACTTCC TTCAACTGGT TTGTGAACCC  1320
GCTGAAGACC TTTGTCTTCT TCATCTGGCG CCGGTACTGG CGCACCCTGG TGCTGCTGCT  1380
ACTGGTGCTG CTCACCGTCT TCCTCCTCCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG  1440
CCAGGTCATC TTCCGTCCCC TCCACAAGTG ACTCTCGCTG ACCTTGGACA CTCACCCAGG  1500
GTGCCAACCC TTCAATGCCT GCTCCTGGAA GTCTTTCTTA CCCATGTGAG CTACCCCAGA  1560
GTCTAGTGCT TCCTCTGAAT AAACCTATCA CAGCCACTG
```

A78 Protein sequence:

Gene name: hypothetical protein FLJ13459

Unigene number: none found
Probeset Accession #: XM_047266
Protein Accession #: XP_047266
Signal sequence: none found
Transmembrane domains: 291-313
C2 domain: 27-86
Cellular Localization: plasma membrane / ER

```
1          11         21         31         41         51
|          |          |          |          |          |
MWIDIFPQDV PAPPPVDIKP RQPISYELRV VIWNTEDVVL DDENPLIGEM SSDIYVKSWV    60
KGLEHDKQET DVHFNSLTGE GNFNWRFVFR FDYLPTEREV SVWRRSGPFA LEEAEFRQPA   120
VLVLQVWDYD RISANDFLGS LELQLPDMVR GARGPELCSV QLARNGAGPR CNLFRCRRLR   180
GWWPVVKLKE AEDVEREAQE AQAGKKKRKQ RRRKGRPEDL EFTDMGGNVY ILTGKVEAEF   240
ELLTVEEAEK RPVGKGRKQP EPLEKPSRPK TSFNWFVNPL KTFVFFIWRR YWRTLVLLLL   300
VLLTVFLLLV FYTIPGQISQ VIFRPLHK
```

A79 DNA SEQUENCE

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
Unigene number: Hs.161031
Probeset Accession #: AL137708
Nucleic Acid Accession #: AL137708
Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT    60
GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCCTTTCTGT CTGTCTCCTT GCTCTGCCCC   120
AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG   180
ATGGCCTGGG CTGGGCCCCT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG   240
CTCTTGTGGG CAAAGCAGGG GAGGCGCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG   300
CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCCTG   360
GGGTCACCGT AGGCCCCATG TAGCACCCTG GTTCCCCTGC CTGTAGGTGA CAGGAGCCAG   420
CCCAGCCAGG TGTGCTCCCT CCCCAGGCCC TAGGCAGGCG GGTACAGGGG CCAGCAGCTG   480
CGCCCGCCCC ACCTTCCTTC CCACCCACAT GCCGAAGGGT GGCCAGGCAG GCAGGTGGAC   540
GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGGAATGTTC TGGCCGCTCC CAGCTGCACC   600
CTGCCCCTAC CTGCCACCAC CTCACCTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCCTGC   660
CAGGAATGCA CCTTTAGCCC AGGCCTGCTC AGTGAGCTCC GCCGACAGCC AGCCCTGCTC   720
CTCCCGCCAT GACCCTGCAG ACCCCTCTGG GCTTCCAAGT TCCTGGGGGC TGCAGTGAAC   780
ATGCTCCACC TGCATGGCTG GCAAACCATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT   840
AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGGATGAGA TGGGACCCCC   900
AGGCAGGGCC CAGGGTCCAG GGCCCAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCCTGG   960
TGGAGGACGC ATCCTACAGT GGGGGCAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT  1020
AGGCTGCCCA GGCCCTGCCT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG  1080
GCTGGGCCTG GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCCTTCAG  1140
CTTCCTGCTG CACAGAACCC TCGCCCCTGG CCACCCCGTG CTGCCTCCTT GCCCTGGCAG  1200
ACCCAGCACT GGCTGCTGCT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC  1260
TCCCAGCTGA CCCAGCCTCC TGGGCCGCTT CTTCCAAACC AGCAGGGTAG AAAGATGGGG  1320
CACCCACCAG TCTCTCCCAG TGCCCCGGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT  1380
ATTCCAGACC TTGTCGCCGG GACCCCCTGT GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG  1440
GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC  1500
CCAGGGCCCC GCTGGGCTCT CATTGCCGGC GCCCTTGCCG CGGGCGTCCT CCTCGTCTCC  1560
TGCCTCCTCT GTGCTGCCTG CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGGACAAG  1620
GAGTCCGTGG GTCTGGGCAG TGCCCGCGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC  1680
TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA  1740
GGCGAGTTCA GCCCCAGGGA TGGTTTAACC CCCACAGAGG CAGGGCGTTG AGGACCTTCC  1800
TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCCAT  1860
GGGCCCGAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT  1920
TTTGGGTGGG TTTGGCCGGT CTCACAGAGC GAAGCCGACG ATTTGTGCCT GTTGGGTGGC  1980
CTGGCCTGGA GGCGGGGGGT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCCAGGG  2040
CTCTGATGAG GCATGATGTC AGCACCACCT GCCCCTTGTC CCAACTCACT CCAGGTGCAA  2100
CCTGATGTGG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCCTGCAG  2160
CTCTCCCTGG AGTTCGACTT TGGAAGCCAG GAGGTGAAGG GCCCCGCTGC GCAGGACCAG  2220
CGGTTCTGCG AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG  2280
TGGGGAGCTG ACAGGGCAGG GGCCCTTGGC TGAGCCCACC CCGCTGGCTC CCAGATCAGG  2340
GTGGGCCTGA GGCAGGCAGC CGACCTGAGG CCTGGGGGCA CCGTGGACCC CTATGCCCGG  2400
GTCAGCGTCT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGCACCG AGGCACGCTC  2460
TGCCCCGTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGGATGGTC GGCTGGGTGG  2520
GCCTGGACGG CTGGATGGGC CTGGGCTGGG TGGGCCTGGG CAGCTGGGTG GGCCTGGGCA  2580
GCTGGGTGGG CCTGAGCTAG GGCAGCAGGG CCTGGCTCAC GCCGCTGCCT CAGATCCCGC  2640
AGGCGGAGCT GCCAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG  2700
GGCATGAGCC CCTGGGTGAG CTCCGTCTGC CACTGGGCAC CGTGGATCTG CAGCATGTTC  2760
TGGAGCACTG GTACCTGCTG GGCCCGCCGG CTGCCACTCA GGTGAGGTGC TGGTCACCAG  2820
GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC  2880
CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAACTCGG CCAGAATCAC CCTCCCGGGC  2940
TGAAGCCCCT CTTGCTGCCC ACAGCCCGAG CAGGTCGGGG AGCTGTGCTT CTCTCTCCGG  3000
TACGTGCCCA GCTCAGGCCG GCTGACCGTG GTGGTGCTGG AGGCTCGAGG CCTGCGTCCA  3060
GGACTTGCAG AGCCCTACGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG  3120
AGAAAGACAG CCACCAAAAA GGGCACGGCG GCCCCCTACT TCAATGAGGC CTTCACCTTC  3180
CTGGTGCCCT TCAGCCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GGACCGCAGC  3240
CTGCCGCTCC GAACTGAGCC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG  3300
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CCCCTGCAGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGCCCATTGC CCAGCGGCAC  3360
CCCCTGCGGC CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGCAGCCCCG CCTTCGCCTG  3420
CGCCTGCCCT TGCCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCCG CTGAGCCCAG  3480
GCACTTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC
```

A80 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
Unigene number: Hs.161031
Probeset Accession #: AL137708
Protein Accession #: CAB70885
Signal sequence: none found
Transmembrane domains: 69-85
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGHPPVSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA    60
STPGPRWALI AGALAAGVLL VSCLLCAACC CCRRHRKKPR DKESVGLGSA RGTTTTHLVR   120
SGSLLTQSRE GLKSRLQSPG QRGEFSPRDG LTPTEAGR
```

A81 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
Unigene number: Hs.2877
Probeset Accession #: X63629
Nucleic Acid Accession #: X63629
Coding sequence: 54-2543 (start and stop codons are underlined)

```
1          11         21         31         41         51
|          |          |          |          |          |
GCGGAACACC GGCCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC    60
TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCGCGG   120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG   180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC   240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG   300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC   360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC   420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT   480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG   540
AGACAGGCTG GTTGTTGTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC   600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA   660
TCATCGTGAC CGACCAGAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA   720
GTGTCTTAGA GGGAGTCCTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG   780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA   840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT   900
CCAGTGGCCT GGACCGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA   960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG  1020
ACAATGCTCC CATGTTTGAC CCCCAGAAGT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG  1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC  1140
GTGCCACCTA CCTTATCATG GGCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC  1200
CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC  1260
AGCACACCCT GTACGTTGAA GTGACCAACG AGGCCCCTTT TGTGCTGAAG CTCCCAACCT  1320
CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAC  1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA  1440
CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG  1500
CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC  1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA  1620
ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG  1680
ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC  1740
ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCTTTC CAGGCCCAGC  1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG  1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG  1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC  1980
ATGTCGAAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG  2040
TCCTGGCTCT GCTGTTCCTC CTGCTGGTGC TGCTTTTGTT GGTGAGAAAG AAGCGGAAGA  2100
TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG  2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG  2220
AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA  2280
TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA  2340
AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG  2400
AGGGCAGCGG CTCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCCTCCGCC TCCGACCAAG  2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT  2520
ACGGTGGCGG GGAGGACGAC TAGGCGGCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC  2580
CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA  2640
GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT  2700
TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC  2760
CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCCAGAA GCCTCTTACC TGCCGTAAAA  2820
TGCTCAACCC TGTGTCCTGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT  2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT  2940
TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG  3000
TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT  3060
ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTTGCGT TGCTATAGAT  3120
GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTTT TATTAAAGAA A
```

A82 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
Unigene number: Hs.2877
Probeset Accession #: X63629
Protein Accession #: CAA45177
Signal sequence: 1-24
Transmembrane domain: 659-675 (second underlined sequence)

Cellular localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG    60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG   120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK   180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT   240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA   300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP   360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL   420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR   480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID   540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD   600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL   660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR   720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF   780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD
```

A83 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
Unigene number: Hs.16085
Probeset Accession #: F07953
Nucleic Acid Accession #: NM_016334
Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCCAGCGTG CTGTGGCCTC    60
GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA   120
CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTTTGGA TTTGGGTGGC TTTTCTTCAT   180
GCGCCAATTG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCCGT   240
GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT   300
GAATAGCAGC TCCCGTTATT TTCACTGGAA AATGAACCTG TGCGTAATTC TGCTGATCCT   360
GGTTTTCATG GTGCCTTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA   420
TAAACAACGA CTGCTTTTTT CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA   480
ACTAGGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT   540
CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTTCTTTCTG GATTTGGTGC   600
TGTCAACTGC CCATACACTT ACATGTCTTA CTTCCTCAGG AATGTGACTG ACACAGATAT   660
TCTAGCCCTG GAACGGCGAC TGCTGCAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG   720
GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG   780
TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT   840
TATTCAACAG GAAGTGGATG CTTTGGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC   900
TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAAATATTT   960
TAATTTTCTT GGTTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT  1020
CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC  1080
TGTGAATTAT CTGGGAATCC AATTTGATGT GAAGTTTTGG TCCCAACACA TTTCCTTCAT  1140
TCTTGTTGGA ATAATCATCG TCACATCCAT CAGAGGATTG CTGATCACTC TTACCAAGTT  1200
CTTTTATGCC ATCTCTAGCA GTAAGTCCTC CAATGTCATT GTCCTGCTAT TAGCACAGAT  1260
AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA  1320
CCGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTTGGTT  1380
TGATGTGATC TTCCTGGTCA GCGCTCTCTC TAGCATACTC TTCCTCTATT TGGCTCACAA  1440
ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC  1500
CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAAATG GAACCAGGGC CTGACATTTT  1560
ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCCCTC  1620
AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACTCAAG  1680
ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG  1740
CCAAGAAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC  1800
TGAGCCAAAC ACGTAGGATT TCCGTTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC  1860
TTGAGATTGA CTCATTAAAA TCAGAGACTG T
```

A84 Protein sequence

Gene name: putative G-protein coupled receptor
Unigene number: Hs.16085
Protein Accession #: NP_057418.1
Signal sequence: none found
Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
```

```
|          |          |          |          |          |
MSFLIDSSIM ITSQILFFGF GWLFFMRQLF KDYEIRQYVV QVIFSVTFAF SCTMFELIIF    60
EILGVLNSSS RYFHWKMNLC VILLILVFMV PFYIGYFIVS NIRLLHKQRL LFSCLLWLTF   120
MYFFWKLGDP FPILSPKHGI LSIEQLISRV GVIGVTLMAL LSGFGAVNCP YTYMSYFLRN   180
VTDTDILALE RRLLQTMDMI ISKKKRMAMA RRTMFQKGEV HNKPSGFWGM IKSVTTSASG   240
SENLTLIQQE VDALEELSRQ LFLETADLYA TKERIEYSKT FKGKYFNFLG YFFSIYCVWK   300
IFMATINIVF DRVGKTDPVT RGIEITVNYL GIQFDVKFWS QHISFILVGI IIVTSIRGLL   360
ITLTKFFYAI SSSKSSNVIV LLLAQIMGMY FVSSVLLIRM SMPLEYRTII TEVLGELQFN   420
FYHRWFDVIF LVSALSSILF LYLAHKQAPE KQMAP
```

A85 DNA SEQUENCE:

Gene name: TTK protein kinase
Unigene number: Hs.169840
Probeset Accession #: M86699
Nucleic Acid Accession #: NM_003318
Coding sequence: 1026-3551(underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GGAATTCCTT TTTTTTTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG    60
CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCCTCCCG GGTTCAAGCG ATTCTCCTGC   120
CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT   180
CTTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACTCCTG   240
ACCTCAGGTG ATCCACTTGC CTTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG   300
TGCCTGGCTG ATTCTTTTTT TGTTGTTGGA TTTTTGAAAC AGGGTCTCCC TTGGTCGCCC   360
AGGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTTCAAGT   420
GATCCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GCGTGCACCA CCACACCCGG   480
CTAATTTTTG TATTTTTATT AGAGACAGGG TTTCACCATG TTGGCCAGGC TGTTCTCAAA   540
CTCCTGGACT CAAGGGATCC GCCTGCCTCC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG   600
AGTCACCATG CCTGACCTTA TAATTCTTAA GTCATTTTTT CTGGTCCATT TCTTCCTTAG   660
GGTCCTCACA ACAAATCTGC ATTAGGCGGT ACAATAATCC TTAACTTCAT GATTCACAAA   720
AGGAAGATGA AGTGATTCAT GATTTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCCT   780
GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA   840
TTTGGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA   900
ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG   960
TGCAGTTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT  1020
CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG  1080
AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAACT GTTAACCAAA  1140
TTATGATGAT GGCAAACAAC CCAGAGGACT GGTTGAGTTT GTTGCTCAAA CTAGAGAAAA  1200
ACAGTGTTCC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTCGTTAC AGTCAAGCAA  1260
TTGAAGCGCT TCCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGCTAGA ATTCAAGTGA  1320
GATTTGCTGA ATTAAAAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG  1380
CCAGAGCAAA CTGCAAGAAA TTTGCTTTTG TTCATATATC TTTTGCACAA TTTGAACTGT  1440
CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG  1500
TACCACTAGA AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC  1560
TTTCAGAGGA GGAAAAGAAG AATTTATCAG CATCTACGGT ATTAACTGCC CAAGAATCAT  1620
TTTCCGGTTC ACTTGGGCAT TTACAGAATA GGAACAACAG TTGTGATTCC AGAGGACAGA  1680
CTACTAAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT  1740
ACCGGAATTC ATTGAGACAA ACTAACAAAA CTAAACAGTC ATGCCCATTT GGAAGAGTCC  1800
CAGTTAACCT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGTACCTT  1860
GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGGTTGTG CCTGGATCTA  1920
AACCAAGTGG AAATGATTCC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT  1980
TCAAGGAACC TCTGGTGTCA GATGAAAAGA GTTCTGAACT TATTATTACT GATTCAATAA  2040
CCCTGAAGAA TAAAACGGAA TCAAGTCTTC TAGCTAAATT AGAAGAAACT AAAGAGTATC  2100
AAGAACCAGA GGTTCCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT  2160
GTATTAACCA GAATCCTGCT GCATCTTCAA ATCACTGGCA GATTCCGGAG TTAGCCCGAA  2220
AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAC  2280
AGTCACCACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTTGT AAGACACCAA  2340
GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT  2400
TTCCACCTGC TTGTCAGTTG TCAACACCTT ATGGCCAACC TGCCTGTTTC CAGCAGCAAC  2460
AGCATCAAAT ACTTGCCACT CCACTTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA  2520
ATGAATGCAT TTCGGTTAAA GGAAGAATTT ATTCCATATT AAAGCAGATA GGAAGTGGAG  2580
GTTCAAGCAA GGTATTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAAATATG  2640
TGAACTTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT  2700
TGAATAAACT ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCACGG  2760
ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA  2820
AGAAAAAATC CATTGATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG  2880
TTCACACAAT CCATCAACAT GGCATTGTTC ACAGTGATCT TAAACCAGCT AACTTTCTGA  2940
TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAAATG CAACCAGATA  3000
CAACAAGTGT TGTTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA  3060
TCAAAGATAT GTCTTCCTCC AGAGAGAATG GGAAATCTAA GTCAAAGATA AGCCCCAAAA  3120
GTGATGTTTG GTCCTTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTC  3180
AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG  3240
AATTTCCCGA TATTCCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTTGT TTAAAAAGGG  3300
ACCCAAAACA GAGGATATCC ATTCCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA  3360
CTCATCCAGT TAACCAAATG GCCAAGGGAA CCACTGAAGA AATGAAATAT GTTCTGGGCC  3420
AACTTGTTGG TCTGAATTCT CCTAACTCCA TTTTGAAAGC TGCTAAAACT TTATATGAAC  3480
ACTATAGTGG TGGTGAAAGT CATAATTCTT CATCCTCCAA GACTTTTGAA AAAAAAAGGG  3540
GAAAAAAATG ATTTGCAGTT ATTCGTAATG TCAGATAGGA GGTATAAAAT ATATTGGACT  3600
GTTATACTCT TGAATCCCTG TGGAAATCTA CATTTGAAGA CAACATCACT CTGAAGTGTT  3660
ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAAAGAAA ACTGTAAAAA TAGCAACCAC  3720
TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC  3780
TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTTG  3840
```

TAAATAAAGT TTTGTGGCTA AAATGA

A86 Protein sequence:

Gene name:	TTK protein kinase
Unigene number:	Hs.169840
Probeset Accession #:	M86699
Protein Accession #:	NP_003309
Signal sequence:	none found
Transmembrane domains:	none found
Protein Kinase Domain:	510-775
Cellular Localization:	cytoplasmic and nuclear

```
1          11         21         31         41         51
|          |          |          |          |          |
MNKVRDIKNK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS    60
VPLSDALLNK LIGRYSQAIE ALPPDKYGQN ESFARIQVRF AELKAIQEPD DARDYFQMAR   120
ANCKKFAFVH ISFAQFELSQ GNVKKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS   180
EEEKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR   240
NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGSKP   300
SGNDSCELRN LKSVQNSHFK EPLVSDEKSS ELIITDSITL KNKTESSLLA KLEETKEYQE   360
PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTFE QPVFSVSKQS   420
PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDFP PACQLSTPYG QPACFQQQQH   480
QILATPLQNL QVLASSSANE CISVKGRIYS ILKQIGSGGS SKVFQVLNEK KQIYAIKYVN   540
LEEADNQTLD SYRNEIAYLN KLQQHSDKII RLYDYEITDQ YIYMVMECGN IDLNSWLKKK   600
KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPANFLIV DGMLKLIDFG IANQMQPDTT   660
SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYY MTYGKTPFQQ   720
IINQISKLHA IIDPNHEIEF PDIPEKDLQD VLKCCLKRDP KQRISIPELL AHPYVQIQTH   780
PVNQMAKGTT EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK   840
K
```

A87 DNA SEQUENCE

Gene name:	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
Unigene number:	Hs.170195
Probeset Accession #:	BE616633
Nucleic Acid Accession #:	NM_001719
Coding sequence:	123-1418 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT    60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG   120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC   180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA   240
GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT   300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC   360
CCATGTTCAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG   420
GCCAGGGCTT CTCCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA   480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG   540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC   600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT   660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG   720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG   780
AGGAGGGCTG GCTGGTGTTT GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC   840
GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA   900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT   960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA  1020
GCCAGAACCG CTCCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG  1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC  1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG  1200
AGGGGGAGTG TGCCTTCCCT CTGAACTCCT ACATGAACGC CACCAACCAC GCCATCGTGC  1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCACGC  1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT  1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT  1440
TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA  1500
CTGCCTTTTG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG  1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA  1620
TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAAAA ACAACGCATA AAGAAAAATG  1680
GCCGGGCCAG GTCATTGGCT GGGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA  1740
TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT  1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA  1860
CAATAAAACG AATGAATG
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A88 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number:	Hs.170195
Probeset Accession #:	BE616633
Protein Accession #:	NP_001710.1
Signal sequence:	1-30
Pfam domains:	TGFb_propeptide [37-281]
Transmembrane domains:	none found
Cellular Localization:	secreted

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1          11         21         31         41         51
|          |          |          |          |          |
MHVRSLRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRLRSQE RREMQREILS    60
ILGLPHRPRP HLQGKHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS   120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY   180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVVNPR   240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS   300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE   360
GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY   420
RNMVVRACGC H
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A89 DNA SEQUENCE:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
Unigene number: Hs.27373
Probeset Accession #: F13036
Nucleic Acid Accession #: AC012478
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCGCGCCG TGCCGCTGCC CGCCCCGCTC CTGCCGCTGC TGCTGCTCGC GCTCCTGGCC    60
GCTCCCGCCG CCCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG   120
CGCGAGTCGC GGCCACCGCC CGGCCCGGGG CCCGGGAACA CCACCCGGTT TGGGTCTGGG   180
GCGGCGGGCG GCAGCGGCAG CTCCAGCTCC AACAGCAGTG GCGACGCCTT GGTGACCCGC   240
ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGCGTTCGCC   300
TTTACCACCC TCCTCATCGC CTGCCTGCTG CTGCGCGTCT TCAGGTCGGG AAAGAGGTTA   360
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGA AATGGCGCCA   420
CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG   480
TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT   540
GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCCAGCAA GATGCAGTGG AAGGCCTGAT   600
GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAAGTTGG   660
TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCGT CGGAGGTGTT   720
GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC   780
TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC   840
TTTGGGCATC CCTTTAAAGT GCCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG   900
CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCATCT   960
GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT  1020
CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAACCATG  1080
AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TTGTGAAGAC  1140
AGAGCAGTGA CTAAGGTTCT CCAGGGTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA  1200
GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC  1260
ACCCATCCTG TCAGGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG  1320
AGGGTGTTTC GGCGTCCGCG GCAGTCTCTG CATGGCGGAG GGTCAGCGGG TACCGCAACT  1380
TGCCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA  1440
ATCTGTCTCC CCTGCTGTGC CGTGGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT  1500
GTCCTTGCGT CATTTGAGCA GAGCCCACAA AAGGCAGCTG CTGCCCACGG GGAGCCTGTC  1560
AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT  1620
GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCACGTGA GGATGTCACT  1680
CACCCTGGAG GAGACTTGGA TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG  1740
GATGGCAGAT GCCAGAAGAT GGTCCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA  1800
TGTGAGAGGC TCACAGGTTC CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT  1860
TCCCCCCGAC AGCCCCTGTT TCTGTCCAGG CCCTGA
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A90 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
Unigene number: Hs.27373
Probeset Accession #: F13036
Protein Accession #: FGENESH predicted
Signal sequence: 1-27
Transmembrane domains: 94-115, 448-469
Cellular Localization: not determined

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1          11         21         31         41         51
|          |          |          |          |          |
MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG    60
AAGGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAFA FTTLLIACLL LRVFRSGKRL   120
KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGCQTLLTVP   180
VPPPFILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV   240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLLPP FGHPFKVPPT STPHGFRQLQ   300
LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLPN PWWHFSATGS PIKTLYTQTM   360
STLGLDVFCG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHHL RLLRECPPLS   420
THFVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK   480
ICLPCCAVEH LREAKRSSVT VLASPEQSPQ KAAAAHGEPV KRGPSGQLTR HTCPGWGITH   540
ANLQTIPDTQ GQEGPREDVT HPGGDLDGVA NFYLEEEGFQ DGRCQKMVLM SEEGPPSLTG   600
CERLTGSHHF SSHSKSWSFL SPRQPLFLSR P
```

EWING

A91 DNA SEQUENCE

Gene name: G protein-coupled receptor 64
Unigene number: Hs.184942

Probeset Accession #: AA435577
Nucleic Acid Accession #: NM_005756
Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA    60
CTCGCGGTCA GGATGGTTTT CTCTGTCAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA   120
GTTTTACTGA CGTTCAAGAT ATTCCTTGTC ATCATTTGTC TTCATGTCGT TCTGGTAACA   180
TCCCTGGAAG AAGATACTGA TAATTCCAGT TTGTCACCAC CACCTGCTAA ATTATCTGTT   240
GTCAGTTTTG CCCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTTACTTTA   300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAATCA CTATAGTAAA AACCTTCAAT   360
GCTTCAGGCG TCAAACCCCA GAGAAATATC TGCAATTTGT CATCTATTTG CAATGACTCA   420
GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT   480
CAACATATAA CGAATGGCAC CTTAACTGGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA   540
GAGCTCAACA AAACCCTGCA AACCCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA   600
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA   660
TGTGCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTCGAC CAATGGAACA CTGCTGCTGT   720
TCTGTCAGGA TACCCTGCCC TTCCTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG   780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA   840
TCCATCCCAG TGGTGCCTCG GGCCACTGTG CTTTCCCAGG TCCCCAAAGC TACCTCTTTT   900
GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTC CCTCTCCAAT AGGGGAGATT   960
CAACCCCTTT CACCCCAGCC TTCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC  1020
CCACAGTCTG AAACGATCTC TTCCCCTATG CCCCAAACCC ATGTCTCCGG CACCCCACCT  1080
CCTGTGAAAG CCTCATTTTC CTCTCCCACC GTGTCTGCCC CTGCGAATGT CAACACTACC  1140
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC  1200
CAAGTGTTGC AGATGGAGAA GGCTCTGTCC TTGGGCAGCC TGGAGCCTAA CCTCGCAGGA  1260
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCCCCGC CTGACATGCT GGCCCCTCTG  1320
GCTCAAAGAT TGCTGAAAGT AGTGGATGAC ATTGGCCTAC AGCTGAACTT TTCAAACACG  1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT  1440
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAAATC TTCAGGTTTC TCTGGAAACC  1500
CAAGCTCCTG AGAACAGTAT TGGCACAATT ACTCTTCCTT CATCGCTGAT GAATAATTTA  1560
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTTTTGA AACACCTGCT  1620
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT  1680
GTTGCAAACC TGACCGTCAG GAACTTGACA AGAAACGTGA CAGTCACATT AAAGCACATC  1740
AACCCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT  1800
GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC  1860
ATCTGTACCT GTAGCCATCT AACAAGCTTC GGCGTTCTGC TGGACCTATC TAGGACATCT  1920
GTGCTGCCTG CTCAAATGAT GGCTCTGACG TTCATTACAT ATATTGGTTG TGGGCTTTCA  1980
TCAATTTTTC TGTCAGTGAC TCTTGTAACC TACATAGCTT TTGAAAAGAT CCGGAGGGAT  2040
TACCCTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCTGGTCTTC  2100
CTCCTGGACT CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA  2160
TTTCTTCATT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCCTAGAAGC ATTCCATATG  2220
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATTCTGC  2280
ATTGTCGGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCCTGACTAT ATCCCCAGAT  2340
AACTATGGGC TTGGATCCTA TGGGAAATTC CCCAATGGTT CACCGGATGA CTTCTGCTGG  2400
ATCAACAACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTTG  2460
CTGAACGTCA GCATGTTCAT TGTGGTCCTG GTTCAGCTCT GTCGAATTAA AAAGAAGAAG  2520
CAACTGGGAG CCCAGCGAAA AACCAGTATT CAAGACCTCA GGAGTATCGC TGGCCTTACA  2580
TTTTTACTGG GAATAACTTG GGGCTTTGCC TTCTTTGCCT GGGGACCAGT TAACGTGACC  2640
TTCATGTATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC  2700
TGTGTGGCCA AAGAAAATGT CAGGAAGCAA TGGAGGCGGT ATCTTTGTTG TGGAAAGTTA  2760
CGGCTGGCTG AAAATTCTGA CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT  2820
GTAAACCAAG GAGTGTCCAG CTCTTCAAAT TCCTTACAGT CAAGCAGTAA CTCCACTAAC  2880
TCCACCACAC TGCTAGTGAA TAATGATTGC TCAGTACACG CAAGCGGGAA TGGAAATGCT  2940
TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGAATG GAGATGTGTG CCTTCACGAT  3000
TTCACTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCCGT  3060
ATGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATTC  3120
CTTTCTTCTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA  3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT  3240
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT  3300
TTTAGACATT TCTGATTTGG TTTCTTATCT TTCATTTTAT AAGAAGGTTG GTTTTAAACA  3360
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAAGG TAGTGAACTT TCAGCTACCT  3420
TTTAAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTTGA CTTCAGCCTG  3480
TTGGTGAGTT TAGTTGTGCA TGCCTTTGTT GTATATAAGC TAAATTCTAG TGACCCATGT  3540
GTCAAAAATC TTACTTCTAC ATTTTTTTGT ATTTATTTTC TACTGTGTAA ATGTATTCCT  3600
TTGTAGAATC ATGGTTGTTT TGTCTCACGT GATAATTCAG AAAATCCTTG CTCGTTCCGC  3660
AAATCCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA  3720
TCAAGAAATA ATGATCCCAG CCAGACTGAG AAAATGTAAG CAGACAGTGC CACAGTTAGC  3780
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA  3840
TGGGTCATGC TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG  3900
GTGCACGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCGCAT  3960
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG  4020
AGAGGGATGA ACTGTCATCC AGACCATGTG TCAGGAAAAT TGTGAACGTA GATGAGGTAC  4080
ATACACTGCC GCTTCTCAAA TCCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC  4140
CTTCTCTTAA AAAGGTACAT ATATATGGAA AAAAATCATA TTGCCGTTCT TTAAAAGGCA  4200
ACTGCATGGT ACATTGTTGA TTGTTATGAC TGGTACACTC TGGCCCAGCC AGAGCTATAA  4260
TTGTTTTTTA AATGTGTCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA  4320
GGGAACTGTC CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA  4380
TATACAGGGT CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC  4440
TTATTAGGAA CATTTCAAAC CCCTTTTAGT TAAGTCTTTC ACTAAGGTTC TCTTGCATAT  4500
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG  4560
CTGACTTGTC TTTGCAATAT TTCTTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT  4620
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AAAATCAAAA ATGTTAAAAT CAATGAAATA AATTTGCAGT TAAGA

A92 Protein sequence

Gene name: G protein-coupled receptor 64
Unigene number: Hs.184942
Protein Accession #: NP_005747.1
Signal sequence: 1-38
GPS domain: 564-615
Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPP PAKLSVVSFA    60
PSSNEVETTS LNDVTLSLLP SNETEKTKIT IVKTFNASGV KPQRNICNLS SICNDSAFFR   120
GEIMFQYDKE STVPQNQHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAQS   180
TLNCTFTIKL NNTMNACAAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI   240
VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSFAEPP DYSPVTHNVP SPIGEIQPLS   300
PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTPPPVKA SFSSPTVSAP ANVNTTSAPP   360
VQTDIVNTSS ISDLENQVLQ MEKALSLGSL EPNLAGEMIN QVSRLLHSPP DMLAPLAQRL   420
LKVVDDIGLQ LNFSNTTISL TSPSLALAVI RVNASSFNTT TFVAQDPANL QVSLETQAPE   480
NSIGTITLPS SLMNNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVISSSVANL   540
TVRNLTRNVT VTLKHINPSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC   600
SHLTSFGVLL DLSRTSVLPA QMMALTFITY IGCGLSSIFL SVTLVTYIAF EKIRRDYPSK   660
ILIQLCAALL LLNLVFLLDS WIALYKMQGL CISVAVFLHY FLLVSFTWMG LEAFHMYLAL   720
VKVFNTYIRK YILKFCIVGW GVPAVVVTII LTISPDNYGL GSYGKFPNGS PDDFCWINNN   780
AVFYITVVGY FCVIPLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG   840
ITWGFAFFAW GFVNVTFMYL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKLRLAE   900
NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNGNASTER   960
NGVSFSVQNG DVCLHDFTGK QHMFNEKEDS CNGKGRMALR RTSKRGSLHF IEQM
```

Fibrosis

A93 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
Unigene number: Hs.12844
Probeset Accession #: N67551
Nucleic Acid Accession #: NM_015507
Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCCTCCCC AGGCCGCGAG    60
CGCCCCTGCC GCGGTGCCTG GCCTCCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACTG   120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG   180
GGGTCCGGCC GGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA   240
ATGCCTCTGC CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC   300
GGGAACGCGG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC   360
TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC   420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC   480
AGATGCTTTC CAGGATACAC CGGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG   540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC   600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG   660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC   720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT   780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC   840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA   900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA   960
GGGTCCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT  1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC  1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC  1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACTTGC AGCCCTTCAA CTATGAAGAG  1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA  1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA  1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT  1380
CTGGTCCAAA GGAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT  1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC  1500
TGGAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA  1560
GGTCACAAGA AAGACATTGG CCGATTGAAA CTTCTCCTAC CTGACCTGCA ACCCCAAAGC  1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCGGAGACA AAGTCGGGAA ACTTCGAGTG  1680
TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG  1740
TGGAAGACAG GGAAAATTCA GTTGTATCAA GGAACTGATG CTACCAAAAG CATCATTTTT  1800
GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT  1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT  1920
TTGACTTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT  1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT  2040
TCTTGTATAA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA  2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT  2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA  2220
TAGAAAAAAA AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC  2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT  2340
TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAAAAA AAAAAAAA
```

A94 Protein sequence:

Gene name:	EGF-like-domain; multiple 6
Unigene number:	Hs.12844
Probeset Accession #:	N67551
Protein Accession #:	NP_056322.2
Signal sequence:	1-21
Transmembrane domains:	none found
MAM domain:	402-546
EGF domain:	80-259
Cellular Localization:	secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRRNSKGV    60
CEATCEPGCK FGECVGPNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRCV NTHGSYKCFC   120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS   180
GKVICPYNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFNTQ   240
GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKNVT   300
PEPTRTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER   360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD   420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFDYRL AGDKVGKLRV   480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV   540
SGLCPDSLLS VDD
```

GLIOBLASTOMA

A95 DNA SEQUENCE

Gene name:	ESTs
Unigene number:	Hs.293616
Probeset Accession #:	AW043782
Nucleic Acid Accession #:	none found

Coding sequence: 38-1075(underlined sequence corresponds to start and stop codon)

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG    60
CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAACAACT TCACCAATGA   120
GTGCAACATA CCAGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA   180
GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA   240
GTCGAAATGT GGCCCAACCT TCTTCCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG   300
CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC   360
AAACCCTCTG CTTTGCTCCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA   420
GAGCTTCATC TGCGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA   480
AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA   540
TTACCCCAGC ATCACCTATG CCATCATCGG CAGCTCCGTC ATTTTTGTGC TGGTGGTGGC   600
CCTGCTGGCA CTGGTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT   660
GCACCGGCTG CAGCACCCTG TGCTGCTGTC CCGCCTGGTG GTCCTGGACC ACCCCCACCA   720
CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA   780
GAATGCGTCG GAAGTAGGCT CCCCACCCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC   840
TGCGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC   900
CGACCTGCCC CCCTACCGCT CCCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC   960
CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCCAGGA  1020
GGGCACTGCT GAGCCCAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC  1080
AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTTG  1140
TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT  1200
AACTATCTCT GCATTCCCCT CCTCCCCCAG ACTTCAGAGA TGTTTTTCTG GCGTCTCAGT  1260
TGACATGATC TGTTGTGCGT CTTTTCTGTC AGGTCACTCT TCCCTTGGGA CCCGAGATCA  1320
CACCCTCATT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG  1380
AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA  1440
CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG  1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAAATT CCATTTGAGC  1560
ATCAAAACCT GCTTTGCACA ATCCTATTTG ATGCCCCCAG TTCAGCAGAG TCAGTGGCCA  1620
AAGAAAACTT TGGACGTGAG TAACACCCTT CAGCAGTCGC AACGTTATTT TGGTTTTGTG  1680
AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTTG CCCAAGAATG  1740
CTCATTCTGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCCTAA AATAGGCAGG  1800
GAGCCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC  1860
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCACC CTCCCAGCTG  1920
ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT  1980
GTATGTCCCT GTGGCCCACA CCCAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC  2040
CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTTGG ACTTGAGGAC  2100
ACTGGTTTCT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC  2160
CTGCACTGTG CACGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG  2220
GGTCAGGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG  2280
AGACAATTTG GAGTCAAGAT TTTCCATTTG GATCTATTTT AAATCTTTTA GAAATGCATT  2340
TGAAACAGTG TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA  2400
AGCTGTCTCT TTTTTTGTTT TTCCTTTAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC  2460
ACACCCTTGC CCCGCTGAGC CCCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG  2520
ACATTTGTGC ATTGTTGCAC TTTGAGGTTA TTATTTATCA AGTTCTTGAA GGAAGCAGAA  2580
AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT  2640
TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT  2700
AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAAATGGAA CCAGGTAGAG  2760
CCACTCCGGG CAGCTGTCAC CCATTCAGAA CTTCTTTCCG CAGCTGAAGA AATGTTCAGT  2820
AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTCAG  2880
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TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA  2940
AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA  3000
AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTTAA AATAGCACTT GAGTTATTTT  3060
CTGAGTAATC CAATAAAGAA CTTTTGATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA  3120
CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC  3180
TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT  3240
GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT  3300
AGATAAGGGA TGCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTTT ATTATAGATT  3360
TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT  3420
TTTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT  3480
TTTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG  3540
AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT  3600
AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA  3660
TTTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG  3720
GAAAGGTTGT GTGTCGTTGC TTTTTGTGTT TTGGTTAGGC TTGGTTTTGT TTTTTAATTT  3780
TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAWG GWMCTAMARM  3840
AAMMAAAAAC AWYWTTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTTAACA CCACTTCGGG  3900
TGGGGCGGCG GGGCCCACGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG  3960
GAAACCCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAAA ACGCGCCGGG  4020
GGAAACCGCA GAGTGTTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG  4080
GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G
```

A96 Protein sequence:

Gene name:	ESTs
Unigene number:	Hs.293616
Probeset Accession #:	AW043782
Protein Accession #:	none found
Signal sequence:	1-17
Transmembrane domains:	169-191
LDLa domains:	28-66, 70-108, 112-149
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD    60
EKECPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC   120
KNGLCIDKSF ICDGQNNCQD NSDEESCESS QEPGSSGQVFV TSENQLVYYP SITYAIIGSS   180
VIFVLVVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ   240
YVASQAEQNA SEVGSPPSYS EALLDQRPAW YDLPPPPYSS DTESLNQADL PPYRSRSGSA   300
NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV
```

LUNG

A97 DNA SEQUENCE

Gene name:	putative GPCR, Weakly similar to dJ365012.1
Unigene number:	Hs.256897
Probeset Accession #:	BE001836
Nucleic Acid Accession #:	BE001836
Coding sequence:	1-2955 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCCGTCA AATCTTTTTC CTTCAACACT GGGAATGATG GGCTAGACCC AGACCCAATC    60
ATGTTAAGTA TGATAGGGAT CAGTGGCCCA GCTGGTGTGG AAGACAAGTG GGTCATACTG   120
GGTTTAGGCC CACATAGCAC TAAAGGTCTT CAACATGCAA TTAGAAGCTC AAATGTTGAC   180
GGGAATATTG TTCACTCTAA AAAAGATGTT TCTATTAGAA TTTACTTACT CTTTCATGAA   240
AACATAGATG CTTCCTCTTT CCTGATTAGT GATGGCCATC AGTTAACCCA AGTGCACTCA   300
GAGAAGTCAA ATTCTGACAC AATCCAGCAA GTAACTATAA AAACTGATGG CCCAGTCGAA   360
GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAAG AGATTTGAGA   420
AATTTTCTGA AGCTCTTGAA GCCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC   480
AGAGCAAAGG CTACCACAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA   540
GACAGCTACA CCTGGTTTCC TCCCTCATGC CTTGATCCCC AGAACTGCTA CCTTCACACG   600
GCTGGAGCAC TCCCAAGCTG TGAATGTCAT CTCAACAACC TCAGCCAGAG TGTCAATTTC   660
TGTGAGAGAA CAAAGATTTG GGGCACTTTC AAAATTAATG AAAGGTTTAC AAATGACCTT   720
TTGAATTCAT CTTCTGCTAT ATACTCCAAA TATGCAAATG GAATTGAAAT TCAACTTAAA   780
AAAGCATATG AAAGAATTCA AGGTTTTGAG TCGGTTCAGG TCACCCAATT TCGAAATGGA   840
AGCATCGTTG CTGGGTATGA AGTTGTTGGC TCCAGCAGTG CATCTGAACT GCTGTCAGCC   900
ATTGAACATG TTGCCGAGAA GGCTAAGACA GCCCTTCACA AGCTGTTTCC ATTAGAAGAC   960
GGCTCTTTCA GAGTGTTCGG AAAAGCCCAG TGTAATGACA TTGTCTTTGG ATTTGGGTCC  1020
AAGGATGATG AATATACCCT GCCCTGCAGC AGTGGCTACA GGGGAAACAT CACAGCCAAG  1080
TGTGAGTCCT CTGGGTGGCA GGTCATCAGG GAGACTTGTG TGCTCTCTCT GCTTGAAGAA  1140
CTGAACAAGA ATTTCAGTAT GATTGTAGGC AATGCCACTG AGGCAGCTGT GTCATCCTTC  1200
GTGCAAAATC TTTCTGTCAT CATTCGGCAA AACCCATCAA CCACAGTGGG GAATCTGGCT  1260
TCGGTGGTGT CGATTCTGAG CAATATTTCA TCTCTGTCAC TGGCCAGCCA TTTCAGGGTG  1320
TCCAATTCAA CAATGGAGGA TGTCATCAGT ATAGCTGACA ATATCCTTAA TTCAGCCTCA  1380
GTAACCAACT GGACAGTCTT ACTGCGGGAA GAAAAGTATG CCAGCTCACG GTTACTAGAG  1440
ACATTAGAAA ACATCAGCAC TCTGGTGCCT CCGACAGCTC TTCCTCTGAA TTTTTCTCGG  1500
AAATTCATTG ACTGGAAAGG GATTCCAGTG AACAAAAGCC AACTCAAAAG GGGTTACAGC  1560
TATCAGATTA AAATGTGTCC CCAAAATACA TCTATTCCCA TCAGAGGCCG TGTGTTAATT  1620
GGGTCAGACC AATTCCAGAG ATCCCTTCCA GAAACTATTA TCAGCATGGC CTCGTTGACT  1680
CTGGGGAACA TTCTACCCGT TTCCAAAAAT GGAAATGCTC AGGTCAATGG ACCTGTGATA  1740
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TCCACGGTTA TTCAAAACTA TTCCATAAAT GAAGTTTTCC TATTTTTTTC CAAGATAGAG  1800
TCAAACCTGA GCCAGCCTCA TTGTGTGTTT TGGGATTTCA GTCATTTGCA GTGGAACGAT  1860
GCAGGCTGCC ACCTAGTGAA TGAAACTCAA GACATCGTGA CGTGCCAATG TACTCACTTG  1920
ACCTCCTTCT CCATATTGAT GTCACCTTTT GTCCCCTCTA CAATCTTCCC CGTTGTAAAA  1980
TGGATCACCT ATGTGGGACT GGGTATCTCC ATTGGAAGTC TCATTTTATG CCTGATCATC  2040
GAGGCTTTGT TTTGGAAGCA GATTAAAAAA AGCCAAACCT CTCACACACG TCGTATTTGC  2100
ATGGTGAACA TAGCCCTGTC CCTCTTGATT GCTGATGTCT GGTTTATTGT TGGTGCCACA  2160
GTGGACACCA CGGTGAACCC TTCTGGAGTC TGCACAGYTG CTGTGTTCTT TACACACTTC  2220
TTCTACCTCT CTTTGTTCTT CTGGATGCTC ATGCTTGGCA TCCTGCTGGC TTACCGGATC  2280
ATCCTCGTGT TCCATCACAT GGCCCAGCAT TTGATGATGG CTGTTGGATT TTGCCTGGGT  2340
TATGGGTGCC CTCTCATTAT ATCTGTCATT ACCATTGCTG TCACGCAACC TAGCAATACC  2400
TACAAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAACC ACTCCTGGCT  2460
TTTGTTGTCC CTGCACTGGC TATTGTGGCT GTGAACTTCG TTGTGGTGCT GCTAGTTCTC  2520
ACAAAGCTCT GGAGGCCGAC TGTTGGGGAA AGACTGAGTC GGGATGACAA GGCCACCATC  2580
ATCCGCGTGG GGAAGAGCCT CCTCATTCTG ACCCCTCTGC TAGGGCTCAC CTGGGGCTTT  2640
GGAATAGGAA CAATAGTGGA CAGCCAGAAT CTGGCTTGGC ATGTTATTTT TGCTTTACTC  2700
AATGCATTCC AGGGATTTTT TATCTTATGC TTTGGAATAC TCTTGGACAG TAAGCTGCGA  2760
CAACTTCTGT TCAACAAGTT GTCTGCCTTA AGTTCTTGGA AGCAAACAGA AAAGCAAAAC  2820
TCATCAGATT TATCTGCCAA ACCCAAATTC TCAAAGCCTT TCAACCCACT GCAAAACAAA  2880
GGCCATTATG CATTTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT  2940
GTCTCAAATG AATAA
```

A98 PROTEIN SEQUENCE

Gene name: putative GPCR, Weakly similar to dJ365O12.1
Unigene number: Hs.256897
Protein Accession #: none found
Signal sequence: 1-17
Pfam domain: 7tm_2 [561-820]
Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MHALLLCFSV LNGASGLSLL QSPVBEYQLL LQVTYRDSKE KRDLRNFLKL LKPPLLWSHG    60
LIRIIRAKAT TDCNSLNGVL QCTCEDSYTW FPPSCLDPQN CYLHTAGALP SCECHLNNLS   120
QSVNFCERTK IWGTFKINER FTNDLLNSSS AIYSKYANGI EIQLKKAYER IQGFESVQVT   180
QFRNGSIVAG YEVVGSSSAS ELLSAIEHVA EKAKTALHKL FPLEDGSFRV FGKAQCNDIV   240
FGFGSKDDEY TLPCSSGYRG NITAKCESSG WQVIRETCVL SLLEELNKNF SMIVGNATEA   300
AVSSFVQNLS VIIRQNPSTT VGNLASVVSI LSNISSLSLA SHFRVSNSTM EDVISIADNI   360
LNSASVTNWT VLLREEKYAS SRLLETLENI STLVPPTALP LNFSRKFIDW KGIPVNKSQL   420
KRGYSYQIKM CPQNTSIPIR GRVLIGSDQF QRSLPETIIS MASLTLGNIL PVSKNGNAQV   480
NGPVISTVIQ NYSINEVFLF FSKIESNLSQ PHCVFWDFSH LQWNDAGCHL VNETQDIVTC   540
QCTHLTSFSI LMSPFVPSTI FPVVKWITYV GLGISIGSLI LCLIIEALFW KQIKKSQTSH   600
TRRICMVNIA LSLLIADVWF IVGATVDTTV NPSGVCTAAV FFTHFFYLSL FFWMLMLGIL   660
LAYRIILVFH HMAQHLMMAV GFCLGYGCPL IISVITIAVT QPSNTYKRKD VCWLNWSNGS   720
KPLLAFVVPA LAIVAVNFVV VLLVLTKLWR PTVGERLSRD DKATIIRVGK SLLILTPLLG   780
LTWGFGIGTI VDSQNLAWHV IFALLNAFQV RIVTITYCIV K
```

A99 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
Unigene number: Hs.16085
Probeset Accession #: F07953
Nucleic Acid Accession #: NM_016334
Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCCAGCGTG CTGTGGCCTC    60
GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA   120
CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTTGGA TTTGGGTGGC TTTTCTTCAT   180
GCGCCAATTG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCCGT   240
GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT   300
GAATAGCAGC TCCCGTTATT TTCACTGGAA AATGAACCTG TGCGTAATTC TGCTGATCCT   360
GGTTTTCATG GTGCCTTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA   420
TAAACAACGA CTGCTTTTTT CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA   480
ACTAGGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT   540
CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTTCTTTCTG GATTTGGTGC   600
TGTCAACTGC CCATACACTT ACATGTCTTA CTTCCTCAGG AATGTGACTG ACACAGATAT   660
TCTAGCCCTG GAACGGCGAC TGCTGCAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG   720
GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG   780
TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT   840
TATTCAACAG GAAGTGGATG CTTTGGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC   900
TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAAATATTT   960
TAATTTTCTT GGTTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT  1020
CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC  1080
TGTGAATTAT CTGGGAATCC AATTTGATGT GAAGTTTTGG TCCCAACACA TTTCCTTCAT  1140
TCTTGTTGGA ATAATCATCG TCACATCCAT CAGAGGATTG CTGATCACTC TTACCAAGTT  1200
CTTTTATGCC ATCTCTAGCA GTAAGTCCTC CAATGTCATT GTCCTGCTAT TAGCACAGAT  1260
AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA  1320
CCGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTTGGTT  1380
TGATGTGATC TTCCTGGTCA GCGCTCTCTC TAGCATACTC TTCCTCTATT TGGCTCACAA  1440
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ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC  1500
CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAAATG GAACCAGGGC CTGACATTTT  1560
ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCCCTC  1620
AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACTCAAG  1680
ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG  1740
CCAAGAAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC  1800
TGAGCCAAAC ACGTAGGATT TCCGTTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC  1860
TTGAGATTGA CTCATTAAAA TCAGAGACTG T
```

A100 Protein sequence

Gene name: putative G-protein coupled receptor
Unigene number: Hs.16085
Protein Accession #: NP_057418.1
Signal sequence: none found
Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446
Cellular Localization: plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MSFLIDSSIM ITSQILFFGF GWLFFMRQLF KDYEIRQYVV QVIFSVTFAF SCTMFELIIF    60
EILGVLNSSS RYFHWKMNLC VILLILVFMV PFYIGYFIVS NIRLLHKQRL LFSCLLWLTF   120
MYFFWKLGDP FPILSPKHGI LSIEQLISRV GVIGVTLMAL LSGFGAVNCP YTYMSYFLRN   180
VTDTDILALE RRLLQTMDMI ISKKKRMAMA RRTMFQKGEV HNKPSGFWGM IKSVTTSASG   240
SENLTLIQQE VDALEELSRQ LFLETADLYA TKERIEYSKT FKGKYFNFLG YFFSIYCVWK   300
IFMATINIVF DRVGKTDPVT RGIEITVNYL GIQFDVKFWS QHISFILVGI IIVTSIRGLL   360
ITLTKFFYAI SSSKSSNVIV LLLAQIMGMY FVSSVLLIRM SMPLEYRTII TEVLGELQFN   420
FYHRWFDVIF LVSALSSILF LYLAHKQAPE KQMAP
```

A101 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
Unigene number: Hs.19322
Probeset Accession #: AA088458
Nucleic Acid Accession #: AA088458
Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA    60
CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG   120
GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC   180
CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG   240
CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC   300
TGTGCCAGCC GGGCCCTGCC CCCGTCCTCC TCCGGGCCCC CCTGCCCTGC CCTGACGTCC   360
ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC   420
CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG   480
GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG   540
GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC   600
AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCCTCTC TGGCTGGAGA CCCCCGGCAG   660
GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCCGCCC TTGCCAGATG GGCTCCCCAG   720
GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG   780
ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCAG CTACTACTGG CCGCTGTCAG   840
TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCCG TTTCCAGCGG TGCCGCCCTG   900
GGTCCCATCT TCAGGGAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC   960
AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC  1020
CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT  1080
GTAAGCGGGG GGTGCCTGCC TGGCTGGGGA GCCCCAGGGA TAGCGGTCGG ACTTCAGGTT  1140
CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT  1200
GGCCTGCATG TGCCTCCCAC AGACCCTGGG GTGATGGCCT TCCCCCTCTT GGCCGGGACG  1260
TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA  1320
GACAGCTCCC AGGCACGTCA TAGGCAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC  1380
CTGGGGTCCT GCTCACCCCC CTTTGCTCTC ACGCCCAGCC TGTCCCCAGG TTTCAGCTGG  1440
GAGAGGCCAC CTCCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG  1500
GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT  1560
GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTCACCA  1620
GAACCAGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG  1680
TCAGTGTGTG TGGGGCGCAG GGCCTCCGAT GCGGGGTCAG TGCGTGGGGG GCGCAGGGCC  1740
CCCGATGCGG GGTCAGTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT  1800
ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC  1860
CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC  1920
TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT  1980
GCCCTCCTAC CCTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG  2040
ACCTCCTGGG CAGGAAAGGG TGCAGGTCCT GAGGGCCTGT GCCCCACAGC CCCAGCACCC  2100
AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCCGTCAGCA  2160
GGCTGGGGTC TGCCCACCAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC  2220
TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG  2280
GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT  2340
GAGACAGGCT GGCACCTCCG GAAAAACTGC CTTTCAGCCT TGGTGTTCCG TGCAAGGTGA  2400
AAAGAAATAG GTCCTCCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC  2460
CACGAGGGGA GAATTTAAAG GCCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT  2520
GCAGACCCTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT  2580
GAGCAGCGTC CCTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT  2640
GCGTGCACAC TGTGATGACA CCCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG  2700
CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA  2760
TTTTGTGTTG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTCACGC  2820
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CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA  2880
CCCCATCTCT ACAARAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT  2940
TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC  3000
TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA  3060
AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA
```

A102 DNA SEQUENCE

Gene name:	TMPRSS3a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Nucleic Acid Accession #:	AB038157
Coding sequence:	202-1566 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTCATGCCC GTGTGAGCCA    60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG   120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC   180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC   240
TCATTCCGAT CGCTTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA   300
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC   360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC   420
TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC   480
GGAGTCTCGG ATTGCAAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG   540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCATGTGCTC CGATGACTGG   600
AAGGGTCACT ACGCAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA   660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT   720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA   780
TGTGCCTCTG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC   840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC   900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCT GTGGATCATC   960
ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT  1020
CTAGTTTCCC TGTTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC  1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA  1140
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC  1200
GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC  1260
TCCCCTGTCC TGAACCACGC GGCCGTCCCT TTGATTTCCA ACAAGATCTG CAACCACAGG  1320
GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC  1380
GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG  1440
AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG  1500
TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA  1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA  1620
TCCTCCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCTTG GAGCTCTGAG  1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT  1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG  1800
AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC  1860
TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT  1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA  1980
CCTCAAATGA TGTGCCTGCT TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC  2040
ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA  2100
AGGGCGGCCT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG  2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC  2220
GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCAGAA  2280
CCAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA  2340
ATGACTCGTT TAAGGCCTAT TTTCATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA  2400
TTGTCCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA  2460
AAAAAAAA
```

A103 Protein sequence:

Gene name:	TMPRSS3a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Protein Accession #:	BAB20077
Signal sequence:	none found
Transmembrane domains:	43-65, 239-261
Tryp_SPc domain:	216-444
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI    60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF   120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK   180
VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH   240
LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR   300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVLNHA   360
AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSCQGD SGGPLVCQER RLWKLVGATS   420
FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT
```

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)
Unigene number: Hs.208229
Probeset Accession #: AI819198
Nucleic Acid Accession #: NM_032551.1
Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCGGC CAACGCCTCC    60
GGCTGCCCGG GCTGTGGCGC CAACGCCTCG GACGGCCCAG TCCCTTCGCC GCGGGCCGTG   120
GACGCCTGGC TCGTGCCGCT CTTCTTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC   180
TCGCTGGTCA TCTACGTCAT CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC   240
ATCGCCAACC TGGCGGCCAC GGACGTGACC TTCCTCCTGT GCTGCGTCCC CTTCACGGCC   300
CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GGCGACTTCA TGTGCAAGTT CGTCAACTAC   360
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC   420
TGGTACGTGA CGGTGTTCCC GTTGCGCGCC CTGCACCGCC GCACGCCCCG CCTGGCGCTG   480
GCTGTCAGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTCGCCCTG   540
CACCGCCTGT CACCCGGGCC GCGCGCCTAC TGCAGTGAGG CCTTCCCCAG CCGCGCCCTG   600
GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC   660
TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCCGGG TCGCCGTGCG CCCCGCGCCC   720
GCCGATAGCG CCCTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAAG   780
GTCTCGCGGC TGGTGGCGGC CGTGGTCCTG CTCTTCGCCG CCTGCTGGGG CCCCATCCAG   840
CTGTTCCTGG TGCTGCAGGC GCTGGGCCCC GCGGGCTCCT GGCACCCACG CAGCTACGCC   900
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCCTACA GCAACTCCGC GCTGAACCCG   960
CTGCTCTACG CCTTCCTGGG CTCGCACTTC CGACAGGCCT TCCGCCGCGT CTGCCCCTGC  1020
GCGCCGCGCC GCCCCCGCCG CCCCCGCCGG CCCGGACCCT CGGACCCCGC AGCCCCACAC  1080
GCGGAGCTGC ACCGCCTGGG GTCCCACCCG GCCCCCGCCA GGGCGCAGAA GCCAGGGAGC  1140
AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA
```

A105 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA
Unigene number: Hs.208229
Protein Accession #: AI819198
Signal sequence: none found
Pfam domains: 7tm_1 [59-323]
Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282
Cellular Localization: plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSPRAV DAWLVPLFFA ALMLLGLVGN    60
SLVIYVICRH KPMRTVTNFY IANLAATDVT FLLCCVPFTA LLYPLPGWVL GDFMCKFVNY   120
IQQVSVQATC ATLTAMSVDR WYVTVFPLRA LHRRTPRLAL AVSLSIWVGS AAVSAPVLAL   180
HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP   240
ADSALQGQVL AERAGAVRAK VSRLVAAVVL LFAACWGPIQ LFLVLQALGP AGSWHPRSYA   300
AYALKTWAHC MSYSNSALNP LLYAFLGSHF RQAFRRVCPC APRRPRRPRR PGPSDPAAPH   360
AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL
```

A106 DNA SEQUENCE

Gene name: integrin, beta 8
Unigene number: Hs.52620
Probeset Accession #: AA479726
Nucleic Acid Accession #: NM_002214
Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

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CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG    60
CTGCCGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT   120
GTTGGCCTCC CTGCCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT   180
TCCCCTCGAC CTCGCCGGCG TACCCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT   240
TAGGGTGGTT TCCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG   300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT   360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT   420
TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG   480
GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT   540
CCGAGCCGCG GGGTCCGCCT GCTAGGCCTG CGGAAAACGT CCTAGCGACA CTCGCCCGCG   600
GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGCGC   660
GGGGCGGGCT GTTTTGCATT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTTG   720
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CACTTGTTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT   840
CCTGTGCCAG GTGCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA   900
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GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA  1020
TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA  1080
ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTTG  1140
ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTTAT  1200
CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTCGTCTTGG ATTTGGCTCA TACGTTGATA  1260
AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT  1320
ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA  1380
TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG  1440
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AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA  1500
AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA  1560
GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACGTCT  1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG  1680
ACAACAACAT TAATGTCATC TTTGCAGTTC AAGGAAAACA ATTTCATTGG TATAAGGATC  1740
TTCTACCCCT CTTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA  1800
ATAATTTGGT AGTGGAAGCC TATCAGAAGC TCATTTCAGA AGTGAAAGTT CAGGTGGAAA  1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC  1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG  1980
TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAACTA TGCAATAATC AAACCTATTG  2040
GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCAG TGTGAGGACA  2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACTTTTCT AGATTCCAAG TGTTTCCAGT  2160
GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC  2220
ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC  2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC  2340
CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT  2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG  2460
TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT  2520
GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT  2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCCTCA CAATTTGTCT CAGGCTATAC  2640
TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAACAACA GCATTATGTC GACCAAACTT  2700
CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTTT CATCATTTTC ATAGTTACAT  2760
TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAATAGTA  2820
ATAAAATTAA GTCCTCATCA GATTACAGAG TGTCAGCCTC AAAAAAGGAT AAGTTGATTC  2880
TGCAAAGTGT TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA  2940
TGGATATCAG CAAATTAAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATTT  3000
TTAAACACTT AATGGGAAAC TGGAATTGTT AATAATTGCT CCTAAAGATT ATAATTTTAA  3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC  3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA  3180
AAAATGTGTC TTACTACTGT TTGAGACTAG TGTCGTTGTA GCACTTTACT GTAATATATA  3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG  3300
TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT  3360
CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAAATA ATCTGGCAAG  3420
TATATTCTAA GGTTGCCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG  3480
ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA  3540
AAAGATTATT GCTTTTTAAA GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT  3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTTT GCCTTTATGT TTTGTTTTCT  3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC  3720
TACTGCCATA AAAAACTAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT  3780
GAATGTTAA
```

A107 Protein sequence:

Gene name:	Integrin, beta 8
Unigene number:	Hs.52620
Probeset Accession #:	AA479726
Protein Accession #:	NP_002205.1
Signal sequence:	1-39
Transmembrane domains:	682-704
EGF domain:	552-584
INB domain:	54-469
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MCGSALAFFT AAFVCLQNDR RGPASFLWAA WVFSLVLCLG QGEDNRCASS NAASCARCLA    60
LGPECGWCVQ EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP   120
GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF   180
SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA   240
VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRLL LVMTDQTSHL ALDSKLAGIV   300
VPNDGNCHLK NNVYVKSTTM EHPSLGQLSE KLIDNNINVI FAVQGKQFHW YKDLLPLLPG   360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR   420
NVTSNDEVLF NVTVTMKKCD VTGGKNYAII KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK   480
CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDQPVC SGRGVCVCGK CSCHKIKLGK   540
VYGKYCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRCQCPSAAA QHCVNSKGQV   600
CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS   660
CALMEQQHYV DQTSECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKIKSSS   720
DYRVSASKKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF
```

A108 DNA sequence

Gene name:	ESTs
Unigene number:	Hs.128899
Probeset Accession #:	AA983251
Nucleic Acid Accession #:	AA983251
Coding sequence:	1-1749 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA    60
GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC   120
GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC   180
GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG   240
```

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CCGCGGCCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGCGCC GCAGGACCCT   300
CGCCTGCGTC CTGGACGTTC CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT   360
TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCCATC AGCGAGTGCA   420
ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA   480
GCTCCTGGAC CTAGGGCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC   540
CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCC GGGGGTCGCC GGGGCCACGA   600
CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCCAG GGTGGTGCCA   660
TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCCTGGAA CGCCGCTTCG CTCCTGCAGC   720
TGCTGCTGGC TGCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC   780
TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC   840
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG   900
GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC   960
CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA  1020
GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC  1080
TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC  1140
CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCCTCTCCCC TGCAGCGGCC CGCCTTGCCC  1200
ATCTACGTGC CGTTCCTCAT TGTTGGCTCC GTGTTTGTCG CCTTTATCAT CTTGGGGTCC  1260
CTGGTGGCAG CCTGTTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA  1320
GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC  1380
CGGGGGTCGT CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC  1440
GGGGCCCGGG CGCCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG  1500
AACAACGTGT ATGTCAACAT GCCCACGAAT TTCTCTGTGC TGAACTGTCA GCAGGCCACC  1560
CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG  1620
CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCCTGCA GCCTGGCTAC  1680
AGGCAGATTC AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG  1740
ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG  1800
GATTCTCGAG GTGGAAGTCC GCACATGTCG GTGGTATTTA TGGCACGATT CCTTTGGATG  1860
GCTTCATTTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT  1920
CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCCTC AGCTGGAGAT GACTGTGATG  1980
TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA  2040
AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT  2100
TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTTATCTCC CTTTTACTGG GACTTTTTTT  2160
TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGCAG  2220
TGGTGCGATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC  2280
AGCCTCCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT  2340
TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA  2400
TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC  2460
TGAGCCTTTT TTTTTTTCTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT  2520
ATTCTAAAAG GAAACCTGTT TGAACTCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA  2580
GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG  2640
GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA  2700
TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC  2760
TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAAACCATT CATCCCCTTC  2820
TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTTT  2880
TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG  2940
TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT  3000
GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA  3060
AAAAATTTTC TTGTCTTAGT TATAAAAATT CAAAGAAATG TGTTACAAAG ATACTTAGTA  3120
TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTTACTTT  3180
GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG  3240
GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCCAC ACTGTTCTTG  3300
ATTTCCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT  3360
CAAATTCAAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAAGAT AACTTTAAGG  3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT  3480
GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATTC  3540
TGTTTCATGA CTGAATAATG TAAAACCAGT GTTGGCAATT GGTATCATCA ATGATACTCA  3600
TTTTTTAATA ACCAAAGGCA GGGGAAAATC ATTTTACTTA TTAATAAATA TTTTATGATG  3660
TGAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

A109 Protein sequence

Gene name:	ESTs
Unigene number:	Hs.128899
Protein Accession #:	none found
Signal sequence:	1-11
Transmembrane domains:	402-424
Cellular Localization:	not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MLSGFLMSPS TQHRAQYTPG GKKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA    60
GEAEKGNRGE PPAWIRAQQQ PRPPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA   120
SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG   180
PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAPRVVP CGALAARPSP HPGTPLRSCS   240
CCWLRCWRRG RGPSGEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE   300
ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPPPV RAWQRCSPEG   360
SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPFLIVGS VFVAFIILGS   420
LVAACCRCL RPKQDPQQSR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS   480
GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGQYL HPPYVGYTVQ   540
HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQKMYPAV TV
```

A110 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG    60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT   120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC   180
ACTTGGGTAC AAACTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA   240
ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC   300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT   360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA   420
GACCCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA   480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT   540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT   600
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAATA   660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAAATAAAT GTTTTTTAAA   720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAA
```

A111 Protein sequence:
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK    60
PLMVIHHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM   120
FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL
```

A112 DNA SEQUENCE
Gene name: Homo sapiens type II membrane serine protease mRNA
Unigene number: Hs.63325
Probeset Accession #: AA411502
Nucleic Acid Accession #: NM_016425
Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC    60
AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA   120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC   180
TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG   240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT   300
GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA   360
GGGAACTGGT TCTCTGCCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT   420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG   480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT   540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG   600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC   660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTCGACCC CCACTGGGTC   720
CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA   780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA   840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC   900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA   960
GCCACCCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT  1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT  1080
GCGTACCAGG GGGAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG  1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG  1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCCAGG AGTATACACC  1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
```

A113 Protein sequence:
Gene name: Homo sapiens type II membrane serine protease mRNA
Unigene number: Hs.63325
Probeset Accession #: AA411502
Protein Accession #: NP_057509
Signal sequence: none found
Transmembrane domains: 31-53
LDLa domain: 54-94
Tryp_SPc domain: 204-429
Cellular Localization: plasma membrane/ER

```
1          11         21         31         41         51
|          |          |          |          |          |
MLQDPDSDQP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY    60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT   120
GNWFSACFDN FTEALAETAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELRMRNSS   180
GPCLSGSLVS LHCLACGKSL KTPRVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV   240
LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIIE FNPMYPKDND IALMKLQFPL   300
TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD   360
AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT   420
KVSAYLNWIY NVWKAEL
```

A114 DNA SEQUENCE:

Gene name: TTK protein kinase
Unigene number: Hs.169840
Probeset Accession #: M86699
Nucleic Acid Accession #: NM_003318
Coding sequence: 1026-3551(underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
GGAATTCCTT TTTTTTTTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG    60
CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCCTCCCG GGTTCAAGCG ATTCTCCTGC   120
CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT   180
CTTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACTCCTG   240
ACCTCAGGTG ATCCACTTGC CTTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG   300
TGCCTGGCTG ATTCTTTTTT TGTTGTTGGA TTTTTGAAAC AGGGTCTCCC TTGGTCGCCC   360
AGGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTTCAAGT   420
GATCCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GCGTGCACCA CCACACCCGG   480
CTAATTTTTG TATTTTTATT AGAGACAGGG TTTCACCATG TTGGCCAGGC TGTTCTCAAA   540
CTCCTGGACT CAAGGGATCC GCCTGCCTCC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG   600
AGTCACCATG CCTGACCTTA TAATTCTTAA GTCATTTTTT CTGGTCCATT TCTTCCTTAG   660
GGTCCTCACA ACAAATCTGC ATTAGGCGGT ACAATAATCC TTAACTTCAT GATTCACAAA   720
AGGAAGATGA AGTGATTCAT GATTTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCCT   780
GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA   840
TTTGGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA   900
ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG   960
TGCAGTTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT  1020
CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG  1080
AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAACT GTTAACCAAA  1140
TTATGATGAT GGCAAACAAC CCAGAGGACT GGTTGAGTTT GTTGCTCAAA CTAGAGAAAA  1200
ACAGTGTTCC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTCGTTAC AGTCAAGCAA  1260
TTGAAGCGCT TCCCCCAGAT AAATATGGCC AAAATGAGAG TTTGCTAGA ATTCAAGTGA  1320
GATTTGCTGA ATTAAAAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG  1380
CCAGAGCAAA CTGCAAGAAA TTTGCTTTTG TTCATATATC TTTTGCACAA TTTGAACTGT  1440
CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG  1500
TACCACTAGA AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC  1560
TTTCAGAGGA GGAAAAGAAG AATTTATCAG CATCTACGGT ATTAACTGCC CAAGAATCAT  1620
TTTCCGGTTC ACTTGGGCAT TTACAGAATA GGAACAACAG TTGTGATTCC AGAGGACAGA  1680
CTACTAAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT  1740
ACCGGAATTC ATTGAGACAA ACTAACAAAA CTAAACAGTC ATGCCCATTT GGAAGAGTCC  1800
CAGTTAACCT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGTACCTT  1860
GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGGTTGTG CCTGGATCTA  1920
AACCAAGTGG AAATGATTCC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT  1980
TCAAGGAACC TCTGGTGTCA GATGAAAAGA GTTCTGAACT TATTATTACT GATTCAATAA  2040
CCCTGAAGAA TAAAACGGAA TCAAGTCTTC TAGCTAAATT AGAAGAAACT AAAGAGTATC  2100
AAGAACCAGA GGTTCCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT  2160
GTATTAACCA GAATCCTGCT GCATCTTCAA ATCACTGGCA GATTCCGGAG TTAGCCCCAA  2220
AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAC  2280
AGTCACCACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTTGT AAGACACCAA  2340
GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT  2400
TTCCACCTGC TTGTCAGTTG TCAACACCTT ATGGCCAACC TGCCTGTTTC CAGCAGCAAC  2460
AGCATCAAAT ACTTGCCACT CCACTTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA  2520
ATGAATGCAT TTCGGTTAAA GGAAGAATTT ATTCCATATT AAAGCAGATA GGAAGTGGAG  2580
GTTCAAGCAA GGTATTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAAATATG  2640
TGAACTTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT  2700
TGAATAAACT ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCACGG  2760
ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA  2820
AGAAAAAATC CATTGATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG  2880
TTCACACAAT CCATCAACAT GGCATTGTTC ACAGTGATCT TAAACCAGCT AACTTTCTGA  2940
TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAAATG CAACCAGATA  3000
CAACAAGTGT TGTTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA  3060
TCAAAGATAT GTCTTCCTCC AGAGAGAATG GGAAATCTAA GTCAAAGATA AGCCCCAAAA  3120
GTGATGTTTG GTCCTTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTC  3180
AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG  3240
AATTTCCCGA TATTCCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTTGT TTAAAAAGGG  3300
ACCCAAAACA GAGGATATCC ATTCCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA  3360
CTCATCCAGT TAACCAAATG GCCAAGGGAA CCACTGAAGA AATGAAATAT GTTCTGGGCC  3420
AACTTGTTGG TCTGAATTCT CCTAACTCCA TTTTGAAAGC TGCTAAAACT TTATATGAAC  3480
ACTATAGTGG TGGTGAAAGT CATAATTCTT CATCCTCCAA GACTTTTGAA AAAAAAGGG  3540
GAAAAAAATG ATTTGCAGTT ATTCGTAATG TCAGATAGGA GGTATAAAAT ATATTGGACT  3600
GTTATACTCT TGAATCCCTG TGGAAATCTA CATTTGAAGA CAACATCACT CTGAAGTGTT  3660
ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAAAGAAA ACTGTAAAAA TAGCAACCAC  3720
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TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC  3780
TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTTG  3840
TAAATAAAGT TTTGTGGCTA AAATGA
```

A115 Protein sequence:

Gene name:	TTK protein kinase
Unigene number:	Hs.169840
Probeset Accession #:	M86699
Protein Accession #:	NP_003309
Signal sequence:	none found
Transmembrane domains:	none found
Protein Kinase Domain:	510-775
Cellular Localization:	cytoplasmic and nuclear

```
1          11         21         31         41         51
|          |          |          |          |          |
MNKVRDIKNK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS    60
VPLSDALLNK LIGRYSQAIE ALPPDKYGQN ESFARIQVRF AELKAIQEPD DARDYFQMAR   120
ANCKKFAFVH ISFAQFELSQ GNVKKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS   180
EEEKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR   240
NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGSKP   300
SGNDSCELRN LKSVQNSHFK EPLVSDEKSS ELIITDSITL KNKTESSLLA KLEETKEYQE   360
PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTFE QPVFSVSKQS   420
PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDFP PACQLSTPYG QPACFQQQQH   480
QILATPLQNL QVLASSSANE CISVKGRIYS ILKQIGSGGS SKVFQVLNEK KQIYAIKYVN   540
LEEADNQTLD SYRNEIAYLN KLQQHSDKII RLYDYEITDQ YIYMVMECGN IDLNSWLKKK   600
KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPANFLIV DGMLKLIDFG IANQMQPDTT   660
SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYY MTYGKTPFQQ   720
IINQISKLHA IIDPNHEIEF PDIPEKDLQD VLKCCLKRDP KQRISIPELL AHPYVQIQTH   780
PVNQMAKGTT EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK   840
K
```

OVARIAN

A116 DNA SEQUENCE

Gene name:	G protein-coupled receptor 39
Unigene number:	Hs.85339
Probeset Accession #:	AA349893
Nucleic Acid Accession #:	NM_001508
Coding sequence:	1-1362 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC    60
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC   120
TTCGTGATGG GCCTTCTGGG GAACAGCGCC ACCATTCGGG TCACCCAGGT GCTGCAGAAG   180
AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC   240
TTGGTGTTCC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC   300
ACGTCCAGCT ACACCCTGTC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC   360
GCTACGCTGC TGCACGTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC   420
TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG   480
GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCCTG   540
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG   600
CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC   660
CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC   720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC   780
ACGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG   840
ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG   900
ATTCGGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG   960
GCGTACATGA TCCTCCTCCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCATCAAC  1020
CCGCTCCTGT ACACGGTGTC CTCGCAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC  1080
TGCCGCCTGT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC  1140
ACCACCGACA GCGCCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC  1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG  1260
TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC  1320
AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA
```

A117 Protein sequence:

Gene name:	G protein-coupled receptor 39
Unigene number:	Hs.85339
Probeset Accession #:	AA349893
Protein Accession #:	NM_001508, NP_001409
Signal sequence:	none found
Pfam domains:	7tm_1 [72-172, 224-344]
Transmembrane domains:	32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK    60
```

```
KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY   120
ATLLHVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL   180
VNVPSHRGLT CNRSSTRHHE QPETSNMSIC TNLSSRWTVF QSSIFGAFVV YLVVLLSVAF   240
MCWNNMQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ   300
IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC   360
CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPQ   420
SKSQSLSLES LEPNSGAKPA NSAAENGFQE HEV
```

A118 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.87223
Probeset Accession #: AA250737
Nucleic Acid Accession #: NM_001203
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGCGGAGA CCGCGGCGCT    60
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT   120
GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTTGATAAA GGTTCAGACT TCTGCTGATT   180
CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC   240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA   300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC   360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA   420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTGCCTGT GGTCACTTCT   480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTCGGG ACACTCCCAT TCCTCATCAA   540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCTACA   600
CTGCCTCCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCTTTACTT   660
ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG   720
TATAAAAGAC AAGAAACCAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC   780
ATTCCTCCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA   840
TCAGGCCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAAACAG   900
ATTGGAAAAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT   960
GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG  1020
ACAGTGTTGA TGAGGCATGA AAACATTTTG GGTTTCATTG CTGCAGATAT CAAAGGGACA  1080
GGGTCCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT  1140
TATCTGAAGT CCACCACCCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC  1200
AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAACC AGCAATTGCC  1260
CATCGAGATC TGAAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACTTG CTGTATTGCT  1320
GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC  1380
ACTCGAGTTG GCACCAAACG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA  1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG  1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC  1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA  1620
CGCCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACTC  1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA  1740
ACACTTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG  1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA  1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC  1920
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG  1980
TCTGTTTGTA GGCGGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT
```

A119 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.72472 / Hs.87223
Probeset Accession #: AA250737 / U89326
Protein Accession #: NP_001194
Signal sequence: 1-13
Transmembrane domains: 128-144
PFAM domains: activin_receptor [30-111], protein kinase [204-491]
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED    60
DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD   120
GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPRYS IGLEQDETYI PPGESLRDLI   180
EQSQSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTEEAS   240
WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS   300
MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILV KKNGTCCIAD LGLAVKFISD   360
TNEVDIPPNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFGLILWEV ARRCVSGGIV   420
EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS   480
RLTALRVKKT LAKMSESQDI KL
```

A120 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
Unigene number: Hs.79136
Probeset Accession #: U41060
Nucleic Acid Accession #: NM_012319.2
Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
```

```
|          |          |          |          |          |          |
CTCGTGCCGA ATTCGGCACG AGACCGCGTG TTCGCGCCTG GTAGAGATTT CTCGAAGACA    60
CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GGCCGTGGGA CAACGAGGCC   120
GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGCCC   180
TCTCTGTCAC AAATCCCCTT CATGAACTAA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA   240
AAATTAGTCC GAATTGGGAA TCTGGCATTA ATGTTGACTT GGCAATTTCC ACACGGCAAT   300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT   360
TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG   420
ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG   480
AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG   540
CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCATGACTCA GATAGTTCAG   600
GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA   660
GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG   720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACTCTTCC   780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACATC AAAGAGCCGG GTGAGCCGGC   840
TGGCTGGTAG GAAAACAAAT GAATCTGTGA GTGAGCCCCG AAAAGGCTTT ATGTATTCCA   900
GAAACACAAA TGAAAATCCT CAGGAGTGTT TCAATGCATC AAAGCTACTG ACATCTCATG   960
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA  1020
TCAACCAAAT TGATGCTAGA TCTTGTCTGA TTCATACAAG TGAAAAGAAG GCTGAAATCC  1080
CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA  1140
TCAGTTTCCT GTCTCTGCTG GGGGTTATCT TAGTGCCTCT CATGAATCGG GTGTTTTTCA  1200
AATTTCTCCT GAGTTTCCTT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT  1260
TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG  1320
CAATGGAAAT GAAAAGAGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA  1380
GTGCCTATTT TGATTCCACG TGGAAGGGTC TAACAGCTCT AGGAGGCCTG TATTTCATGT  1440
TTCTTGTTGA ACATGTCCTC ACATTGATCA AACAATTTAA AGATAAGAAG AAAAAGAATC  1500
AGAAGAAACC TGAAAATGAT GATGATGTGG AGATTAAGAA GCAGTTGTCC AAGTATGAAT  1560
CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC  1620
GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAAG  1680
AAGAGGTCAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG  1740
GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA  1800
TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCACCATC  1860
CTCACAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTCGCCACTT  1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAATTT CAGCGATGGC CTAGCAATTG  1980
GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC  2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA  2100
AGCAGGCTGT CCTTTATAAT GCATTGTCAG CCATGCTGGC GTATCTTGGA ATGGCAACAG  2160
GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTGCA CTTACTGCTG  2220
GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA  2280
GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTTACA GAATGCTGGG ATGCTTTTGG  2340
GTTTTGGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTT CGTATAAATT  2400
TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT  2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATTT  2520
TTGTATTGAA TATTGCTGTC TGTTACAAAG TCAGTTAAAG GTACGTTTTA ATATTTAAGT  2580
TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG  2640
TAAACAAGAG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAAAAATGT CTTTAATGCT  2700
TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG  2760
TGTTTAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA  2820
AGCAAAGAAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT  2880
AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAAGG  2940
CAGAATTAGT ATAGAGTACA TTCATTAAAC ATTTTTGTCA GGATTATTTC CCGTAAAAAC  3000
GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT  3060
AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG  3120
TTCGTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT  3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTTCTGGTT ACCTGGTTTA  3240
CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAAACT ACACTAAGTA  3300
TCATTTGATT CGATTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTGT  3360
GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA  3420
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G
```

A121 PROTEIN SEQUENCE

Gene name:	LIV-1 protein, estrogen regulated
Unigene number:	Hs.79136
Protein Accession #:	NP_036451
Signal sequence:	1-21
Pfam domain:	Zip[591-743]
Transmembrane domains:	330-346, 352-368, 427-444, 663-679, 688-703, 730-745
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MARKLSVILI LTFALSVTNP LHELKAAAFP QTTEKISPNW ESGINVDLAI STRQYHLQQL    60
FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHDHHS DHEHHSDHER HSDHEHHSDH   120
EHHSDHDHHS HHNHAASGKN KRKALCPDHD SDSSGKDPRN SQGKGAHRPE HASGRRNVKD   180
SVSASEVTST VYNTVSEGTH FLETIETPRP GKLFPKDVSS STPPSVTSKS RVSRLAGRKT   240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LTSHGMGIQV PLNATEFNYL CPAIINQIDA   300
RSCLIHTSEK KAEIPPKTYS LQIAWVGGFI AISIISFLSL LGVILVPLMN RVFFKFLLSF   360
LVALAVGTLS GDAFLHLLPH SHASHHHSHS HEEPAMEMKR GPLFSHLSSQ NIEESAYFDS   420
TWKGLTALGG LYFMFLVEHV LTLIKQFKDK KKKNQKKPEN DDDVEIKKQL SKYESQLSTN   480
EEKVDTDDRT EGYLRADSQE PSHFDSQQPA VLEEEEVMIA HAHPQEVYNE YVPRGCKNKC   540
HSHFHDTLGQ SDDLIHHHHD YHHILHHHHH QNHHPHSHSQ RYSREELKDA GVATLAWMVI   600
MGDGLHNFSD GLAIGAAFTE GLSSGLSTSV AVFCHELPHE LGDFAVLLKA GMTVKQAVLY   660
NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS   720
```

RWGYFFLQNA GMLLGFGIML LISIFEHKIV FRINF

A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
Unigene number: Hs.12844
Probeset Accession #: N67551
Nucleic Acid Accession #: NM_015507
Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCCTCCCC AGGCCGCGAG    60
CGCCCCTGCC GCGGTGCCTG GCCTCCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACTG   120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG   180
GGGTCCGGCC GGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA   240
ATGCCTCTGC CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC   300
GGGAACGCGG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC   360
TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC   420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC   480
AGATGCTTTC CAGGATACAC CGGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG   540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC   600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG   660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC   720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT   780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC   840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA   900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA   960
GGGTCCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT  1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC  1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC  1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACTTGC AGCCCTTCAA CTATGAAGAG  1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA  1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA  1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT  1380
CTGGTCCAAA GGAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT  1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC  1500
TGGAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC CGCCTTGGCA  1560
GGTCACAAGA AAGACATTGG CCGATTGAAA CTTCTCCTAC CTGACCTGCA ACCCCAAAGC  1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCGGAGACA AAGTCGGGAA ACTTCGAGTG  1680
TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG  1740
TGGAAGACAG GGAAAATTCA GTTGTATCAA GGAACTGATG CTACCAAAAG CATCATTTTT  1800
GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT  1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT  1920
TTGACTTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT  1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT  2040
TCTTGTATAA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA  2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT  2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA  2220
TAGAAAAAAA AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC  2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT  2340
TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAAAAA AAAAAAAA
```

A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6
Unigene number: Hs.12844
Probeset Accession #: N67551
Protein Accession #: NP_056322.2
Signal sequence: 1-21
Transmembrane domains: none found
MAM domain: 402-546
EGF domain: 80-259
Cellular Localization: secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRRNSKGV    60
CEATCEPGCK FGECVGPNKC RCPPGYTGKT CSQDVNECGM KPRPCQHRCV NTHGSYKCFC   120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS   180
GKVICPYNRR CVNTPGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFNTQ   240
GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKNVT   300
PEPTRTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER   360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD   420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFDYRL AGDKVGKLRV   480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV   540
SGLCPDSLLS VDD
```

A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
Unigene number: Hs.170195
Probeset Accession #: BE616633
Nucleic Acid Accession #: NM_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT    60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG   120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC   180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA   240
GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT   300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC   360
CCATGTTCAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG   420
GCCAGGGCTT CTCCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA   480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG   540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC   600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT   660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG   720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG   780
AGGAGGGCTG GCTGGTGTTT GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC   840
GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA   900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT   960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA  1020
GCCAGAACCG CTCCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG  1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC  1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG  1200
AGGGGGAGTG TGCCTTCCCT CTGAACTCCT ACATGAACGC CACCAACCAC GCCATCGTGC  1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCACGC  1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT  1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT  1440
TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA  1500
CTGCCTTTTG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG  1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA  1620
TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAAAA ACAACGCATA AAGAAAAATG  1680
GCCGGGCCAG GTCATTGGCT GGGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA  1740
TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT  1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA  1860
CAATAAAACG AATGAATG
```

A125 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number:	Hs.170195
Probeset Accession #:	BE616633
Protein Accession #:	NP_001710.1
Signal sequence:	1-30
Pfam domains:	TGFb_propeptide [37-281]
Transmembrane domains:	none found
Cellular Localization:	secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MHVRSLRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRLRSQE RREMQREILS    60
ILGLPHRPRP HLQGKHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS   120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY   180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVVNPR   240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS   300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE   360
GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY   420
RNMVVRACGC H
```

A126 DNA SEQUENCE

Gene name:	integrin, beta 8
Unigene number:	Hs.52620
Probeset Accession #:	AA479726
Nucleic Acid Accession #:	NM_002214
Coding sequence:	680-2990 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG    60
CTGCCGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT   120
GTTGGCCTCC CTGCCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT   180
TCCCCTCGAC CTCGCCGGCG TACCCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT   240
TAGGGTGGTT TCCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG   300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT   360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT   420
TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG   480
GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT   540
CCGAGCCGCG GGGTCCGCCT GCTAGGCCTG CGGAAAACGT CCTAGCGACA CTCGCCCGCG   600
GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGCGC   660
GGGGCGGGCT GTTTTGCATT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTTG   720
TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTCCT CTGGGCAGCC TGGGTGTTTT   780
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CACTTGTTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT   840
CCTGTGCCAG GTGCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA   900
TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT   960
GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA  1020
TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA  1080
ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTTG  1140
ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTTAT  1200
CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTCGTCTTGG ATTTGGCTCA TACGTTGATA  1260
AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT  1320
ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA  1380
TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG  1440
AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA  1500
AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA  1560
GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACGTCT  1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG  1680
ACAACAACAT TAATGTCATC TTTGCAGTTC AAGGAAAACA ATTTCATTGG TATAAGGATC  1740
TTCTACCCCT CTTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA  1800
ATAATTTGGT AGTGGAAGCC TATCAGAAGC TCATTTCAGA AGTGAAAGTT CAGGTGGAAA  1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC  1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG  1980
TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAACTA TGCAATAATC AAACCTATTG  2040
GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCAG TGTGAGGACA  2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACTTTTCT AGATTCCAAG TGTTTCCAGT  2160
GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC  2220
ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC  2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC  2340
CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT  2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG  2460
TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT  2520
GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT  2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCCTCA CAATTTGTCT CAGGCTATAC  2640
TTGATCAGTG CAAACCTCA TGTGCTCTCA TGGAACAACA GCATTATGTC GACCAAACTT  2700
CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTTT CATCATTTTC ATAGTTACAT  2760
TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAATAGTA  2820
ATAAAATTAA GTCCTCATCA GATTACAGAG TGTCAGCCTC AAAAAAGGAT AAGTTGATTC  2880
TGCAAAGTGT TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA  2940
TGGATATCAG CAAATTAAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATTT  3000
TTAAACACTT AATGGGAAAC TGGAATTGTT AATAATTGCT CCTAAAGATT ATAATTTTAA  3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC  3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA  3180
AAAATGTGTC TTACTACTGT TTGAGACTAG TGTCGTTGTA GCACTTTACT GTAATATATA  3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG  3300
TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT  3360
CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAAATA ATCTGGCAAG  3420
TATATTCTAA GGTTGCCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG  3480
ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA  3540
AAAGATTATT GCTTTTTAAA GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT  3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTTT GCCTTTATGT TTTGTTTTCT  3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC  3720
TACTGCCATA AAAAACTAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT  3780
GAATGTTAA
```

A127 Protein sequence:

Gene name:	Integrin, beta 8
Unigene number:	Hs.52620
Probeset Accession #:	AA479726
Protein Accession #:	NP_002205.1
Signal sequence:	1-39
Transmembrane domains:	682-704
EGF domain:	552-584
INB domain:	54-469
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MCGSALAFFT AAFVCLQNDR RGPASFLWAA WVFSLVLGLG QGEDNRCASS NAASCARCLA    60
LGPECGWCVQ EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP   120
GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF   180
SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA   240
VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRLL LVMTDQTSHL ALDSKLAGIV   300
VPNDGNCHLK NNVYVKSTTM EHPSLGQLSE KLIDNNINVI FAVQGKQFHW YKDLLPLLPG   360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR   420
NVTSNDEVLF NVTVTMKKCD VTGGKNYAII KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK   480
CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDQPVC SGRGVCVCGK CSCHKIKLGK   540
VYGKYCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRCQCPSAAA QHCVNSKGQV   600
CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS   660
CALMEQQHYV DQTSECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKIKSSS   720
DYRVSASKKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF
```

A128 DNA SEQUENCE

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942
Probeset Accession #: AA435577
Nucleic Acid Accession #: NM_005756
Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA    60
CTCGCGGTCA GGATGGTTTT CTCTGTCAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA   120
GTTTTACTGA CGTTCAAGAT ATTCCTTGTC ATCATTTGTC TTCATGTCGT TCTGGTAACA   180
TCCCTGGAAG AAGATACTGA TAATTCCAGT TTGTCACCAC CACCTGCTAA ATTATCTGTT   240
GTCAGTTTTG CCCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTTACTTTA   300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAATCA CTATAGTAAA AACCTTCAAT   360
GCTTCAGGCG TCAAACCCCA GAGAAATATC TGCAATTTGT CATCTATTTG CAATGACTCA   420
GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT   480
CAACATATAA CGAATGGCAC CTTAACTGGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA   540
GAGCTCAACA AAACCCTGCA AACCCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA   600
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA   660
TGTGCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTCGAC CAATGGAACA CTGCTGCTGT   720
TCTGTCAGGA TACCCTGCCC TTCCTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG   780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA   840
TCCATCCCAG TGGTGCCTCG GGCCACTGTG CTTTCCCAGG TCCCCAAAGC TACCTCTTTT   900
GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTC CCTCTCCAAT AGGGGAGATT   960
CAACCCCTTT CACCCCAGCC TTCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC  1020
CCACAGTCTG AAACGATCTC TTCCCCTATG CCCCAAACCC ATGTCTCCGG CACCCCACCT  1080
CCTGTGAAAG CCTCATTTTC CTCTCCCACC GTGTCTGCCC CTGCGAATGT CAACACTACC  1140
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC  1200
CAAGTGTTGC AGATGGAGAA GGCTCTGTCC TTGGGCAGCC TGGAGCCTAA CCTCGCAGGA  1260
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCCCCGC CTGACATGCT GGCCCCTCTG  1320
GCTCAAAGAT TGCTGAAAGT AGTGGATGAC ATTGGCCTAC AGCTGAACTT TTCAAACACG  1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT  1440
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAAATC TTCAGGTTTC TCTGGAAACC  1500
CAAGCTCCTG AGAACAGTAT TGGCACAATT ACTCTTCCTT CATCGCTGAT GAATAATTTA  1560
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TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT  1680
GTTGCAAACC TGACCGTCAG GAACTTGACA AGAAACGTGA CAGTCACATT AAAGCACATC  1740
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GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC  1860
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TCAATTTTTC TGTCAGTGAC TCTTGTAACC TACATAGCTT TTGAAAAGAT CCGGAGGGAT  2040
TACCCTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCTGGTCTTC  2100
CTCCTGGACT CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA  2160
TTTCTTCATT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCCTAGAAGC ATTCCATATG  2220
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATTCTGC  2280
ATTGTCGGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCCTGACTAT ATCCCCAGAT  2340
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ATCAACAACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTTG  2460
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TGTGTGGCCA AAGAAAATGT CAGGAAGCAA TGGAGGCGGT ATCTTTGTTG TGGAAAGTTA  2760
CGGCTGGCTG AAAATTCTGA CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT  2820
GTAAACCAAG GAGTGTCCAG CTCTTCAAAT TCCTTACAGT CAAGCAGTAA CTCCACTAAC  2880
TCCACCACAC TGCTAGTGAA TAATGATTGC TCAGTACACG CAAGCGGGAA TGGAAATGCT  2940
TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGAATG GAGATGTGTG CCTTCACGAT  3000
TTCACTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCCGT  3060
ATGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATTC  3120
CTTTCTTCTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA  3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT  3240
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT  3300
TTTAGACATT TCTGATTTGG TTTCTTATCT TTCATTTTAT AAGAAGGTTG GTTTTAAACA  3360
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAAGG TAGTGAACTT TCAGCTACCT  3420
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TTGGTGAGTT TAGTTGTGCA TGCCTTTGTT GTATATAAGC TAAATTCTAG TGACCCATGT  3540
GTCAAAAATC TTACTTCTAC ATTTTTTTGT ATTTATTTTC TACTGTGTAA ATGTATTCCT  3600
TTGTAGAATC ATGGTTGTTT TGTCTCACGT GATAATTCAG AAAATCCTTG CTCGTTCCGC  3660
AAATCCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA  3720
TCAAGAAATA ATGATCCCAG CCAGACTGAG AAAATGTAAG CAGACAGTGC CACAGTTAGC  3780
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA  3840
TGGGTCATGG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG  3900
GTGCACGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCGCAT  3960
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG  4020
AGAGGGATGA ACTGTCATCC AGACCATGTG TCAGGAAAAT TGTGAACGTA GATGAGGTAC  4080
ATACACTGCC GCTTCTCAAA TCCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC  4140
CTTCTCTTAA AAAGGTACAT ATATATGGAA AAAAATCATA TTGCCGTTCT TTAAAAGGCA  4200
ACTGCATGGT ACATTGTTGA TTGTTATGAC TGGTACACTC TGGCCCAGCC AGAGCTATAA  4260
TTGTTTTTTA AATGTGTCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA  4320
GGGAACTGTC CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA  4380
TATACAGGGT CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC  4440
TTATTAGGAA CATTTCAAAC CCCTTTTAGT TAAGTCTTTC ACTAAGGTTC TCTTGCATAT  4500
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG  4560
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CTGACTTGTC TTTGCAATAT TTCTTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT  4620
AAAATCAAAA ATGTTAAAAT CAATGAAATA AATTTGCAGT TAAGA
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A129 Protein sequence

Gene name: G protein-coupled receptor 64
Unigene number: Hs.184942
Protein Accession #: NP_005747.1
Signal sequence: 1-38
GPS domain: 564-615
Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
Cellular Localization: plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPP PAKLSVVSFA    60
PSSNEVETTS LNDVTLSLLP SNETEKTKIT IVKTFNASGV KPQRNICNLS SICNDSAFFR   120
GEIMFQYDKE STVPQNQHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAQS   180
TLNCTFTIKL NNTMNACAAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI   240
VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSFAEPP DYSPVTHNVP SPIGEIQPLS   300
PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTPPPVKA SFSSPTVSAP ANVNTTSAPP   360
VQTDIVNTSS ISDLENQVLQ MEKALSLGSL EPNLAGEMIN QVSRLLHSPP DMLAPLAQRL   420
LKVVDDIGLQ LNFSNTTISL TSPSLALAVI RVNASSFNTT TFVAQDPANL QVSLETQAPE   480
NSIGTITLPS SLMNNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVISSSVANL   540
TVRNLTRNVT VTLKHINPSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC   600
SHLTSFGVLL DLSRTSVLPA QMMALTFITY IGCGLSSIFL SVTLVTYIAF EKIRRDYPSK   660
ILIQLCAALL LLNLVFLLDS WIALYKMQGL CISVAVFLHY FLLVSFTWMG LEAFHMYLAL   720
VKVFNTYIRK YILKFCIVGW GVPAVVVTII LTISPDNYGL GSYGKFPNGS PDDFCWINNN   780
AVFYITVVGY FCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG   840
ITWGFAFFAW GPVNVTFMYL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKLRLAE   900
NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNGNASTER   960
NGVSFSVQNG DVCLHDFTGK QHMFNEKEDS CNGKGRMALR RTSKRGSLHF IEQM
```

A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
Unigene number: Hs.285529
Probeset Accession #: AA460530
Nucleic Acid Accession #: NM_003667
Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

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GTGGCGGCAA CCGGCACCTC AGTCCCCGCC GCGCTTCTCC TCGCCGCCCA CGCCGTGGGG    60
TCAGGAACGC GGCGTCTGGC GCTGCAGACG CCCGCTGAGT TGCAGAAGCC CACGGAGCGG   120
CGCCCGGCGC GCCACGGCCC GTAGCAGTCC GGTGCTGCTC TCCGCCCGCG TCCGGCTCGT   180
GGCCCCCTAC TTCGGGCACC ATGGACACCT CCCGGCTCGG TGTGCTCCTG TCCTTGCCTG   240
TGCTGCTGCA GCTGGCGACC GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT   300
GCCCCACACA CTGTCATTGC GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG   360
ACCTGGGGCT CTCGGAGCTG CCTTCCAACC TCAGCGTCTT CACCTCCTAC CTAGACCTCA   420
GTATGAACAA CATCAGTCAG CTGCTCCCGA ATCCCCTGCC CAGTCTCCGC TTCCTGGAGG   480
AGTTACGTCT TGCGGGAAAC GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT   540
ACAGTCTTAA AGTTCTTATG CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC   600
TGCAGAATTT GCGAAGCCTT CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC   660
CCCCAAGCTG TTTCAGTGGC CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT   720
TAACAGAAAT CCCCGTCCAG GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG   780
CCCTGAACAA AATACACCAC ATACCAGACT ATGCCTTTGG AAACCTCTCC AGCTTGGTAG   840
TTCTACATCT CCATAACAAT AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC   900
ACAGCCTAGA GACTTTAGAT TTAAATTACA ATAACCTTGA TGAATTCCCC ACTGCAATTA   960
GGACACTCTC CAACCTTAAA GAACTAGGAT TTCATAGCAA CAATATCAGG TCGATACCTG  1020
AGAAAGCATT TGTAGGCAAC CCTTCTCTTA TTACAATACA TTTCTATGAC AATCCCATCC  1080
AATTTGTTGG GAGATCTGCT TTTCAACATT TACCTGAACT AAGAACACTG ACTCTGAATG  1140
GTGCCTCACA AATAACTGAA TTTCCTGATT TAACTGGAAC TGCAAACCTG GAGAGTCTGA  1200
CTTTAACTGG AGCACAGATC TCATCTCTTC CTCAAACCGT CTGCAATCAG TTACCTAATC  1260
TCCAAGTGCT AGATCTGTCT TACAACCTAT TAGAAGATTT ACCCAGTTTT TCAGTCTGCC  1320
AAAAGCTTCA GAAAATTGAC CTAAGACATA ATGAAATCTA CGAAATTAAA GTTGACACTT  1380
TCCAGCAGTT GCTTAGCCTC CGATCGCTGA ATTTGGCTTG GAACAAAATT GCTATTATTC  1440
ACCCCAATGC ATTTTCCACT TTGCCATCCC TAATAAAGCT GGACCTATCG TCCAACCTCC  1500
TGTCGTCTTT TCCTATAACT GGGTTACATG GTTTAACTCA CTTAAAATTA ACAGGAAATC  1560
ATGCCTTACA GAGCTTGATA TCATCTGAAA ACTTTCCAGA ACTCAAGGTT ATAGAAATGC  1620
CTTATGCTTA CCAGTGCTGT GCATTTGGAG TGTGTGAGAA TGCCTATAAG ATTTCTAATC  1680
AATGGAATAA AGGTGACAAC AGCAGTATGG ACGACCTTCA TAAGAAAGAT GCTGGAATGT  1740
TTCAGGCTCA AGATGAACGT GACCTTGAAG ATTTCCTGCT TGACTTTGAG GAAGACCTGA  1800
AAGCCCTTCA TTCAGTGCAG TGTTCACCTT CCCCAGGCCC CTTCAAACCC TGTGAACACC  1860
TGCTTGATGG CTGGCTGATC AGAATTGGAG TGTGGACCAT AGCAGTTCTG GCACTTACTT  1920
GTAATGCTTT GGTGACTTCA ACAGTTTTCA GATCCCCTCT GTACATTTCC CCCATTAAAC  1980
TGTTAATTGG GGTCATCGCA GCAGTGAACA TGCTCACGGG AGTCTCCAGT GCCGTGCTGG  2040
CTGGTGTGGA TGCGTTCACT TTTGGCAGCT TTGCACGACA TGGTGCCTGG TGGGAGAATG  2100
GGGTTGGTTG CCATGTCATT GGTTTTTTGT CCATTTTTGC TTCAGAATCA TCTGTTTTCC  2160
TGCTTACTCT GGCAGCCCTG GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTTGAAA  2220
CGAAAGCTCC ATTTTCTAGC CTGAAAGTAA TCATTTTGCT CTGTGCCCTG CTGGCCTTGA  2280
CCATGGCCGC AGTTCCCCTG CTGGGTGGCA GCAAGTATGG CGCCTCCCCT CTCTGCCTGC  2340
CTTTGCCTTT TGGGGAGCCC AGCACCATGG GCTACATGGT CGCTCTCATC TTGCTCAATT  2400
CCCTTTGCTT CCTCATGATG ACCATTGCCT ACACCAAGCT CTACTGCAAT TTGGACAAGG  2460
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GAGACCTGGA GAATATTTGG GACTGCTCTA TGGTAAAACA CATTGCCCTG TTGCTCTTCA  2520
CCAACTGCAT CCTAAACTGC CCTGTGGCTT TCTTGTCCTT CTCCTCTTTA ATAAACCTTA  2580
CATTTATCAG TCCTGAAGTA ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTTCCTGCAT  2640
GTCTCAATCC CCTTCTCTAC ATCTTGTTCA ATCCTCACTT TAAGGAGGAT CTGGTGAGCC  2700
TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAACT  2760
CTGATGATGT CGAAAAACAG TCCTGTGACT CAACTCAAGC CTTGGTAACC TTTACCAGCT  2820
CCAGCATCAC TTATGACCTG CCTCCCAGTT CCGTGCCATC ACCAGCTTAT CCAGTGACTG  2880
AGAGCTGCCA TCTTTCCTCT GTGGCATTTG TCCCATGTCT CTAATTAATA TGTGAAGGAA  2940
AATGTTTTCA AAGGTTGAGA ACCTGAAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA  3000
ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA
```

A131 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
Unigene number: Hs.285529
Protein Accession #: NP_003658.1
Signal sequence: 1-22
Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
Cellular Localization: plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL    60
PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLM   120
LQNNQLRHVP TEALQNLRSL QSLRLDANHI SYVPPSCFSG LHSLRHLWLD DNALTEIPVQ   180
AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD   240
LNYNNLDEFP TAIRTLSNLK ELGFHSNNIR SIPEKAFVGN PSLITIHFYD NPIQFVGRSA   300
FQHLPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS   360
YNLLEDLPSF SVCQKLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIIHPNAFST   420
LPSLIKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPELKV IEMPYAYQCC   480
AFGVCENAYK ISNQWNKGDN SSMDDLHKKD AGMFQAQDER DLEDFLLDFE EDLKALHSVQ   540
CSPSPGPFKP CEHLLDGWLI RIGVWTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA   600
AVNMLTGVSS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLLTLAAL   660
ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEP   720
STMGYMVALI LLNSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC   780
PVAFLSFSSL INLTFISPEV IKFILLVVVP LPACLNPLLY ILFNPHFKED LVSLRKQTYV   840
WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS   900
VAFVPCL
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A132 DNA SEQUENCE

Gene name: parathyroid hormone receptor 2
Unigene number: Hs.159499
Probeset Accession #: U25128
Nucleic Acid Accession #: NM_005048
Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

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|          |          |          |          |          |
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TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT   120
TCTTCCTACA GCCGTTCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG   180
GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCCAGCTG GATTCTGATG GCACCATTAC   240
TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC   300
AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTTGTTG   360
GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCCATGC CCTCCTTATA TTTATGACTT   420
CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA   480
CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT   540
CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC   600
CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTTACTTCA GACGATTGCA   660
TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCATGCTGA GAGCTACAAG   720
CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT   780
AATAATGCAG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA   840
TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG   900
GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCGGACAC   960
CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC  1020
ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGCGAGGTGC TGGGAACTTA GTGCTGGAGA  1080
CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT  1140
TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA  1200
CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG  1260
AGTGCATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT  1320
CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA  1380
CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT  1440
CTCCGTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCCGC AGATGCGGCT CAGTGCTCAC  1500
CACCGTGACG CACAGCACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT  1560
TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC  1620
TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCCTGCCA CACTCTTTCC ACGAGGAGAC  1680
CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT  1740
GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAAACT GAGGATGTTC TCTGAATGGA  1800
CATTTGTGGC TGACTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG  1860
ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT  1920
TTTTAGGCTC CATGAATTGG CTCCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT  1980
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GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT  2040
GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG  2100
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ATTTTCCTTT TAGAAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC  2220
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GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT  2340
TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTCAC  2400
ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC  2460
TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCCTCAGTT AGTCAGCTTG TGTCTGCAAA  2520
TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG  2580
TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAAAAATTT GTTTTAAAAA  2640
T
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A133 PROTEIN SEQUENCE

Gene name:	parathyroid hormone receptor 2
Unigene number:	Hs.159499
Protein Accession #:	NP_005039.1
Signal sequence:	1-25
Pfam domain:	7tm_2 [141-420]
Transmembrane domains:	177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419
Cellular Localization:	plasma membrane

```
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|          |          |          |          |          |
MAGLGASLHV WGWLMLGSCL LARAQLDSDG TITIEEQIVL VLKAKVQCEL NITAQLQEGE   60
GNCFPEWDGL ICWPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA  120
NYSDCLRFLQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH  180
MHLFVSFMLR ATSIFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV  240
VMFIYFLATN YYWILVEGLY LHNLIFVAFF SDTKYLWGFI LIGWGFPAAF VAAWAVARAT  300
LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK  360
LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFFVS IIYCYCNGEV  420
QAEVKKMWSR WNLSVDWKRT PPCGSRRCGS VLTTVTHSTS SQSQVAASTR MVLISGKAAK  480
IASRQPDSHI TLPGYVWSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RPMESNPDTE  540
GCQGETEDVL
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A134 DNA sequence

Gene name:	ESTs
Unigene number:	Hs.128899
Probeset Accession #:	AA983251
Nucleic Acid Accession #:	AA983251
Coding sequence:	1-1749 (underlined sequences correspond to start and stop codons)

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GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC  120
GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC  180
GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG  240
CCGCGGCCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCCT  300
CGCCTGCGTC CTGGACGTTC CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT  360
TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCCATC AGCGAGTGCA  420
ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA  480
GCTCCTGGAC CTAGGGCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC  540
CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCC GGGGGTCGCC GGGGCCACGA  600
CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCCAG GGTGGTGCCA  660
TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCCTGGAA CGCCGCTTCG CTCCTGCAGC  720
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TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC  840
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GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC  960
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GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC 1080
TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC 1140
CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCCTCTCCCC TGCAGCGGCC CGCCTTGCCC 1200
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AACAACGTGT ATGTCAACAT GCCCACGAAT TTCTCTGTGC TGAACTGTCA GCAGGCCACC 1560
CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG 1620
CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCCTGCA GCCTGGCTAC 1680
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CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCCTC AGCTGGAGAT GACTGTGATG 1980
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TGGTGCGATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC 2280
AGCCTCCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT 2340
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TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA  2400
TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC  2460
TGAGCCTTTT TTTTTTTCTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT  2520
ATTCTAAAAG GAAACCTGTT TGAACTCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA  2580
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TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG  2940
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GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA  3060
AAAAATTTTC TTGTCTTAGT TATAAAAATT CAAAGAAATG TGTTACAAAG ATACTTAGTA  3120
TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTTACTTT  3180
GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG  3240
GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCCAC ACTGTTCTTG  3300
ATTTCCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT  3360
CAAATTCAAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAAGAT AACTTTAAGG  3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT  3480
GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATTC  3540
TGTTTCATGA CTGAATAATG TAAAACCAGT GTTGGCAATT GGTATCATCA ATGATACTCA  3600
TTTTTTAATA ACCAAAGGCA GGGGAAAATC ATTTTACTTA TTAATAAATA TTTTATGATG  3660
TGAAAAAAAA AAAAAAAAAA AAAAAAAAAA
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A135 Protein sequence

Gene name: ESTs
Unigene number: Hs.128899
Protein Accession #: none found
Signal sequence: 1-11
Transmembrane domains: 402-424
Cellular Localization: not determined

```
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|          |          |          |          |          |
MLSGFLMSPS TQHRAQYTPG GKKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA    60
GEAEKGNRGE PPAWIRAQQQ PRPPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA   120
SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG   180
PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAPRVVP CGALAARPSP HPGTPLRSCS   240
CCWLRCWRRG RGPSGEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE   300
ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPPPV RAWQRCSPEG   360
SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPFLIVGS VFVAFIILGS   420
LVAACCRCL RPKQDPQQSR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS   480
GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGQYL HPPYVGYTVQ   540
HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQKMYPAV TV
```

A136 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Nucleic Acid Accession #: NM_000450
Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

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GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT   120
CAGCAAAGGT ACACACACCT GGTTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC   180
TCCATATTGA GCTATTCACC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG   240
TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT   300
GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA   360
GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA   420
GCTGCCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT   480
TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAT TGTGAACTGT   540
ACAGCCCTGG AATCCCCTGA GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAAACTTC   600
AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG   660
ACCATGCAGT GTATGTCCTC TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT   720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCCTGGA   780
AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTTGA ACTAATGGGA   840
GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA   900
GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC   960
CCTGCTGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG  1020
TTGCAGGGAC CAGCCCAGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAATCCCA  1080
GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT  1140
CTTCCTAGTG CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG  1200
GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC  1260
GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG  1320
GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCTTCAGC  1380
TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA  1440
TGGACAGAAG AGGTTCCTTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCCGGGA  1500
AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCCTGT  1560
CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG  1620
TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA  1680
CTTTCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA  1740
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TGCTTACGGA AAGCAAAGAA ATTTGTTCCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A137 Protein sequence:

Gene name:	Selectin E (endothelial adhesion molecule 1)
Unigene number:	Hs.89546
Probeset Accession #:	M24736
Protein Accession #:	NP_000441
Signal sequence:	1-22
Transmembrane domains:	555-573
C-lectin domain:	23-139
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRYTHLVAI QNKEEIEYLN    60
SILSYSPSYY WIGIRKVNNV WVWVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK   120
DVGMWNDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC   180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV   240
ECDAVTNPAN GFVECFQNPG SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK   300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPAQVECT TQGQWTQQIP   360
VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN   420
EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ   480
WTEEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW   540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRK CLRKAKKFVP ASSCQSLESD   600
GSYQKPSYIL
```

A138 DNA SEQUENCE:

Gene name:	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number:	Hs.100686
Probeset Accession #:	AA487468
Nucleic Acid Accession #:	AA487468
Coding sequence:	55-555 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG    60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT   120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC   180
ACTTGGGTAC AAACTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA   240
ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC   300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT   360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA   420
GACCCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA   480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT   540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT   600
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAATA   660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAAATAAAT GTTTTTTAAA   720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAA
```

A139 Protein sequence:

Gene name:	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number:	Hs.100686
Probeset Accession #:	AA487468
Protein Accession #:	none found
Signal sequence:	1-23
Transmembrane domains:	none found
Cellular Localization:	secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK    60
PLMVIHHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM   120
FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL
```

A140 DNA SEQUENCE

Gene name:	TMPRSS3a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Nucleic Acid Accession #:	AB038157
Coding sequence:	202-1566 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTCATGCCC GTGTGAGCCA    60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG   120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC   180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC   240
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TCATTCCGAT CGCTTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA   300
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC   360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC   420
TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC   480
GGAGTCTCGG ATTGCAAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG   540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCATGTGCTC CGATGACTGG   600
AAGGGTCACT ACGCAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA   660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT   720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA   780
TGTGCCTCTG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC   840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC   900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCT GTGGATCATC   960
ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT  1020
CTAGTTTCCC TGTTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC  1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA  1140
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC  1200
GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC  1260
TCCCCTGTCC TGAACCACGC GGCCGTCCCT TTGATTTCCA ACAAGATCTG CAACCACAGG  1320
GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC  1380
GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG  1440
AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG  1500
TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA  1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA  1620
TCCTCCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCTTG GAGCTCTGAG  1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT  1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG  1800
AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC  1860
TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT  1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA  1980
CCTCAAATGA TGTGCCTGCT TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC  2040
ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA  2100
AGGGCGGCCT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG  2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC  2220
GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCAGAA  2280
CCAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA  2340
ATGACTCGTT TAAGGCCTAT TTTCATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA  2400
TTGTCCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA  2460
AAAAAAAA
```

A141 Protein sequence:

Gene name:	TMPRSS3a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Protein Accession #:	BAB20077
Signal sequence:	none found
Transmembrane domains:	43-65, 239-261
Tryp_SPc domain:	216-444
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI    60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF   120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK   180
VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH   240
LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR   300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVLNHA   360
AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSCQGD SGGPLVCQER RLWKLVGATS   420
FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT
```

A142 DNA SEQUENCE

Gene name:	ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
Unigene number:	Hs.105484
Probeset Accession #:	AA314779
Nucleic Acid Accession #:	none found
Coding sequence:	103-579 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT    60
CTGAGATCCT TGCACTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG   120
CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG   180
AGACCCAGCT GTGCTCCTGG ATGGTTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG   240
AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCAGT CTTACGGAAA CGGAGCCCAC   300
CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT   360
CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG   420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC   480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC   540
AACAAGCGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT   600
AACTCCTGCA CCAGCCCCGT CCTCTTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT   660
TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA   720
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GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG   780
CCCCGCCATC CCTTTCCACA GTATCCTTCT TCCCTCCTCC CCTGTCTCTG GCTGTCTCGA   840
GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT   900
AAAGATTTGA AGACAGAAGG AAGAAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT   960
ACACCCTTCT GCCCTCTCTC CATTGCCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG  1020
TTTTTCCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA  1080
TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA
```

A143 Protein sequence:

```
Gene name:                ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
Unigene number:           Hs.105484
Probeset Accession #:     AA314779
Protein Accession #:      none found
Signal sequence:          1-22
Transmembrane domains:    none found
C-type lectin domain:     47-156
Cellular Localization:    secreted
```

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1           11          21          31          41          51
|           |           |           |           |           |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSN CYGYFRKLRN WSDAELECQS    60
YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG   120
KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP
```

A144 DNA SEQUENCE

```
Gene name:                    Cadherin 3, P-cadherin (placental)
Unigene number:               Hs.2877
Probeset Accession #:         X63629
Nucleic Acid Accession #:     X63629
Coding sequence:              54-2543 (start and stop codons are underlined)
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```
1           11          21          31          41          51
|           |           |           |           |           |
GCGGAACACC GGCCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC    60
TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCGCGG   120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG   180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC   240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG   300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC   360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC   420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT   480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG   540
AGACAGGCTG GTTGTTGTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC   600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA   660
TCATCGTGAC CGACCAGAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA   720
GTGTCTTAGA GGGAGTCCTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG   780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA   840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT   900
CCAGTGGCCT GGACCGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA   960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG  1020
ACAATGCTCC CATGTTTGAC CCCCAGAAGT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG  1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC  1140
GTGCCACCTA CCTTATCATG GGCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC  1200
CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC  1260
AGCACACCCT GTACGTTGAA GTGACCAACG AGGCCCCTTT TGTGCTGAAG CTCCCAACCT  1320
CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAC  1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA  1440
CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG  1500
CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC  1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA  1620
ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG  1680
ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC  1740
ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCTTTC CAGGCCCAGC  1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG  1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG  1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC  1980
ATGTCGAAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG  2040
TCCTGGCTCT GCTGTTCCTC CTGCTGGTGC TGCTTTTGTT GGTGAGAAAG AAGCGGAAGA  2100
TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG  2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG  2220
AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA  2280
TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA  2340
AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG  2400
AGGGCAGCGG CTCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCCTCCGCC TCCGACCAAG  2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT  2520
ACGGTGGCGG GGAGGACGAC TAGGCGGCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC  2580
CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA  2640
GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT  2700
TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC  2760
CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCCAGAA GCCTCTTACC TGCCGTAAAA  2820
TGCTCAACCC TGTGTCCTGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT  2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT  2940
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TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG  3000
TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT  3060
ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTTGCGT TGCTATAGAT  3120
GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTTT TATTAAAGAA A
```

A145 Protein sequence:

Gene name:	Cadherin 3, P-cadherin (placental)
Unigene number:	Hs.2877
Probeset Accession #:	X63629
Protein Accession #:	CAA45177
Signal sequence:	1-24
Transmembrane domain:	659-675
Cellular localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG    60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG   120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK   180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT   240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA   300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP   360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL   420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR   480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID   540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD   600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL   660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR   720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF   780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD
```

A146 DNA SEQUENCE:

Gene name:	TTK protein kinase
Unigene number:	Hs.169840
Probeset Accession #:	M86699
Nucleic Acid Accession #:	NM_003318
Coding sequence:	1026-3551(underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GGAATTCCTT TTTTTTTTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG    60
CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCCTCCCG GGTTCAAGCG ATTCTCCTGC   120
CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT   180
CTTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACTCCTG   240
ACCTCAGGTG ATCCACTTGC CTTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG   300
TGCCTGGCTG ATTCTTTTTT TGTTGTTGGA TTTTTGAAAC AGGGTCTCCC TTGGTCGCCC   360
AGGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTTCAAGT   420
GATCCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GCGTGCACCA CCACACCCGG   480
CTAATTTTTG TATTTTTATT AGAGACAGGG TTTCACCATG TTGGCCAGGC TGTTCTCAAA   540
CTCCTGGACT CAAGGGATCC GCCTGCCTCC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG   600
AGTCACCATG CCTGACCTTA TAATTCTTAA GTCATTTTTT CTGGTCCATT TCTTCCTTAG   660
GGTCCTCACA ACAAATCTGC ATTAGGCGGT ACAATAATCC TTAACTTCAT GATTCACAAA   720
AGGAAGATGA AGTGATTCAT GATTTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCCT   780
GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA   840
TTTGGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA   900
ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG   960
TGCAGTTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT  1020
CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG  1080
AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAACT GTTAACCAAA  1140
TTATGATGAT GGCAAACAAC CCAGAGGACT GGTTGAGTTT GTTGCTCAAA CTAGAGAAAA  1200
ACAGTGTTCC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTCGTTAC AGTCAAGCAA  1260
TTGAAGCGCT TCCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGCTAGA ATTCAAGTGA  1320
GATTTGCTGA ATTAAAAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG  1380
CCAGAGCAAA CTGCAAGAAA TTTGCTTTTG TTCATATATC TTTTGCACAA TTTGAACTGT  1440
CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG  1500
TACCACTAGA AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC  1560
TTTCAGAGGA GGAAAAGAAG AATTTATCAG CATCTACGGT ATTAACTGCC CAAGAATCAT  1620
TTTCCGGTTC ACTTGGGCAT TTACAGAATA GGAACAACAG TTGTGATTCC AGAGGACAGA  1680
CTACTAAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT  1740
ACCGGAATTC ATTGAGACAA ACTAACAAAA CTAAACAGTC ATGCCCATTT GGAAGAGTCC  1800
CAGTTAACCT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGTACCTT  1860
GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGGTTGTG CCTGGATCTA  1920
AACCAAGTGG AAATGATTCC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT  1980
TCAAGGAACC TCTGGTGTCA GATGAAAAGA GTTCTGAACT TATTATTACT GATTCAATAA  2040
CCCTGAAGAA TAAAACGGAA TCAAGTCTTC TAGCTAAATT AGAAGAAACT AAAGAGTATC  2100
AAGAACCAGA GGTTCCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT  2160
GTATTAACCA GAATCCTGCT GCATCTTCAA ATCACTGGCA GATTCCGGAG TTAGCCCGAA  2220
AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAC  2280
AGTCACCACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTTGT AAGACACCAA  2340
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GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT  2400
TTCCACCTGC TTGTCAGTTG TCAACACCTT ATGGCCAACC TGCCTGTTTC CAGCAGCAAC  2460
AGCATCAAAT ACTTGCCACT CCACTTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA  2520
ATGAATGCAT TTCGGTTAAA GGAAGAATTT ATTCCATATT AAAGCAGATA GGAAGTGGAG  2580
GTTCAAGCAA GGTATTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAAATATG  2640
TGAACTTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT  2700
TGAATAAACT ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCACGG  2760
ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA  2820
AGAAAAAATC CATTGATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG  2880
TTCACACAAT CCATCAACAT GGCATTGTTC ACAGTGATCT TAAACCAGCT AACTTTCTGA  2940
TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAAATG CAACCAGATA  3000
CAACAAGTGT TGTTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA  3060
TCAAAGATAT GTCTTCCTCC AGAGAGAATG GGAAATCTAA GTCAAAGATA AGCCCCAAAA  3120
GTGATGTTTG GTCCTTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTC  3180
AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG  3240
AATTTCCCGA TATTCCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTTGT TTAAAAAGGG  3300
ACCCAAAACA GAGGATATCC ATTCCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA  3360
CTCATCCAGT TAACCAAATG GCCAAGGGAA CCACTGAAGA AATGAAATAT GTTCTGGGCC  3420
AACTTGTTGG TCTGAATTCT CCTAACTCCA TTTTGAAAGC TGCTAAAACT TTATATGAAC  3480
ACTATAGTGG TGGTGAAAGT CATAATTCTT CATCCTCCAA GACTTTTGAA AAAAAAGGG  3540
GAAAAAAATG ATTTGCAGTT ATTCGTAATG TCAGATAGGA GGTATAAAAT ATATTGGACT  3600
GTTATACTCT TGAATCCCTG TGGAAATCTA CATTTGAAGA CAACATCACT CTGAAGTGTT  3660
ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAAAGAAA ACTGTAAAAA TAGCAACCAC  3720
TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC  3780
TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTTG  3840
TAAATAAAGT TTTGTGGCTA AAATGA
```

A147 Protein sequence:

Gene name:	TTK protein kinase
Unigene number:	Hs.169840
Probeset Accession #:	M86699
Protein Accession #:	NP_003309
Signal sequence:	none found
Transmembrane domains:	none found
Protein Kinase Domain:	510-775
Cellular Localization:	cytoplasmic and nuclear

```
1          11         21         31         41         51
|          |          |          |          |          |
MNKVRDIKNK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS    60
VPLSDALLNK LIGRYSQAIE ALPPDKYGQN ESFARIQVRF AELKAIQEPD DARDVFQMAR   120
ANCKKFAPVH ISFAQFELSQ GNVKKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS   180
EEEKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR   240
NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGSKP   300
SGNDSCELRN LKSVQNSHFK EPLVSDEKSS ELIITDSITL KNKTESSLLA KLEETKEYQE   360
PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTFE QPVFSVSKQS   420
PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDFP PACQLSTPYG QPACFQQQQH   480
QILATPLQNL QVLASSSANE CISVKGRIYS ILKQICSGGS SKVFQVLNEK KQIYAIKYVN   540
LEEADNQTLD SYRNEIAYLN KLQQHSDKII RLYDYEITDQ YIYMVMECGN IDLNSWLKKK   600
KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPANFLIV DGMLKLIDFG IANQMQPDTT   660
SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYY MTYGKTPFQQ   720
IINQISKLHA IIDPNHEIEF PDIPEKDLQD VLKCCLKRDP KQRISIPELL AHPYVQIQTH   780
PVNQMAKGTT EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK   840
K
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A148 DNA SEQUENCE

Gene name:	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number:	Hs.258583
Probeset Accession #:	NM_012152
Nucleic Acid Accession #:	NM_012152
Coding sequence:	43-1104 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
CTTCTTTAAA TTTCTTTCTA GGATGTTCAC TTCTTCTCCA CAATGAATGA GTGTCACTAT    60
GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTCGA TGACTGGACA   120
GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT   180
TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC   240
TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCCTG   300
ATGTTTAACA CAGGCCCAGT TTCAAAAACT TTGACTGTCA ACCGCTGGTT TCTCCGTCAG   360
GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG   420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA   480
CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTTATGG GGCCGGTCCC CACACTGGGC   540
TGGAATTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCCATTTA CAGCAGGAGT   600
TACCTTGTTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC   660
CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG   720
TCCATCAGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG   780
GCGTTTGTGG TATGCTGGAC CCCGGGCCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC   840
AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC   900
GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG   960
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA  1020
GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA  1080
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GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCCACCCA GGTGATGACT 1140
GTCTTAGG

A149 Protein sequence:

Gene name:	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number:	Hs.258583
Probeset Accession #:	NM_012152
Protein Accession #:	NP_036284
Signal sequence:	none found
Transmembrane domains:	31-53, 66-88, 150-172, 190-211, 239-261, 277-295
Cellular Localization:	plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNSL VIAAVIKNRK    60
FHFPFYYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL   120
LVIAVERHMS IMRMRVHSNL TKKRVTLLIL LVWAIAIFMG AVPTLGWNCL CNISACSSLA   180
PIYSRSYLVF WTVSNLMAFL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT   240
VMTVLGAFVV CWTPGLVVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVNP IIYSYKDEDM   300
YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS
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Prostate

A150 DNA SEQUENCE

Gene name:	ESTs
Unigene number:	Hs.293616
Probeset Accession #:	AW043782
Nucleic Acid Accession #:	none found

Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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1          11         21         31         41         51
|          |          |          |          |          |
AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG    60
CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAACAACT TCACCAATGA   120
GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA   180
GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA   240
GTCGAAATGT GGCCCAACCT TCTTCCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG   300
CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC   360
AAACCCTCTG CTTTGCTCCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA   420
GAGCTTCATC TGCGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA   480
AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA   540
TTACCCCAGC ATCACCTATG CCATCATCGG CAGCTCCGTC ATTTTTGTGC TGGTGGTGGC   600
CCTGCTGGCA CTGGTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT   660
GCACCGGCTG CAGCACCCTG TGCTGCTGTC CCGCCTGGTG GTCCTGGACC ACCCCCACCA   720
CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA   780
GAATGCGTCG GAAGTAGGCT CCCCACCCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC   840
TGCGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC   900
CGACCTGCCC CCCTACCGCT CCCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC   960
CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCCAGGA  1020
GGGCACTGCT GAGCCCAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC  1080
AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTTG  1140
TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT  1200
AACTATCTCT GCATTCCCCT CCTCCCCCAG ACTTCAGAGA TGTTTTTCTG GCGTCTCAGT  1260
TGACATGATC TGTTGTGCGT CTTTTCTGTC AGGTCACTCT TCCCTTGGGA CCCGAGATCA  1320
CACCCTCATT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG  1380
AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA  1440
CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG  1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAAATT CCATTTGAGC  1560
ATCAAAACCT GCTTTGCACA ATCCTATTTG ATGCCCCCAG TTCAGCAGAG TCAGTGGCCA  1620
AAGAAAACTT TGGACGTGAG TAACACCCTT CAGCAGTCGC AACGTTATTT TGGTTTTGTG  1680
AAGGACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAAATTTG CCCAAGAATG  1740
CTCATTCTGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCCTAA AATAGGCAGG  1800
GAGCCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC  1860
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCACC CTCCCAGCTG  1920
ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT  1980
GTATGTCCCT GTGGCCCACA CCCAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC  2040
CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTTGG ACTTGAGGAC  2100
ACTGGTTTCT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC  2160
CTGCACTGTG CACGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG  2220
GGTCAGGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG  2280
AGACAATTTG GAGTCAAGAT TTTCCATTTG GATCTATTTT AAATCTTTTA GAAATGCATT  2340
TGAAACAGTG TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA  2400
AGCTGTCTCT TTTTTTGTTT TTCCTTTAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC  2460
ACACCCTTGC CCCGCTGAGC CCCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG  2520
ACATTTGTGC ATTGTTGCAC TTTGAGGTTA TTATTTATCA AGTTCTTGAA GGAAGCAGAA  2580
AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT  2640
TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT  2700
AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAAATGGAA CCAGGTAGAG  2760
CCACTCCGGG CAGCTGTCAC CCATTCAGAA CTTCTTTCCG CAGCTGAAGA AATGTTCAGT  2820
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AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTCAG  2880
TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA  2940
AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA  3000
AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTTAA AATAGCACTT GAGTTATTTT  3060
CTGAGTAATC CAATAAAGAA CTTTTGATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA  3120
CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC  3180
TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT  3240
GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT  3300
AGATAAGGGA TGCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTTT ATTATAGATT  3360
TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT  3420
TTTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT  3480
TTTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG  3540
AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT  3600
AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA  3660
TTTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG  3720
GAAAGGTTGT GTGTCGTTGC TTTTTGTGTT TTGGTTAGGC TTGGTTTTGT TTTTTAATTT  3780
TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAWG GWMCTAMARM  3840
AAMMAAAAAC AWYWTTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTTAACA CCACTTCGGG  3900
TGGGGCGGCG GGGCCCACGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG  3960
GAAACCCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAAA ACGCGCCGGG  4020
GGAAACCGCA GAGTGTTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG  4080
GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G
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A151 Protein sequence:

Gene name:	ESTs
Unigene number:	Hs.293616
Probeset Accession #:	AW043782
Protein Accession #:	none found
Signal sequence:	1-17
Transmembrane domains:	169-191
LDLa domains:	28-66, 70-108, 112-149
Cellular Localization:	plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD    60
EKECPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC   120
KNGLCIDKSF ICDGQNNCQD NSDEESCESS QEPGSGQVFV TSENQLVYYP SITYAIIGSS   180
VIFVLVVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ   240
YVASQAEQNA SEVGSPPSYS EALLDQRPAW YDLPPPPYSS DTESLNQADL PPYRSRSGSA   300
NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV
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A152 DNA SEQUENCE

Gene name:	Transmembrane protease, serine 2 (TMPRSS2)
Unigene number:	Hs.105807
Probeset Accession #:	T48536
Nucleic Acid Accession #:	NM_005656.1

Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC AGCAAGATGG    60
CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT GGATACCAAC   120
CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG   180
CTCAGTACTA CCCGTCCCCC GTGCCCCAGT ACGCCCCGAG GGTCCTGACG CAGGCTTCCA   240
ACCCCGTCGT CTGCACGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA   300
AGAAAGCACT GTGCATCACC TTGACCCTGG GGACCTTCCT CGTGGGAGCT GCGCTGGCCG   360
CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGCGACT   420
CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG CGTGTCACAC TGCCCCGGCG   480
GGGAGGACGA GAATCGGTGT GTTCGCCTCT ACGGACCAAA CTTCATCCTT CAGATGTACT   540
CATCTCAGAG GAAGTCCTGG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC   600
GGGCGGCCTG CAGGGACATG GGCTATAAGA ATAATTTTTA CTCTAGCCAA GGAATAGTGG   660
ATGACAGCGG ATCCACCAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT   720
ATAAAAAACT GTACCACAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT   780
TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG   840
CGCTCCCGGG GGCCTGGCCC TGGCAGGTCA GCCTGCACGT CCAGAACGTC CACGTGTGCG   900
GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC   960
TTAACAATCC ATGGCATTGG ACGGCATTTG CGGGGATTTT GAGACAATCT TTCATGTTCT  1020
ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA  1080
AGAACAATGA CATTGCGCTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA  1140
AACCAGTGTG TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT  1200
CCGGGTGGGG GGCCACCGAG GAGAAAGGGA AGACCTCAGA AGTGCTGAAC GCTGCCAAGG  1260
TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC  1320
CAGCCATGAT CTGTGCCGGC TTCCTGCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG  1380
GAGGGCCTCT GGTCACTTCG AACAACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG  1440
GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTCACGG  1500
ACTGGATTTA TCGACAAATG AAGGCAAACG GCTAATCCAC ATGGTCTTCG TCCTTGACGT  1560
CGTTTTACAA GAAAACAATG GGGCTGGTTT TGCTTCCCCG TGCATGATTT ACTCTTAGAG  1620
ATGATTCAGA GGTCACTTCA TTTTTATTAA ACAGTGAACT TGTCTGGCTT TGGCACTCTC  1680
TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCCAGCC TGCTCTCCCT AACCCCTTGT  1740
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CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG  1800
GTTGGAGGCT GCCCCCATTG AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGGA  1860
TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT  1920
GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTTGGTAGTG  1980
TCCCCAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTC TTAGAGCCTT AGCAGCCCTG  2040
GATGGTGGCC AGAAATAAAG GGACCAGCCC TTCATGGGTG GTGACGTGGT AGTCACTTGT  2100
AAGGGGAACA GAAACATTTT TGTTCTTATG GGGTGAGAAT ATAGACAGTG CCCTTGGTGC  2160
GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA  2220
CATTGGGTGG GGCTCCTGGG AGGGAGACTC AGCCTTCCTC CTCATCCTCC CTGACCCTGC  2280
TCCTAGCACC CTGGAGAGTG AATGCCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC  2340
ATGTCGGCCT CTTCAGGCCT GATAGTCATT GGAAATTGAG GTCCATGGGG GAAATCAAGG  2400
ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC  2460
CTGAGTTCAA AGCCATCTT
```

A153 Protein sequence:

Gene name:	Transmembrane protease, serine 2 (TMPRSS2)
Unigene number:	Hs.105807
Probeset Accession #:	T48536
Protein Accession #:	NP_005647.1
Signal sequence:	none found
Transmembrane domains:	85-107
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA    60
SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC   120
DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VCQDDWNENY   180
GRAACRDMGY KNNFYSSQGI VDDSGSTSFM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR   240
CLACGVNLNS SRQSRIVGGE SALPGAWPWQ VSLHVQNVHV CGGSIITPEW IVTAAHCVEK   300
PLNNPWHWTA FAGILRQSFM FYGAGYQVQK VISHPNYDSK TKNNDIALMK LQKPLTFNDL   360
VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNLI   420
TPAMICAGFL QGNVDSCQGD SGGPLVTSNN NIWWLIGDTS WGSGCAKAYR PGVYGNVMVF   480
TDWIYRQMKA NG
```

A154 DNA SEQUENCE

Gene name:	Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
Unigene number:	Hs.129179
Probeset Accession #:	AI694767
Nucleic Acid Accession #:	AI694767
Coding sequence:	130-1086 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
CAGAGAGGCT GTATTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG    60
GGGGTCACAC ATTCCTTCCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTCACAGTTC   120
AGCTTCTTCA TGATGGTGGA TCCCAATGGC AATGAATCCA GTGCTACATA CTTCATCCTA   180
ATAGGCCTCC CTGGTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCCATT GTGCTCCCTC   240
TACCTTATTG CTGTGCTAGG TAACTTGACA ATCATCTACA TTGTGCGGAC TGAGCACAGC   300
CTGCATGAGC CCATGTATAT ATTTCTTTGC ATGCTTTCAG GCATTGACAT CCTCATCTCC   360
ACCTCATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT   420
GATGCTTGTC TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG   480
CTGCTGGCCA TGGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGCG CCATGCCACA   540
GTACTTACGT TGCCTCGTGT CACCAAAATT GGTGTGGCTG CTGTGGTGCG GGGGGCTGCA   600
CTGATGGCAC CCCTTCCTGT CTTCATCAAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT   660
TCCCATTCCT ACTGCCTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC   720
AATGTCGTCT ATGGCCTTAT CGTCATCATC TCCGCCATTG GCCTGGACTC ACTTCTCATC   780
TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTTGGGCT TGACACGTGA AGCCCAGGCC   840
AAGGCATTTG GCACTTGCGT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC   900
ATTGGATTGT CCATGGTGCA TCGCTTTAGC AAGCGGCGTG ACTCTCCACT GCCCGTCATC   960
TTGGCCAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG  1020
ACAAAGGAGA TTCGACAGCG CATCCTTCGA CTTTTCCATG TGGCCACACA CGCTTCAGAG  1080
CCCTAGGTGT CAGTGATCAA ACTTCTTTTC CATTCAGAGT CCTCTGATTC AGATTTTAAT  1140
GTTAACATTT TGGAAGACAG TATTCAGAAA AAAAATTTCC TTAATAAAAA TACAACTCAG  1200
ATCCTTCAAA TATGAAACTG GTTGGGGAAT CTCCATTTTT TCAATATTAT TTTCTTCTTT  1260
GTTTTCTTGC TACATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC  1320
TTTTCATTTT ACCATGCAGT CCAAATCTAA ACTGCTTCTA CTGATGGTTT ACAGCATTCT  1380
GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAAGGAAAA  1440
TAAACACAGA ATATAATAAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA  1500
ACTCCCAACC ACATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG  1560
AAATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA  1620
AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT  1680
ATGGACCCTG TTTTTCCTAT TTAATTTTCT TATCAACCCT TTAATTAGGC AAAGATATTA  1740
TTAGTACCCT CATTGTAGCC ATGGGAAAAT TGATGTTCAG TGGGGATCAG TGAATTAAAT  1800
GGGGTCATAC AAGTATAAAA ATTAAAAAAA AAAGACTTCA TGCCCAATCT CATATGATGT  1860
GGAAGAACTG TTAAAGAGAC CAACAGGGTA GTGGGTTAGA GATTTCCAGA GTCTTACATT  1920
TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGTATTTAG GAATTTCCTG  1980
GCAACAGAAC TCATGGCTTT AATCCCACTA GCTATTGCTT ATTGTCCTGG TCCAATTGCC  2040
AATTACCTGT GTCTTGGAAG AAGTGATTTC TAGGTTCACC ATTATGGAAG ATTCTTATTC  2100
AGAAAGTCTG CATAGGGCTT ATAGCAAGTT ATTTATTTTT AAAAGTTCCA TAGGTGTTTC  2160
TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGAA TGGCAGGTGT  2220
TGAAGATAAC ATTGGCCTTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGGG AATCTTCAGG  2280
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ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGGAACAGGG ACTTTGAGAC CGGGAAAGCA  2340
ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA  2400
ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACTC AAATTACATA  2460
TACTAAAACA TGTGATCATA TATGTGGTAA GTTTCATTTT CTTTTTCAAT CCTCAGGTTC  2520
CCTGATATGG ATTCCTATNA CATGCTTTCA TCCCCTTTTG TAATGGATAT CATATTTGGA  2580
AATGCCTATT TAATACTTGT ATTTGCTGCT GGACTGTAAG CCCATGAGGG CACTGTTTAT  2640
TATTGAATGT CATCTCTGTT CATCATTGAC TGCTCTTTGC TCATCATTGA ATCCCCCAGC  2700
AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTTCA TCAAACCTGA  2760
TTCCTTCTGT GCTGAACACA TAGCCAGGCA ATTTTCCAGC CTTCTTTGAG TTGGGTATTA  2820
TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAAGTGAC ATGTGCAATT TTTATACCTG  2880
GCTCATAAAA CCCTCCCATG TGCAGCCTTT CATGTTGACA TTAAATGTGA CTTGGGAAGC  2940
TATGTGTTAC ACAGAGTTAA TTAACCNGAA AGGCCTGGNA ATTTTTTGNN AANNAAACTG  3000
TGGCCNNGAG GCCCNCAACC CTTTTTNNNA ATTTGGCAAN NTCCCACTTT GTANTTTGGT  3060
AAGGAGGCCA GTTGGATAAG TGAAAAATAA AGTACTATTG TGTC
```

A155 PROTEIN SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
Unigene number: Hs.129179
Protein Accession #: not available
Signal sequence: none found
Pfam domain: 7tm_1 [43-293]
Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295
Cellular Localization: not determined

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1          11         21         31         41         51
|          |          |          |          |          |
MVDPNGNESS ATYFILIGLP GLEEAQFWLA FPLCSLYLIA VLGNLTIIYI VRTEHSLHEP    60
MYIFLCMLSG IDILISTSSM PKMLAIFWFN STTIQFDACL LQMFAIHSLS GMESTVLLAM   120
AFDRYVAICH PLRHATVLTL PRVTKIGVAA VVRGAALMAP LPVFIKQLPF CRSNILSHSY   180
CLHQDVMKLA CDDIRVNVVY GLIVIISAIG LDSLLISFSY LLILKTVLGL TREAQAKAFG   240
TCVSHVCAVF IFYVPFIGLS MVHRFSKRRD SPLPVILANI YLLVPPVLNP IVYGVKTKEI   300
RQRILRLFHV ATHASEP
```

A156 DNA SEQUENCE

Gene name: vasoactive intestinal peptide receptor 1
Unigene number: Hs.198726
Probeset Accession #: X77777
Nucleic Acid Accession #: NM_004624.1
Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

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TCGGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTCGCCCGCC TCACTCATGC    60
CTCCTCCTCC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGGTCGGCG GTTACGCGGC   120
TGGTGGTCGC GGCGGCCGGG GCTCGCTCTC GGGGAGGCCG GGGCGGATCT CGCGGCGCAG   180
GCGGCGGCGG CCGAGGTGGG GTCGCGCGGC GGAGGCGGCT CGAGCTTCGT GCTGCGCGCT   240
CGCTCTTGGG CTCCTCGCTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC   300
ACAAGCAGTG CCTGGAGGAG GCCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT   360
GGGACAACCT CACCTGCTGG CCAGCCACCC CTCGGGGCCA GGTAGTTGTC TTGGCCTGTC   420
CCCTCATCTT CAAGCTCTTC TCCTCCATTC AAGGCCGCAA TGTAAGCCGC AGCTGCACCG   480
ACGAAGGCTG GACGCACCTG GAGCCTGGCC CGTACCCCAT TGCCTGTGGT TTGGATGACA   540
AGGCAGCGAG TTTGGATGAG CAGCAGACCA TGTTCTACGG TTCTGTGAAG ACCGGCTACA   600
CCATTGGCTA CGGCCTGTCC CTCGCCACCC TTCTGGTCGC CACAGCTATC CTGAGCCTGT   660
TCAGGAAGCT CCACTGCACG CGGAACTACA TCCACATGCA CCTCTTCATA TCCTTCATCC   720
TGAGGGCTGC CGCTGTCTTC ATCAAAGACT TGGCCCTCTT CGACAGCGGG GAGTCGGACC   780
AGTGCTCCGA GGGCTCGGTG GGCTGTAAGG CAGCCATGGT CTTTTTCCAA TATTGTGTCA   840
TGGCTAACTT CTTCTGGCTG CTGGTGGAGG GCCTCTACCT GTACACCCTG CTTGCCGTCT   900
CCTTCTTCTC TGAGCGGAAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA   960
GCACATTCAC CATGGTGTGG ACCATCGCCA GGATCCATTT TGAGGATTAT GGTCTGCTCA  1020
GGTGCTGGGA CACCATCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCCTCACCT  1080
CCATCTTGGT AAACTTCATC CTGTTTATTT GCATCATCCG AATCCTGCTT CAGAAACTGC  1140
GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATACTC AAGGCTAGCC AGGTCCACAC  1200
TCCTGCTGAT CCCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CCGGACAATT  1260
TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTCGTGGG GTCTTTCCAG GGTTTTGTGG  1320
TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC  1380
GGCGCTGGCA CCTGCAGGGC GTCCTGGGCT GGAACCCCAA ATACCGGCAC CCGTCGGGAG  1440
GCAGCAACGG CGCCACGTGC AGCACGCAGG TTTCCATGCT GACCCGCGTC AGCCCAGGTG  1500
CCCGCCGCTC CTCCAGCTTC CAAGCCGAAG TCTCCCTGGT CTGACCACCA GGATCCCAGC  1560
CCAAGCGGCC CCTCCCGCCC CTTCCCACTC GCAGCAGACG CCGGGGACAG AGGCCTGCCC  1620
GGGCGCGCCA GCCCCGGCCC TGGGCTCGGA GGCTGCCCCC GGCCCCCTGG TCTCTGGTCC  1680
GGACACTCCT AGAGAACGCA GCCCTAGAGC CTGCCTGGAG CGTTTCTAGC AAGTGAGAGA  1740
GATGGGAGCT CCTCTCCTGG AGGATGCAGG TGGAACTCAG TCATTAGACT CCTCCTCCAA  1800
AGGCCCCCTA CGCCAATCAA GGGCAAAAAG TCTACATACT TTCATCCTGA CTCTGCCCCC  1860
TGCTGGCTCT TCTGCCCAAT TGGAGGAAAG CAACCGGTGG ATCCTCAAAC AACACTGGTG  1920
TGACCTGAGG GCAGAAAGGT TCTGCCCGGG AAGGTCACCA GCACCAACAC CACGGTAGTG  1980
CCTGAAATTT CACCATTGCT GTCAAGTTCC TTTGGGTTAA GCATTACCAC TCAGGCATTT  2040
GACTGAAGAT GCAGCTCACT ACCCTATTCT CTCTTTACGC TTAGTTATCA GCTTTTTAAA  2100
GTGGGTTATT CTGGAGTTTT TGTTTGGAGA GCACACCTAT CTTAGTGGTT CCCCACCGAA  2160
GTGGACTGGC CCCTGGGTCA GTCTGGTGGG AGGACGGTGC AACCCAAGGA CTGAGGGACT  2220
CTGAAGCCTC TGGGAAATGA GAAGGCAGCC ACCAGCGAAT GCTAGGTCTC GGACTAAGCC  2280
TACCTGCTCT CCAAGTCTCA GTGGCTTCAT CTGTCAAGTG GGACTCTGTC ACACCAGCCA  2340
TTCTTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTTGTCCACC  2400
CACCTATGTG CCAACTGTTG TAACTAGGCT CAGAGATGTG CACCCATGGG CTCTGACAGA  2460
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AAGCAGATCC TCACCCTGCT ACACATACAG GATTTGAACT CAGATCTGTC TGATAGGAAT  2520
GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT AACCAGCCAG ATCCTCTTGG  2580
TTATTTGTTT ACCACTTGTA TTATTAATGC CATTATCCCT GAATTCCCCT TGCCACCCCA  2640
CCCTCCCTGG AGTGTGGCTG AGGAGGCCTC CATCTCATGT ATCATCTGGA TAGGAGCCTG  2700
CTGGTCACAG CCTCCTCTGT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA  2760
CCTCTGCCAG AAGATCCCCT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT  2820
GGAAAAAAAA AAAA
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A157 Protein sequence:

Gene name:	vasoactive intestinal peptide receptor 1
Unigene number:	Hs.198726
Probeset Accession #:	X77777
Protein Accession #:	JC2195
Signal sequence:	none found
Transmembrane domains:	181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPPPLLSLR RLGGGWSAVT RLVVAAAGAR SRGGRGGSRG AGGGGRGGVA RRRRLELRAA    60
RSLLGSSLQE ECDYVQMIEV QHKQCLEEAQ LENETIGCSK MWDNLTCWPA TPRGQVVVLA   120
CPLIFKLFSS IQGRNVSRSC TDEGWTHLEP GPYPIACGLD DKAASLDEQQ TMFYGSVKTG   180
YTIGYGLSLA TLLVATAILS LFRKLHCTRN YIHMHLFISF ILRAAAVFIK DLALFDSGES   240
DQCSEGSVGC KAAMVFFQYC VMANFFWLLV EGLYLYTLLA VSFFSERKYF WGYILIGWGV   300
PSTFTMVWTI ARIHFEDYGL LRCWDTINSS LWWIIKGPIL TSILVNFILF ICIIRILLQK   360
LRPPDIRKSD SSPYSRLARS TLLLIPLFGV HYIMFAFFPD NFKPEVKMVF ELVVGSFQGF   420
VVAILYCFLN GEVQAELRRK WRRWHLQGVL GWNPKYRHPS GGSNGATCST QVSMLTRVSP   480
GARRSSSFQA EVSLV
```

A158 DNA SEQUENCE

Gene name:	ESTs
Unigene number:	Hs.29383
Probeset Accession #:	AW207206
Nucleic Acid Accession #:	AL133619

Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCCA GCTCGCCGAC CCCGGGCTCT    60
CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG   120
CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG   180
CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG   240
GAAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCTCCCCA GGCACACTCA   300
ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA   360
GGGGGAACAC AGGACGGGGA GCCCCTCCAG ACTGTCCTTG CCCACCTGGC TGCACTGGCC   420
CCTGTATGCC AACCCAGTGG GTACAGGTTC TGGGGGACCT GGACAGATGC CGCTACCTCT   480
AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCACG TGCTGCTCTC GGGAAGCCCA   540
GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT   600
CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG   660
CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCCTCAC   720
ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG   780
GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCCTGT TTCCTTGCCA CTTGTCCAAG   840
GCACTTCCCC ATCCTGACAG CGGCCCCCAC CCAGCCCAGG ATCCTGGGCT GTGGTCTCAA   900
GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA   960
TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCCAGGGA  1020
GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG  1080
CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCAGTGC TGGGGACGCT  1140
GACAGGACAC GGGAAGAGGC CATGCTTTCC CTCGGGACCT GCTGTTCCAT GTGTCCCAAG  1200
CCCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG  1260
GGCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC  1320
AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGCG  1380
GGCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG  1440
TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC  1500
TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCCAGA AGGCGGACCT GGAAGAGGAG  1560
CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCCTGGGG TACAAGGGCA GGCCAGAAAG  1620
GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC  1680
AGGCAGATGG GGCCGGGGGC ACACCCCCCA ATGATCCTGC CCCTTCCCCT GCGAAAGCCC  1740
ACCACACTTA GGCAGTGCGA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCAG  1800
ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC  1860
CCGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCCAA GGTCTCCACC  1920
AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA  1980
CTGAAGCAGA CCCCGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG  2040
AAACGGCGCC TGCATCGCTC AGTGCTTTGA
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A159 Protein sequence:

Gene name:	ESTs
Unigene number:	Hs.29383
Probeset Accession #:	AW207206
Protein Accession #:	T43457
Signal sequence:	none found
Transmembrane domains:	303-322
Cellular Localization:	not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL    60
QQQHSEMLAK LHEEIEHLKR ENKGEPARGP RPALPPQAHS TLPLPQHRNT AINSSTRLGS   120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAATS SRGWTMLCSQ AQHVLLSGSP   180
GPEVIAGRQV ATGCSPDLPP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH   240
MLGAQGIWTH SIQGSLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSGPH PAQDPGLWSQ   300
AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVEGGP FPSRCGNSSE   360
LFWAKCGPSR QPQPCSAGDA DRTREEAMLS LGTCCSMCPK PSCFPDGPSG NHLSRASAPL   420
GARWVCINGV WVEPGGPSPA RLKEGSSRTH RPGGKRGRLA GGSADTVRSP ADSLSMSSFQ   480
SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGQARK   540
EKAEASNAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ   600
TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA   660
LKQTPKNNFA ERQKRLQAMQ KRRLHRSVL
```

A160 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
Unigene number: Hs.79136
Probeset Accession #: U41060
Nucleic Acid Accession #: NM_012319.2
Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

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|          |          |          |          |          |
CTCGTGCCGA ATTCGGCACG AGACCGCGTG TTCGCGCCTG GTAGAGATTT CTCGAAGACA    60
CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GGCCGTGGGA CAACGAGGCC   120
GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTTGATCCTG ACCTTTGCCC   180
TCTCTGTCAC AAATCCCCTT CATGAACTAA AAGCAGCTGC TTTCCCCCAG ACCACTGAGA   240
AAATTAGTCC GAATTGGGAA TCTGGCATTA ATGTTGACTT GGCAATTTCC ACACGGCAAT   300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT   360
TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG   420
ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG   480
AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG   540
CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCCAGA CCATGACTCA GATAGTTCAG   600
GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA   660
GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG   720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACTCTTCC   780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACATC AAAGAGCCGG GTGAGCCGGC   840
TGGCTGGTAG GAAAACAAAT GAATCTGTGA GTGAGCCCCG AAAAGGCTTT ATGTATTCCA   900
GAAACACAAA TGAAAATCCT CAGGAGTGTT TCAATGCATC AAAGCTACTG ACATCTCATG   960
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA  1020
TCAACCAAAT TGATGCTAGA TCTTGTCTGA TTCATACAAG TGAAAAGAAG GCTGAAATCC  1080
CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA  1140
TCAGTTTCCT GTCTCTGCTG GGGGTTATCT TAGTGCCTCT CATGAATCGG GTGTTTTTCA  1200
AATTTCTCCT GAGTTTCCTT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT  1260
TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG  1320
CAATGGAAAT GAAAAGAGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA  1380
GTGCCTATTT TGATTCCACG TGGAAGGGTC TAACAGCTCT AGGAGGCCTG TATTTCATGT  1440
TTCTTGTTGA ACATGTCCTC ACATTGATCA AACAATTTAA AGATAAGAAG AAAAAGAATC  1500
AGAAGAAACC TGAAAATGAT GATGATGTGG AGATTAAGAA GCAGTTGTCC AAGTATGAAT  1560
CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC  1620
GAGCAGACTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAAG  1680
AAGAGGTCAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG  1740
GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA  1800
TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCACCATC  1860
CTCACAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTCGCCACTT  1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAATTT CAGCGATGGC CTAGCAATTG  1980
GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC  2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA  2100
AGCAGGCTGT CCTTTATAAT GCATTGTCAG CCATGCTGGC GTATCTTGGA ATGGCAACAG  2160
GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTTGCA CTTACTGCTG  2220
GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA  2280
GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTTACA GAATGCTGGG ATGCTTTTGG  2340
GTTTTGGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTT CGTATAAATT  2400
TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT  2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATTT  2520
TTGTATTGAA TATTGCTGTC TGTTACAAAG TCAGTTAAAG GTACGTTTTA ATATTTAAGT  2580
TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG  2640
TAAACAAGAG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAAAAATGT CTTTAATGCT  2700
TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG  2760
TGTTTAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA  2820
AGCAAAGAAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT  2880
AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAAGG  2940
CAGAATTAGT ATAGAGTACA TTCATTAAAC ATTTTTGTCA GGATTATTTC CCGTAAAAAC  3000
GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT  3060
AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG  3120
TTCGTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT  3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTTCTGGTT ACCTGGTTTA  3240
CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAAACT ACACTAAGTA  3300
TCATTTGATT CGATTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTGT  3360
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GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420
GATGTTTCTT TTTACACAA TAAATTCCTT ATATCAGCTT G

A161 PROTEIN SEQUENCE

Gene name:	LIV-1 protein, estrogen regulated
Unigene number:	Hs.79136
Protein Accession #:	NP_036451
Signal sequence:	1-21
Pfam domain:	Zip[591-743]
Transmembrane domains:	330-346, 352-368, 427-444, 663-679, 688-703, 730-745
Cellular Localization:	plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MARKLSVILI LTFALSVTNP LHELKAAAFP QTTEKISPNW ESGINVDLAI STRQYHLQQL    60
FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHDHHS DHEHHSDHER HSDHEHHSDH   120
EHHSDHDHHS HHNHAASGKN KRKALCPDHD SDSSGKDPRN SQGKGAHRPE HASGRRNVKD   180
SVSASEVTST VYNTVSEGTH FLETIETPRP GKLFPKDVSS STPPSVTSKS RVSRLAGRKT   240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LTSHGMGIQV PLNATEFNYL CPAIINQIDA   300
RSCLIHTSEK KAEIPPKTYS LQIAWVGGFI AISIISFLSL LGVILVPLMN RVFFKFLLSF   360
LVALAVGTLS GDAFLHLLPH SHASHHHSHS HEEPAMEMKR GPLFSHLSSQ NIEESAYFDS   420
TWKGLTALGG LYFMFLVEHV LTLIKQFKDK KKKNQKKPEN DDDVEIKKQL SKYESQLSTN   480
EEKVDTDDRT EGYLRADSQE PSHFDSQQPA VLEEEEVMIA HAHPQEVYNE YVPRGCKNKC   540
HSHFHDTLGQ SDDLIHHHHD YHHILHHHHH QNHHPHSHSQ RYSREELKDA GVATLAWMVI   600
MGDGLHNFSD GLAIGAAFTE GLSSGLSTSV AVFCHELPHE LGDFAVLLKA GMTVKQAVLY   660
NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS   720
RWGYFFLQNA GMLLGFGIML LISIFEHKIV FRINF
```

A162 DNA sequence

Gene name:	bone morphogenetic protein receptor IB (ALK-6)
Unigene number:	Hs.87223
Probeset Accession #:	AA250737
Nucleic Acid Accession #:	NM_001203
Coding sequence:	274-1782 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGCGGAGA CCGCGGCGCT    60
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT   120
GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTTGATAAA GGTTCAGACT TCTGCTGATT   180
CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC   240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA   300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC   360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA   420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTGCCTGT GGTCACTTCT   480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTCGGG ACACTCCCAT TCCTCATCAA   540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCTACA   600
CTGCCTCCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCTTTACTT   660
ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG   720
TATAAAAGAC AAGAAACCAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC   780
ATTCCTCCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA   840
TCAGGCCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAAACAG   900
ATTGGAAAAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT   960
GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG  1020
ACAGTGTTGA TGAGGCATGA AAACATTTTG GGTTTCATTG CTGCAGATAT CAAAGGGACA  1080
GGGTCCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT  1140
TATCTGAAGT CCACCACCCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC  1200
AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAACC AGCAATTGCC  1260
CATCGAGATC TGAAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACTTG CTGTATTGCT  1320
GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC  1380
ACTCGAGTTG GCACCAAACG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA  1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG  1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC  1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA  1620
CGCCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACTC  1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA  1740
ACACTTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG  1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA  1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC  1920
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG  1980
TCTGTTTGTA GGCGGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT
```

A163 Protein sequence

Gene name:	bone morphogenetic protein receptor IB (ALK-6)
Unigene number:	Hs.72472 / Hs.87223
Probeset Accession #:	AA250737 / U89326
Protein Accession #:	NP_001194
Signal sequence:	1-13
Transmembrane domains:	128-144
PFAM domains:	activin_receptor [30-111], protein kinase [204-491]
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED    60
DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD   120
GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPRYS IGLEQDETYI PPGESLRDLI   180
EQSQSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTEEAS   240
WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS   300
MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILV KKNGTCCIAD LGLAVKFISD   360
TNEVDIPPNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFGLILWEV ARRCVSGGIV   420
EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS   480
RLTALRVKKT LAKMSESQDI KL
```

A164 DNA sequence

Gene name: ESTs
Unigene number: Hs.157601
Probeset Accession #: W07459
Nucleic Acid Accession #: AC005383
Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT    60
TTTTATTTGC AGACCTGGGC CGATGCCGCT TTAAAAAACG CGAGGGGCTC TATGCACCTC   120
CCTGGCGGTA GTTCCTCCGA CCTCAGCCGG GTCGGGTCGT GCCGCCCTCT CCCAGGAGAG   180
ACAAACAGGT GTCCCACGTG GCAGCCGCGC CCCGGGCGCC CCTCCTGTGA TCCCGTAGCG   240
CCCCCTGGCC CGAGCCCGCC CCGGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG   300
TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCCTTTCC TGTTGCTGGA GGCCGTCTGT   360
GTTTTCCTGT TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA   420
GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC   480
ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCGGGAAAG GGAGCTTTGA AAGGTCCAAG   540
CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA   600
GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCCCT TGGATTCATT TTCAACCCAA   660
CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA   720
CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC   780
CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG   840
CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG   900
GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCACG TGCTGTTGGC TGAGCAGGTG   960
GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC  1020
ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG  1080
GAGTTCGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCCTTGC GGTGCTGGCT  1140
GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCCTAA CCCACCCTGC CACCTGCTAC  1200
AGGACCACCT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT  1260
CCAGAAGGAC TGGACGGCTA CCAGTGCCTC TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC  1320
TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCCTGCT GGACAGCTCT  1380
GCGGGCACCA CTCTGGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG  1440
GCCGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG  1500
CTGGTGGCGG TGCCTGTGGG GGAGTACCAG GATGTGCCTG ACCTGGTCTG GAGCCTCGAT  1560
GGCATTCCCT TCCGTGGTGG CCCCACCCTG ACGGGCAGTG CCTTGCGGCA GGCGGCAGAG  1620
CGTGGCTTCG GGAGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTTTTG  1680
CTCACTGAGT CACACTCCGA GGATGAGGTT GCGGGCCCAG CGCGTCACGC AAGGGCGCGA  1740
GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCCGTGCGGG CAGAGCTGGA GGAGATCACA  1800
GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAAATCCCT  1860
GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG CGGCCAGGGT GCCGGACACA AGCCCTGGAC  1920
CTCGTCTTCA TGTTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG  1980
AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCGGC  2040
CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCCACCCGG  2100
GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCCTACCTAG GTGGGGTGGG CTCAGCCGGC  2160
ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCCTGGT  2220
GTCCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT  2280
GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA  2340
AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CGGGATTCCC TGATCCACGT GGCAGCTTAC  2400
GCCGACCTGC GGTACCACCA GGACGTGCTC ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG  2460
CCAGTCAACC TCTGCAAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAAT  2520
GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG  2580
TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATTC TTCAGACGCC CCTGAGGCAC  2640
ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCCTCCCA GCAACTACAG AGAAGGCCTG  2700
GGCACTGAAA TGGTGCCTAC CTTCTGGAAT GTCTGTGCCC CAGGTCCTTA GAATGTCTGC  2760
TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC  2820
ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTGAAAAGTT  2880
TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CCTTGTTGAG GCTATGTCAT  2940
CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCCTGAAG ACTTAAATTT AGCGGCCTGA  3000
CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCCAGCAG  3060
AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAAGCA  3120
GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAAGGGGG  3180
CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAAGA GACTTGGAAA  3240
GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT  3300
TGTGCATGGG CCCAGGTCTG GAGGGCCACG TAAAATCGTT CTGAGTCGTG AGCAGTGTCC  3360
ACCTTGAAGG TCTTC
```

A165 Protein sequence

Gene name:	ESTs
Unigene number:	Hs.157601
Protein Accession #:	none found
Signal sequence:	1-17
Transmembrane domains:	none found
VGW domains:	49-223; 341-518; 529-706
EGF domains:	298-333; 715-748
Cellular Localization:	secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN    60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAPQFSSTPH LEFPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAPGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS   780
RTPPSNYREG LGTEMVPTFW NVCAPGP
```

A166 DNA sequence

Gene name:	Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
Unigene number:	Hs.37744
Probeset Accession #:	AA011176
Nucleic Acid Accession #:	AF272890
Coding Sequence:	87-1520 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
TGCTACCCGC GCCCGGGCTT CTGGGGTGTT CCCCAACCAC GGCCCAGCCC TGCCACACCC    60
CCCGCCCCCG GCCTCCGCAG CTCGGCATGG GCGCGGGGGT GCTCGTCCTG GGCGCCTCCG   120
AGCCCGGTAA CCTGTCGTCG GCCGCACCGC TCCCCGACGG CGCGGCCACC GCGGCGCGGC   180
TGCTGGTGCC CGCGTCGCCG CCCGCCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCCGAGC   240
CGCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGCTGAT GGCGCTCATC GTGCTGCTCA   300
TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCCGCGG CTGCAGACGC   360
TCACCAACCT CTTCATCATG TCCCTGGCCA GCGCCGACCT GGTCATGGGG CTGCTGGTGG   420
TGCCGTTCGG GGCCACCATC GTGGTGTGGG GCCGCTGGGA GTACGGCTCC TTCTTCTGCG   480
AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA   540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCAGAGC CTGCTGACGC   600
GCGCGCGGGC GCGGGGCCTC GTGTGCACCG TGTGGGCCAT CTCGGCCCTG GTGTCCTTCC   660
TGCCCATCCT CATGCACTGG TGGCGGGCGG AGAGCGACGA GGCGCGCCGC TGCTACAACG   720
ACCCCAAGTG CTGCGACTTC GTCACCAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT   780
CCTTCTACGT GCCCCTGTGC ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCGAGGCCC   840
AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCCGTTT CCTCGGCGGC CCAGCGCGGC   900
CGCCCTCGCC CTCGCCCTCG CCCGTCCCCG CGCCCGCGCC GCCGCCCGGA CCCCCGCGCC   960
CCGCCGCCGC CGCCGCCACC GCCCCGCTGG CCAACGGGCG TGCGGGTAAG CGGCGGCCCT  1020
CGCGCCTCGT GGCCCTACGC GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG  1080
TCTTCACGCT CTGCTGGCTG CCCTTCTTCC TGGCCAACGT GGTGAAGGCC TTCCACCGCG  1140
AGCTGGTGCC CGACCGCCTC TTCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCCT  1200
TCAACCCCAT CATCTACTGC CGCAGCCCCG ACTTCCGCAA GGCCTTCCAG GGACTGCTCT  1260
GCTGCGCGCG CAGGGCTGCC CGCCGGCGCC ACGCGACCCA CGGAGACCGG CCGCGCGCCT  1320
CGGGCTGTCT GGCCCGGCCC GGACCCCCGC CATCGCCCGG GGCCGCCTCG GACGACGACG  1380
ACGACGATGT CGTCGGGGCC ACGCCGCCCG CGCGCCTGCT GGAGCCCTGG GCCGGCTGCA  1440
ACGGCGGGGC GGCGGCGGAC AGCGACTCGA GCCTGGACGA GCCGTGCCGC CCCGGCTTCG  1500
CCTCGGAATC CAAGGTGTAG GGCCCGGCGC GGGGCGCGGA CTCCGGGCAC GGCTTCCCAG  1560
GGGAACGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAACTCGA AGCCCACAAT  1620
CCTCGTCTGA ATCATCCGAG GCAAAGAGAA AAGCCACGGA CCGTTGCACA AAAAGGAAAG  1680
TTTGGGAAGG GATGGGAGAG TGGCTTGCTG ATGTTCCTTG TTG
```

A167 Protein sequence

Gene name:	Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
Unigene number:	Hs.37744
Protein Accession #:	AA011176
Signal sequence:	none found
Transmembrane domains:	62-84, 95-117, 135-157, 177-198, 226-248
Pfam domian:	7tm_1 [75-377]
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGAGVLVLGA SEPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQWTAG    60
MGLLMALIVL LIVAGNVLVI VAIAKTPRLQ TLTNLFIMSL ASADLVMGLL VVPFGATIVV   120
```

```
WGRWEYGSFF CELWTSVDVL CVTASIETLC VIALDRYLAI TSPFRYQSLL TRARARGLVC   180
TVWAISALVS FLPILMHWWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM   240
AFVYLRVFRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAATAP   300
LANGRAGKRR PSRLVALREQ KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVPDRLFV   360
FFNWLGYANS AFNPIIYCRS PDFRKAFQGL LCCARRAARR RHATHGDRPR ASGCLARPGP   420
PPSPGAASDD DDDDVVGATP PARLLEPWAG CNGGAAADSD SSLDEPCRPG FASESKV
```

A168 DNA sequence

Gene name: CEGP1
Unigene number: Hs.222399
Probeset Accession #: AA256485
Nucleic Acid Accession #: AJ400877
Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCGTCCGCG CACACCTCCC CGCGCCGCCG CCGCCACCGC CCGCACTCCG CCGCCTCTGC    60
CCGCAACCGC TGAGCCATCC ATGGGGGTCG CGGGCCGCAA CCGTCCCGGG GCGGCCTGGG   120
CGGTGCTGCT GCTGCTGCTG CTGCTGCCGC CACTGCTGCT GCTGGCGGGG GCCGTCCCGC   180
CGGGTCGGGG CCGTGCCGCG GGGCCGCAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG   240
ATGACTGCCA TGCCGACGCC CTGTGTCAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA   300
AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC   360
TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT   420
TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG   480
AGAACAATGG CGGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGCTGCT   540
GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG   600
GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCCAAGGG   660
GCAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA   720
TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG   780
GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG   840
AGCGAGAGGA CACTGTCCTG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG   900
ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG   960
ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCCTGTT GGATTCACTC  1020
TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT  1080
GTGATCATTT CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAAGGATTTA  1140
AATTATTAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT  1200
GTGACCACAG CTGCATCAAC CACCCTGGCA CATTTGCTTG TGCTTGCAAC CGAGGGTACA  1260
CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT  1320
GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA  1380
AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT  1440
CACCCCGTGT GTCCCTGCAC TGCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT  1500
GTCACTCTGG CATTCACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA  1560
AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTTCCCGAG GGTCTGCGAC  1620
CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT  1680
GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT  1740
TTATCACTGT TGAGTTTGAG CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTTGTGACC  1800
TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA  1860
AGGCCGTCCA CAGGGAGCAG TTTCACCTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA  1920
AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCTG TGGAGTGGGC CAGGGTCATG  1980
CAGAAAACCA ATGTGTCAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT  2040
GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT  2100
GCCCAAGACC AGGAAATTCT GGGGCCCTGA AGACCCCAGA AGCTTGGAAT ATGTCTGAAT  2160
GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGCACCT TGCCAGCTCT  2220
GTGCCCTGGG CACGTTCCAG CCTGAAGCTG GTCGAACTTC CTGCTTCCCC TGTGGAGGAG  2280
GCCTTGCCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT  2340
GTTCACCTGG ACATTTCTAC AACACCACCA CTCACCGATG TATTCGTTGC CCAGTGGGAA  2400
CATACCAGCC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG  2460
ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG  2520
GAGATTTCAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG  2580
AGTGTACGTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATCGTG GTCCCTGAGA  2640
TCTTCCTGCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT  2700
CCAATTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT  2760
CCAGGTCAAA GAAGCTGTGG ATTCAGTTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT  2820
TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCAGGA ACTCATTGAA GACATAGTTC  2880
GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAAACTTA  2940
TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCCAGG  3000
AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT  3060
TTTTGAGACC TTACAAATGA CTCAGCCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG  3120
GGTTGGTGGG ACAGAGCTGT CTTCCTTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCCTC  3180
CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGGTAAATT  3240
GAACTTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT  3300
CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGGACT  3360
TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCCTCC TCAAGGAGTC  3420
TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACTTCAGC TTCCTCTAGC  3480
CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG  3540
CAAGAGGGGA GGGAAGGAGA CCCCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG  3600
ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACTTG  3660
AGTTCTAAGC AGTGCTCGTG AAAAAAAAAA GCAGAAAGAA TTAGAAATAA ATAAAAACTA  3720
AGCACTTCTG GAGACAT
```

A169 Protein sequence

Gene name: CEGP1
Unigene number: Hs.222399

WO03042661 [file:///E:/WO03042661.pcp] Page 913 of 1385

Probeset Accession #: AA256485
Protein Accession #: CAB92285
Signal sequence: 1-31
Transmembrane domains: none
PFAM domains: EGF-like_domains [49-84,132-167,177-213,286-321,407-442] CUB_domain [809-918]
Cellular Localization: may be secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MGVAGRNRPG AAWAVLLLLL LLPPLLLLAG AVPPGRGRAA GPQEDVDECA QGLDDCHADA    60
LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNYR CTCFDGFMLA   120
HDGHNCLDVD ECLENNGGCQ HTCVNVMGSY ECCCKEGFFL SDNQHTCIHR SEEGLSCMNK   180
DHGCSHICKE APRGSVACEC RPGFELAKNQ RDCILTCNHG NGGCQHSCDD TADGPECSCH   240
PQYKMHTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCDRTCKDT   300
STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK   360
SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQQVCVN   420
TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL   480
SSDVTTIRTS VTFKLNEGKC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGKQV   540
PGAPGRPSTP KEMFITVEPE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ   600
FHLQLSGMNL DVAKKPPRTS ERQAESCGVG QGHAENQCVS CRAGTYYDGA RERCILCPNG   660
TFQNEEGQMT CEPCPRPGNS GALKTPEAWN MSECGGLCQP GEYSADGFAP CQLCALGTFQ   720
PEAGRTSCPP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYQPEFG   780
KNNCVSCPGN TTTDFDGSTN ITQCKNRRCG GELGDFTGYI ESPNYPGNYP ANTECTWTIN   840
PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSSNSVTTY ETCQTYERPI AFTSRSKKLW   900
IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLIKALFDV   960
LAHPQNYFKY TAQESREMFP RSFIRLLRSK VSRFLRPYK
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A170 DNA sequence

Gene name: DEME-6 protein (KIAA0452)
Unigene number: Hs.125783
Probeset Accession #: AL039402
Nucleic Acid Accession #: AF007170
Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

```
1          11         21         31         41         51
|          |          |          |          |          |
AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC    60
CTGGACCAGT GCATGACCGC CCTGGACCTC TTCCTCACCA ACCAGTTCTC AGAAGCACTC   120
AGCTACCTCA AGCCCAGAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC   180
CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG   240
ATGAAGGAGG CACAGATGCT GTGTCAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC   300
TTCAGCAGCC TGGTGAACCG CCCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCACGCT   360
GAGGTCTGCT ATGCAGAGTG CCTGCTGCAG CGAGCAGCCC TGACCTTCCT GCAGGACGAG   420
AACATGGTGA GCTTCATCAA AGGCGGCATC AAAGTTCGAA ACAGCTACCA GACCTACAAG   480
GAGCTGGACA GCCTTGTTCA GTCCTCACAA TACTGCAAGG GTGAGAACCA CCCGCACTTT   540
GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCCTACT   600
AGGATCCTGA GGCTGTTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG   660
CAGCTGGAGG AGGGAGCGTC AGGGCACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCCTG   720
CTGTGCTACC ACACCTTCCT CACCTTCGTG CTCGGTACTG GGAACGTCAA CATCGAGGAG   780
GCCGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCCTA AGGGTGCCAT CTTCCTGTTC   840
TTTGCAGGGA GGATTGAAGT CATTAAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG   900
GAGTGCTGTG AGGCCCAGCA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG   960
ATGTGGTGCT TCACCTACAA GGGCCAGTGG AAGATGTCCT ACTTCTACGC CGACCTGCTC  1020
AGCAAGGAGA ACTGCTGGTC CAAGGCCACC TACATTTACA TGAAGGCCGC CTACCTCAGC  1080
ATGTTTGGGA AGGAGGACCA CAAGCCGTTC GGGGACGACG AAGTGGAATT ATTTCGAGCT  1140
GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC  1200
CGGAAGTCCC GGCGCTACTT CTCCTCCAAC CCTATCTCGC TGCCAGTGCC TGCTCTGGAA  1260
ATGATGTACA TCTGGAACGG CTACGCCCTG ATTGGGAAGC AGCCGAAACT CACGGATGGG  1320
ATACTTGAGA TTATCACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCCAGA GAACGAGTAC  1380
TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC  1440
CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA  1500
TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCCTGCTGCT TATGGAGCAA  1560
GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAAACTA CAAGAATTAC  1620
TCCATGGAGT CAAGGACACA CTTTCGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC  1680
CTAGAGAACA GCAGCAGATC CATGGTCTCA TCAGTGTCCT TGTAGCTTTG TGCAGCAGTT  1740
CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCCT  1800
CCCCCTGCCC TGCCCTGCCT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG  1860
TGTATCCGTG CAGAAGCCGA GCTGGCATTT TCACCAGTGT AGCCAAGGGC CTTTGCCAAG  1920
GGCAGAGCAG GTGGAGCCCT CTGCCTGCCC TATCACACAT ACGGGTACTT GCTTTTCACT  1980
GTGATGTTTA AGAGAATGTA TGAACAGTTT ACATTTTCCT TAGAAATACA TTGATGGGAT  2040
CACAGTTGGC TTTAAAAACC AACAACAATC AACCACCTGT AAGTCTTTGT CTTCACCTAT  2100
TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAATTG CTTTTCAAAT  2160
TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCTTCAGA GGACCTGAGG AATGCCTGGG  2220
AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTTGGGC ATGAGGATGT ACACAGACAC  2280
CCACTACCTT ACTACTCACA CTTCATTTCA CTCCTTTTGT AAATTTCCAA TTTAAAAATC  2340
AAGCACGTCT TTTTAGTGAG ATAAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC  2400
AGTAGAAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG  2460
AAATTTGGGG GGCAGGAGGA GGTTCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA  2520
CTGAAACCAC TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTCCAAGGTA  2580
CATTTGCTTA CTGACAGCAT TTTTGTTAAA ACTGTTATTC TTGAAAAAAA AAAAAAAAAA  2640
AA
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A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)
Unigene number: Hs.125783
Probeset Accession #: AL039402
Protein Accession #: AAC39582
Signal sequence: none
Transmembrane domains: 210-226
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MTALDLFLTN QFSEALSYLK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMMKEA    60
QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAEVCY AECLLQRAAL TFLQDENMVS   120
FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSMLPTRILR   180
LLEFVGFSGN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFVLGTG NVNIEEAEKL   240
LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEECCE AQQHWKQFHH MCYWELMWCF   300
TYKGQWKMSY FYADLLSKEN CWSKATYIYM KAAYLSMFGK EDHKPFGDDE VELFRAVPGL   360
KLKIAGKSLP TEKFAIRKSR RYFSSNPISL PVPALEMMYI WNGYAVIGKQ PKLTDGILEI   420
ITKAEEMLEK GPENEYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY   480
LIPNALLELA LLLMEQDRNE EAIKLLESAK QNYKNYSMES RTHFRIQAAT LQAKSSLENS   540
SRSMVSSVSL
```

A172 DNA sequence
Gene name: EST
Unigene number: Hs.200102
Probeset Accession #: AL117406
Nucleic Acid Accession #: none found
Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
ATGACTAGGA AGAGGACATA CTGGGTGCCC AACTCTTCTG GTGGCCTCGT GAATCGTGGC    60
ATCGACATAG GCGATGACAT GGTTTCAGGA CTTATTTATA AAACCTATAC TCTCCAAGAT   120
GGCCCCTGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCCACCG   180
TGGGGGAAGT ATGATGCTGC CTTGAGAACC ATGATTCCCT TCCGTCCCAA GCCGAGGTTT   240
CCTGCCCCCC AGCCCCTGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC   300
ACCCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCCTCCACTG   360
TCAGTCCATG ATGCCTCAGA CAAAAATGTC CAAAGGCTTC ACCGCCTTTG GGAAGAAGAA   420
GTCTCAAGGC GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA   480
ACAAGGTTGA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG   540
CCAATATTGA TTATACCAAA GATCCTGGAA TATTCAGAAG AGCAGTTGGG GAATGTTGTC   600
CATGGAGTGG GACTCTGCTT TGCCCTTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC   660
TCCTCCAGTT GGATCATCAA CCAACGCACA GCCATCAGGT TCCGAGCAGC TGTTTCCTCC   720
TTTGCCTTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC   780
ATCAGCTTCT TCACCGGTGA TGTAAACTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA   840
GTACTGATCA CCTGCGCATC GCTGGTCATC TGCAGCATTT CTTCCTACTT CATTATTGGA   900
TACACTGCAT TTATTGCCAT CTTATGCTAT CTCCTGGTTT TCCCACTGGC GGTATTCATG   960
ACAAGAATGG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT  1020
GTGACCAGTG AAGTTCTCAC TTGCATTAAG CTGATTAAAA TGTACACATG GGAGAAACCA  1080
TTTGCAAAAA TCATTGAAGG TATGGAAAGT CTGACTTTCT GCTCCAAACC TGGTGATGGC  1140
ATGGCCTTCA GCATGCTGGC CTCCTTGAAT CTCCTTCGGC TGTCAGTGTT CTTTGTGCCT  1200
ATTGCAGTCA AAGGTCTCAC GAATTCCAAG TCTGCAGTGA TGAGGTTCAA GAAGTTTTTC  1260
CTCCAGGAGA GCCCTGTTTT CTATGTCCAG ACATTACAAG ACCCCAGCAA AGCTCTGGTC  1320
TTTGAGGAGG CCACCTTGTC ATGGCAACAG ACCTGTCCCG GGATCGTCAA TGGGGCACTG  1380
GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCCTAGAGA TGCCCTCGGG  1440
CCAGAGGAAG AAGGGAACAG CCTGGGCCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC  1500
AAGGGGATGA TGTTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAGAGCAG CCTGTTGTCA  1560
GCCATCCTGG AGGAGATGCA CTTGCTCGAG GGCTCGGTGG GGGTGCAGGG AAGCCTGGCC  1620
TATGTCCCCC AGCAGGCCTG GATCGTCAGC GGGAACATCA GGGAGAACAT CCTCATGGGA  1680
GGCGCATATG ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC  1740
CTGGAACTTC TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCCT CAACCTCTCT  1800
GGGGGGCAGA AACAGAGGAT CAGCCTGGCC CGCGCCGTCT ATTCCGACCG TCAGATCTAC  1860
CTGCTGGACG ACCCCCTGTC TGCTGTGGAC GCCCACGTGG GGAAGCACAT TTTTGAGGAG  1920
TGCATTAAGA AGACACTCAG GGGGAAGACG GTCGTCCTGG TGACCCACCA GCTGCAGTAC  1980
TTAGAATTTT GTGGCCAGAT CATTTTGTTG GAAAATGGGA AAATCTGTGA AAATGGAACT  2040
CACAGTGAGT TAATGCAGAA AAAGGGGAAA TATGCCCAAC TTATCCAGAA GATGCACAAG  2100
GAAGCCACTT CGGACATGTT GCAGGACACA GCAAAGATAG CAGAGAAGCC AAAGGTAGAA  2160
AGTCAGGCTC TGGCCACCTC CCTGGAAGAG TCTCTCAACG GAAATGCTGT GCCGGAGCAT  2220
CAGCTCACAC AGGAGGAGGA GATGGAAGAA GGCTCCTTGA GTTGGAGGGT CTACCACCAC  2280
TACATCCAGG CAGCTGGAGG TTACATGGTC TCTTGCATAA TTTTCTTCTT CGTGGTGCTG  2340
ATCGTCTTCT TAACGATCTT CAGCTTCTGG TGGCTGAGCT ACTGGTTGGA GCAGGGCTCG  2400
GGGACCAATA GCAGCCGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTGCAGAC  2460
AATCCTCAAC TGTCCTTCTA CCAGCTGGTG TACGGGCTCA ACGCCCTGCT CCTCATCTGT  2520
GTGGGGGTCT GCTCCTCAGG GATTTTCACC AAAGTCACGA GGAAGGCATC CACGGCCCTG  2580
CACAACAAGC TCTTCAACAA GGTTTTCCGC TGCCCCATGA GTTTCTTTGA CACCATCCCA  2640
ATAGGCCGGC TTTTGAACTG CTTCGCAGGG GACTTGGAAC AGCTGGACCA GCTCTTGCCC  2700
ATCTTTTCAG AGCAGTTCCT GGTCCTGTCC TTAATGGTGA TCGCCGTCCT GTTGATTGTC  2760
AGTGTGCTGT CTCCATATAT CCTGTTAATG GGAGCCATAA TCATGGTTAT TTGCTTCATT  2820
TATTATATGA TGTTCAAGAA GGCCATCGGT GTGTTCAAGA GACTGGAGAA CTATAGCCGG  2880
TCTCCTTTAT TCTCCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGTCTAT  2940
GGAAAAACTG AAGACTTCAT CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC  3000
CTGCTGTTGT TTCTATCTTC CACACGATGG ATGGCATTGA GGCTGGAGAT CATGACCAAC  3060
CTTGTGACCT TGGCTGTTGC CCTGTTCGTG GCTTTTGGCA TTTCCTCCAC CCCCTACTCC  3120
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TTTAAAGTCA TGGCTGTCAA CATCGTGCTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC  3180
CGGATTGGCT TGGAGACAGA GGCACAGTTC ACGGCTGTAG AGAGGATACT GCAGTACATG  3240
AAGATGTGTG TCTCGGAAGC TCCTTTACAC ATGGAAGGCA CAAGTTGTCC CCAGGGGTGG  3300
CCACAGCATG GGGAAATCAT ATTTCAGGAT TATCACATGA AATACAGAGA CAACACACCC  3360
ACCGTGCTTC ACGGCATCAA CCTGACCATC CGCGGCCACG AAGTGGTGGG CATCGTGGGA  3420
AGGACGGGCT CTGGGAAGTC CTCCTTGGGC ATGGCTCTCT TCCGCCTGGT GGAGCCCATG  3480
GCAGGCCGGA TTCTCATTGA CGGCGTGGAC ATTTGCAGCA TCGGCCTGGA GGACTTGCGG  3540
TCCAAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC  3600
CTAGATCCCT TTGACCGTCA CACTGACCAG CAGATCTGGG ATGCCTTGGA GAGGACATTC  3660
CTGACCAAGG CCATCTCAAA GTTCCCCAAA AAGCTGCATA CAGATGTGGT GGAAAACGGT  3720
GGAAACTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGGCTGT GCTTCGCAAC  3780
TCCAAGATCA TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCCTG  3840
ATCCAGCGCA CAATCCGTGA AGCCTTCCAG GGCTGCACCG TGCTCGTCAT TGCCCACCGT  3900
GTCACCACTG TGCTGAACTG TGACCACATC CTGGTTATGG GCAATGGGAA GGTGGTAGAA  3960
TTTGATCGGC CGGAGGTACT GCGGAAGAAG CCTGGGTCAT TGTTCGCAGC CCTCATGGCC  4020
ACAGCCACTT CTTCACTGAG ATAAGGAGAT GTGGAGACTT CATGGAGGCT GGCAGCTGAG  4080
CTCAGAGGTT CACACAGGTG CAGCTTCGAG GCCCACAGTC TGCGACCTTC TTGTTTGGAG  4140
ATGAGAACTT CTCCTGGAAG CAGGGGTAAA TGTAGGGGGG GTGGGGATTG CTGGATGGAA  4200
ACCCTGGAAT AGGCTACTTG ATGGCTCTCA AGACCTTAGA ACCCCAGAAC CATCTAAGAC  4260
ATGGGATTCA GTGATCATGT GGTTCTCCTT TTAACTTACA TGCTGAATAA TTTTATAATA  4320
AGGTAAAAGC TTATAGTTTT CTGATCTGTG TTAGAAGTGY TGCAAATGCT GTACTGACTT  4380
TGTAAAATAT AAAACTAAGG AAAACTCAAA AAAAAAAAAA AAAAAAA
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A173 Protein sequence

Gene name: EST
Unigene number: Hs.200102
Probeset Accession #: AL117406
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943,1018-1034
PFAM domains: ABC_transporter [502-673], ABC_membrane_region [163-432, 771-1060] ATP-binding_domains [508-516, 1139-1147]
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MTRKRTYWVP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQERNP EAPGRAAVPP    60
WGKYDAALRT MIPFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLDENTIPPL   120
SVHDASDKNV QRLHRLWEBE VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFCIASVLG   180
PILIIPKILE YSEEQLGNVV HGVGLCFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS   240
FAFEKLIQFK SVIHITSGEA ISFFTGDVNY LFEGVCYGPL VLITCASLVI CSISSYFIIG   300
YTAFIAILCY LLVFPLAVFM TRMAVKAQHH TSEVSDQRIR VTSEVLTCIK LIKMYTWEKP   360
FAKIIEGMES LTFCSKPGDG MAFSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRFKKFF   420
LQESPVFYVQ TLQDPSKALV FEEATLSWQQ TCPGIVNGAL ELERNGHASE GMTRPRDALG   480
PEEEGNSLGP ELHKINLVVS KGMMLGVCGN TGSGKSSLLS AILEEMHLLE GSVGVQGSLA   540
YVPQQAWIVS GNIRENILMG GAYDKARYLQ VLHCCSLNRD LELLPFGDMT EIGERGLNLS   600
GGQKQRISLA RAVYSDRQIY LLDDPLSAVD AHVGKHIFEE CIKKTLRGKT VVLVTHQLQY   660
LEFCGQIILL ENGKICENGT HSELMQKKGK YAQLIQKMHK EATSDMLQDT AKIAEKPKVE   720
SQALATSLEE SLNGNAVPEH QLTQEEEMEE GSLSWRVYHH YIQAAGGYMV SCIIFFFVVL   780
IVFLTIFSFW WLSYWLEQGS GTNSSRESNG TMADLGNIAD NPQLSFYQLV YGLNALLLIC   840
VGVCSSGIFT KVTRKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLLP   900
IFSEQFLVLS LMVIAVLLIV SVLSPYILLM GAIIMVICFI YYMMFKKAIG VFKRLENYSR   960
SPLFSHILNS LQGLSSIHVY GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALRLEIMTN  1020
LVTLAVALFV AFGISSTPYS FKVMAVNIVL QLASSFQATA RIGLETEAQF TAVERILQYM  1080
KMCVSEAPLH MEGTSCPQGW PQHGEIIFQD YHMKYRDNTP TVLHGINLTI RGHEVVGIVG  1140
RTGSGKSSLG MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRFN  1200
LDPFDRHTDQ QIWDALERTF LTKAISKFPK KLHTDVVENG GNFSVGERQL LCIARAVLRN  1260
SKIILIDEAT ASIDMETDTL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNGKVVE  1320
FDRPEVLRKK PGSLFAALMA TATSSLR
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A174 DNA sequence

Gene name: ESTs
Unigene number: Hs.128899
Probeset Accession #: AA983251
Nucleic Acid Accession #: AA983251
Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

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ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA    60
GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC   120
GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC   180
GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG   240
CCGCGGCCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCCT   300
CGCCTGCGTC CTGGACGTTC CCGGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT   360
TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCCATC AGCGAGTGCA   420
ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA   480
GCTCCTGGAC CTAGGGCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC   540
CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCC GGGGGTCGCC GGGGCCACGA   600
CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCCAG GGTGGTGCCA   660
TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCCTGGAA CGCCGCTTCG CTCCTGCAGC   720
TGCTGCTGGC TGCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC   780
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TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC   840
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG   900
GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC   960
CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA  1020
GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC  1080
TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC  1140
CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCCTCTCCCC TGCAGCGGCC CGCCTTGCCC  1200
ATCTACGTGC CGTTCCTCAT TGTTGGCTCC GTGTTTGTCG CCTTTATCAT CTTGGGGTCC  1260
CTGGTGGCAG CCTGTTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA  1320
GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC  1380
CGGGGGTCGT CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC  1440
GGGGCCCGGG CGCCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG  1500
AACAACGTGT ATGTCAACAT GCCCACGAAT TTCTCTGTGC TGAACTGTCA GCAGGCCACC  1560
CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG  1620
CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCCTGCA GCCTGGCTAC  1680
AGGCAGATTC AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG  1740
ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG  1800
GATTCTCGAG GTGGAAGTCC GCACATGTCG GTGGTATTTA TGGCACGATT CCTTTGGATG  1860
GCTTCATTTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT  1920
CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCCTC AGCTGGAGAT GACTGTGATG  1980
TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA  2040
AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT  2100
TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTTATCTCC CTTTTACTGG GACTTTTTTT  2160
TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGCAG  2220
TGGTGCGATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC  2280
AGCCTCCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT  2340
TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA  2400
TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCCAGCC  2460
TGAGCCTTTT TTTTTTTCTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT  2520
ATTCTAAAAG GAAACCTGTT TGAACTCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA  2580
GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG  2640
GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA  2700
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TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAAACCATT CATCCCCTTC  2820
TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTTT  2880
TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG  2940
TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT  3000
GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA  3060
AAAAATTTTC TTGTCTTAGT TATAAAAATT CAAAGAAATG TGTTACAAAG ATACTTAGTA  3120
TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTTACTTT  3180
GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG  3240
GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCCAC ACTGTTCTTG  3300
ATTTCCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT  3360
CAAATTCAAG TGAATTTATT TGTGTGTTCT TTACTTATAT AAAAAAAGAT AACTTTAAGG  3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT  3480
GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATTC  3540
TGTTTCATGA CTGAATAATG TAAAACCAGT GTTGGCAATT GGTATCATCA ATGATACTCA  3600
TTTTTTAATA ACCAAAGGCA GGGGAAAATC ATTTTACTTA TTAATAAATA TTTTATGATG  3660
TGAAAAAAAA AAAAAAAAAA AAAAAAAAAA
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A175 Protein sequence

Gene name:	ESTs
Unigene number:	Hs.128899
Protein Accession #:	none found
Signal sequence:	1-11
Transmembrane domains:	402-424
Cellular Localization:	not determined

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1          11         21         31         41         51
|          |          |          |          |          |
MLSGFLMSPS TQHRAQYTPG GKKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA    60
GEAEKGNRGE PPAWIRAQQQ PRPPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA   120
SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG   180
PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAPRVVP CGALAARPSP HPGTPLRSCS   240
CCWLRCWRRG RGPSGEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE   300
ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPPPV RAWQRCSPEG   360
SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPFLIVGS VFVAFIILGS   420
LVAACCCRCL RPKQDPQQSR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS   480
GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGQYL HPPYVGYTVQ   540
HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQKMYPAV TV
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A176 DNA SEQUENCE

Gene name:	ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
Unigene number:	Hs.19322
Probeset Accession #:	AA088458
Nucleic Acid Accession #:	AA088458
Coding sequence:	862-1995 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA    60
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CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG   120
GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC   180
CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG   240
CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC   300
TGTGCCAGCC GGGCCCTGCC CCCGTCCTCC TCCGGGCCCC CCTGCCCTGC CCTGACGTCC   360
ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC   420
CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG   480
GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG   540
GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC   600
AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCCTCTC TGGCTGGAGA CCCCCGGCAG   660
GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCCGCCC TTGCCAGATG GGCTCCCCAG   720
GCCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG   780
ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCAG CTACTACTGG CCGCTGTCAG   840
TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCCG TTTCCAGCGG TGCCGCCCTG   900
GGTCCCATCT TCAGGGAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC   960
AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC  1020
CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT  1080
GTAAGCGGGG GGTGCCTGCC TGGCTGGGGA GCCCCAGGGA TAGCGGTCGG ACTTCAGGTT  1140
CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT  1200
GGCCTGCATG TGCCTCCCAC AGACCCTGGG GTGATGGCCT TCCCCCTCTT GGCCGGGACG  1260
TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA  1320
GACAGCTCCC AGGCACGTCA TAGGCAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC  1380
CTGGGGTCCT GCTCACCCCC CTTTGCTCTC ACGCCCAGCC TGTCCCCAGG TTTCAGCTGG  1440
GAGAGGCCAC CTCCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG  1500
GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT  1560
GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTCACCA  1620
GAACCAGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG  1680
TCAGTGTGTG TGGGGCGCAG GGCCTCCGAT GCGGGGTCAG TGCGTGGGGG GCGCAGGGCC  1740
CCCGATGCGG GGTCAGTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT  1800
ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC  1860
CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC  1920
TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT  1980
GCCCTCCTAC CCTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG  2040
ACCTCCTGGG CAGGAAAGGG TGCAGGTCCT GAGGGCCTGT GCCCCACAGC CCCAGCACCC  2100
AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCCGTCAGCA  2160
GGCTGGGGTC TGCCCACCAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC  2220
TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG  2280
GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT  2340
GAGACAGGCT GGCACCTCCG GAAAAACTGC CTTTCAGCCT TGGTGTTCCG TGCAAGGTGA  2400
AAAGAAATAG GTCCTCCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC  2460
CACGAGGGGA GAATTTAAAG GCCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT  2520
GCAGACCCTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT  2580
GAGCAGCGTC CCTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT  2640
GCGTGCACAC TGTGATGACA CCCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG  2700
CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA  2760
TTTTGTGTTG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTCACGC  2820
CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA  2880
CCCCATCTCT ACAARAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT  2940
TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC  3000
TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA  3060
AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA
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A177 DNA SEQUENCE

Gene name:	Cadherin 3, P-cadherin (placental)
Unigene number:	Hs.2877
Probeset Accession #:	X63629
Nucleic Acid Accession #:	X63629
Coding sequence:	54-2543 (start and stop codons are underlined)

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1          11         21         31         41         51
|          |          |          |          |          |
GCGGAACACC GGCCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC    60
TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCGCGG   120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG   180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC   240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG   300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC   360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC   420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT   480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG   540
AGACAGGCTG GTTGTTGTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC   600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA   660
TCATCGTGAC CGACCAGAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA   720
GTGTCTTAGA GGGAGTCCTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG   780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA   840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT   900
CCAGTGGCCT GGACCGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA   960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG  1020
ACAATGCTCC CATGTTTGAC CCCCAGAAGT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG  1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC  1140
GTGCCACCTA CCTTATCATG GGCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC  1200
CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC  1260
AGCACACCCT GTACGTTGAA GTGACCAACG AGGCCCCTTT TGTGCTGAAG CTCCCAACCT  1320
CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAC  1380
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CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA  1440
CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG  1500
CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC  1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA  1620
ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG  1680
ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC  1740
ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCTTTC CAGGCCCAGC  1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG  1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG  1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC  1980
ATGTCGAAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG  2040
TCCTGGCTCT GCTGTTCCTC CTGCTGGTGC TGCTTTTGTT GGTGAGAAAG AAGCGGAAGA  2100
TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG  2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG  2220
AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA  2280
TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA  2340
AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG  2400
AGGGCAGCGG CTCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCCTCCGCC TCCGACCAAG  2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT  2520
ACGGTGGCGG GGAGGACGAC TAGGCGGCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC  2580
CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA  2640
GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT  2700
TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC  2760
CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCCAGAA GCCTCTTACC TGCCGTAAAA  2820
TGCTCAACCC TGTGTCCTGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT  2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT  2940
TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG  3000
TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT  3060
ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTTGCGT TGCTATAGAT  3120
GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTTT TATTAAAGAA A
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A178 Protein sequence:

Gene name:	Cadherin 3, P-cadherin (placental)
Unigene number:	Hs.2877
Probeset Accession #:	X63629
Protein Accession #:	CAA45177
Signal sequence:	1-24
Transmembrane domain:	659-675
Cellular localization:	plasma membrane

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|          |          |          |          |          |
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QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG   120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK   180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT   240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA   300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP   360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL   420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR   480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID   540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD   600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL   660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR   720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF   780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD
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A179 DNA SEQUENCE

Gene name:	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number:	Hs.258583
Probeset Accession #:	NM_012152
Nucleic Acid Accession #:	NM_012152
Coding sequence:	43-1104 (underlined sequences correspond to start and stop codons)

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CTTCTTTAAA TTTCTTTCTA GGATGTTCAC TTCTTCTCCA CAATGAATGA GTGTCACTAT    60
GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTCGA TGACTGGACA   120
GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT   180
TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC   240
TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCCTG   300
ATGTTTAACA CAGGCCCAGT TTCAAAAACT TTGACTGTCA ACCGCTGGTT TCTCCGTCAG   360
GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG   420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA   480
CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTTATGG GGGCGGTCCC CACACTGGGC   540
TGGAATTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCCATTTA CAGCAGGAGT   600
TACCTTGTTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC   660
CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG   720
TCCATCAGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG   780
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GCGTTTGTGG TATGCTGGAC CCCGGGCCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC   840
AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC   900
GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG   960
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGCCGTC CCTCTCGCAT CCCCTCCACA  1020
GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA  1080
GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCCACCCA GGTGATGACT  1140
GTCTTAGG
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A180 Protein sequence:

Gene name:	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number:	Hs.258583
Probeset Accession #:	NM_012152
Protein Accession #:	NP_036284
Signal sequence:	none found
Transmembrane domains:	31-53, 66-88, 150-172, 190-211, 239-261, 277-295
Cellular Localization:	plasma membrane

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|          |          |          |          |          |
MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNSL VIAAVIKNRK    60
FHFPFYYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL   120
LVIAVERHMS IMRMRVHSNL TKKRVTLLIL LVWAIAIFMG AVPTLGWNCL CNISACSSLA   180
PIYSRSYLVF WTVSNLMAFL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT   240
VMTVLGAFVV CWTPGLVVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVNP IIYSYKDEDM   300
YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS
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A181 DNA SEQUENCE

Gene name:	ESTs
Unigene number:	Hs.162859
Probeset Accession #:	AA569531
Nucleic Acid Accession #:	AA569531
Coding sequence:	1-504 (underlined sequences correspond to start and stop codons)

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CATTCTGAAG CCAACAGGAG AACCAAGACC AAAACTTTAT TGTCTCTGCT TTCATTTCTT   120
GATGAAACCT CTGGACTAAG CACACATCTT CCTTGTTTAT CTCTCTCAAA GGAGTGTGGA   180
GTGCTTCATC TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC   240
CAGCTATACC TGTGGGACAT GGGTGGTTTT ACAATATTTA AGAACCTGTG GATGAGCCTC   300
ATACCCAGAG GGAACAAACG CTCCCCAAAA AGAGTTACAG AAACCATCCT GAGAGATTTT   360
AAGCAGAAGC AAAGTTCAAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC   420
CTCTCTTCAT TCTGGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTTGGGCA   480
GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTTCTTCA   540
GCTACGTTGT CCCAGCACTT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC   600
AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTATC TACTGAGCTG CTACCATATC   660
CCAGCTACTC CTTGCATGTT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT   720
TATGTAATAT CACAGACAAG GAAACTGAAC GCAGAAATGT TTTATTTCTT GCCAAACATC   780
ACATGAGGAT GAACAATGAA ACCGATTTGA AACCAGGATT GTCTGATTCC AACATCTCTG   840
GGTCCTTTTT CACTCTGATA TGCTGCAATT AAAAAGCCAT TTCTAAGACT GT
```

A182 Protein sequence:

Gene name:	ESTs
Unigene number:	Hs.162859
Probeset Accession #:	AA569531
Protein Accession #:	none found
Signal sequence:	1-46
Transmembrane domains:	none found
Cellular Localization:	not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MTYSYSFFRP ELIVNHLNYV HSEANRRTKT KTLLSLLSFL DETSGLSTHL PCLSLSKECG    60
VLHLDIHGKK EDMRITQQSS QLYLWDMGGF TIFKNLWMSL IPRGNKRSPK RVTETILRDF   120
KQKQSSKIQE ERRRESAGPN LSSFWFVGNA GRGDRPQIWA GSKQFSG
```

A183 DNA SEQUENCE

Gene name:	ESTs
Unigene number:	Hs.179809
Probeset Accession #:	N95796
Nucleic Acid Accession #:	XM_050197
Coding sequence:	310-1971 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCCGGGTGAC    60
AGCCGCGCGC CTCGGCCAGG ATCTGAGTGA TGAGACGTGT CCCCACTGAG GTGCCCCACA   120
GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAAGGGCT GGCAGAAATG   180
GGCGCCTGGC TGATTCCTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCCG CAGCTTCTGG   240
AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCCTGAGC CCTACCCGCC   300
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TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCGCCTGC TGCGGCACCG GAAAGCCCAG   360
CTCTTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCGC AGGCATCACC   420
TATGTGCCGC CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTCATGAC CATGGTGCTG   480
GGCATTGGTC CAGTGCTGGG CCTGGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACCAC   540
TGGCGTGGAC GCTATGGCCG CCGCCGGCCC TTCATCTGGG CACTGTCCTT GGGCATCCTG   600
CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGCTGTG CCCGGATCCC   660
AGGCCCCTGG AGCTGGCACT GCTCATCCTG GGCGTGGGGC TGCTGGACTT CTGTGGCCAG   720
GTGTGCTTCA CTCCACTGGA GGCCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT   780
CGCCAGGCCT ACTCTGTCTA TGCCTTCATG ATCAGTCTTG GGGGCTGCCT GGGCTACCTC   840
CTGCCTGCCA TTGACTGGGA CACCAGTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG   900
TGCCTCTTTG GCCTGCTCAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGCTGGTG   960
GCTGAGGAGG CAGCGCTGGG CCCCACCGAG CCAGCAGAAG GGCTGTCGGC CCCCTCCTTG  1020
TCGCCCCACT GCTGTCCATG CCGGGCCCGC TTGGCTTTCC GGAACCTGGG CGCCCTGCTT  1080
CCCCGGCTGC ACCAGCTGTG CTGCCGCATG CCCCGCACCC TGCGCCGGCT CTTCGTGGCT  1140
GAGCTGTGCA GCTGGATGGC ACTCATGACC TTCACGCTGT TTTACACGGA TTTCGTGGGC  1200
GAGGGGCTGT ACCAGGGCGT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT  1260
GATGAAGGCG TTCGGATGGG CAGCCTGGGG CTGTTCCTGC AGTGCGCCAT CTCCCTGGTC  1320
TTCTCTCTGG TCATGGACCG GCTGGTGCAG CGATTCGGCA CTCGAGCAGT CTATTTGGCC  1380
AGTGTGGCAG CTTTCCCTGT GGCTGCCGGT GCCACATGCC TGTCCCACAG TGTGGCCGTG  1440
GTGACAGCTT CAGCCGCCCT CACCGGGTTC ACCTTCTCAG CCCTGCAGAT CCTGCCCTAC  1500
ACACTGGCCT CCCTCTACCA CCGGGAGAAG CAGGTGTTCC TGCCCAAATA CCGAGGGGAC  1560
ACTGGAGGTG CTAGCAGTGA GGACAGCCTG ATGACCAGCT TCCTGCCAGG CCCTAAGCCT  1620
GGAGCTCCCT TCCCTAATGG ACACGTGGGT GCTGGAGGCA GTGGCCTGCT CCCACCTCCA  1680
CCCGCGCTCT GCGGGGCCTC TGCCTGTGAT GTCTCCGTAC GTGTGGTGGT GGGTGAGCCC  1740
ACCGAGGCCA GGGTGGTTCC GGGCCGGGGC ATCTGCCTGG ACCTCGCCAT CCTGGATAGT  1800
GCCTTCCTGC TGTCCCAGGT GGCCCCATCC CTGTTTATGG GCTCCATTGT CCAGCTCAGC  1860
CAGTCTGTCA CTGCCTATAT GGTGTCTGCC GCAGGCCTGG GTCTGGTCGC CATTTACTTT  1920
GCTACACAGG TAGTATTTGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAAACTTCC  1980
AGCACATTGG GGTGGAGGGC CTGCCTCACT GGGTCCCAGC TCCCCGCTCC TGTTAGCCCC  2040
ATGGGGCTGC CGGGCTGGCC GCCAGTTTCT GTTGCTGCCA AAGTAATGTG GCTCTCTGCT  2100
GCCACCCTGT GCTGCTGAGG TGCGTAGCTG CACAGCTGGG GGCTGGGGCG TCCCTCTCCT  2160
CTCTCCCCAG TCTCTAGGGC TGCCTGACTG GAGGCCTTCC AAGGGGGTTT CAGTCTGGAC  2220
TTATACAGGG AGGCCAGAAG GGCTCCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT  2280
ACCCAGGCTC AGGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTTT  2340
GGGAGCTGAA TAAACTCAGT CACCTGGTTT CCCATCTCTA AGCCCCTTAA CCTGCAGCTT  2400
CGTTTAATGT AGCTCTTGCA TGGGAGTTTC TAGGATGAAA CACTCCTCCA TGGGATTTGA  2460
ACATATGAAA GTTATTTGTA GGGGAAGAGT CCTGAGGGGC AACACACAAG AACCAGGTCC  2520
CCTCAGCCCC ACAGGCACTG GTCTTTTTTG CTNGANTCCA CCCCCCCCCT CTTTACCCTT  2580
TT
```

A184 Protein sequence:

Gene name:	ESTs
Unigene number:	Hs.179809
Probeset Accession #:	N95796
Protein Accession #:	XP_050197
Signal sequence:	none
Transmembrane domains:	21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MVQRLWVSRL LRHRKAQLLL VNLLTFGLEV CLAAGITYVP PLLLEVGVEE KFMTMVLGIG    60
PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL   120
ELALLILGVG LLDFCGQVCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA   180
IDWDTSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH   240
CCPCRARLAF RNLGALLPRL HQLCCRMPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL   300
YQGVPRAEPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG TRAVYLASVA   360
AFPVAAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA SLYHREKQVF LPKYRGDTGG   420
ASSEDSLMTS FLPGPKPGAP FPNGHVGAGG SGLLPPPPAL CGASACDVSV RVVVGEPTEA   480
RVVPGRGICL DLAILDSAFL LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIYFATQ   540
VVFDKSDLAK YSA
```

A185 DNA SEQUENCE

Gene name:	ESTs
Unigene number:	Hs.11260
Probeset Accession #:	R73640
Nucleic Acid Accession #:	AK002126
Coding sequence:	1-1593 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGTTCGCC GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTTGCT GGTGCTCCTC    60
TGCTGTGCTA TCTCTGTCCT GTACATGTTG GCCTGCACCC CAAAAGGTGA CGAGGAGCAG   120
CTGGCACTGC CCAGGGCCAA CAGCCCCACG GGGAAGGAGG GGTACCAGGC CGTCCTTCAG   180
GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC   240
AAGGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT   300
GCTGCTGGCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAAA CCCAGGCCGA CCTCCTGGCC   360
TTCCTGCACT CGCAGGTGGA CAAGGCAGAG GTGAATGCTG GCGTCAAGCT GGCCACAGAG   420
TATGCAGCAG TGCCTTTCGA TAGCTTTACT CTACAGAAGG TGTACCAGCT GGAGACTGGC   480
CTTACCCGCC ACCCCGAGGA GAAGCCTGTG AGGAAGGACA AGCGGGATGA GTTGGTGGAA   540
GCCATTGAAT CAGCCTTGGA GACCCTGAAC AATCCTGCAG AGAACAGCCC CAATCACCGT   600
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CCTTACACGG CCTCTGATTT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA   660
TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACACGAAT TCAAACGGCT CATCTTATTT   720
CGACCATTCG GCCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT   780
ATCAATGTTA TCGTGCCTCT AGCAAAAAGG GTGGACAAGT TCCGGCAGTT CATGCAGAAT   840
TTCAGGGAGA TGTGCATTGA GCAGGATGGG AGAGTCCATC TCACTGTTGT TTACTTTGGG   900
AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTTGAAAACA CTTCCAAAGC TGCCAACTTC   960
AGGAACTTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAGGG ACTTGATGTT  1020
GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTTCTCTTTT TCTGTGATGT GGACATCTAC  1080
TTCACATCTG AATTCCTCAA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT  1140
TATCCAGTTC TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGATGCAGTC  1200
CCTCCCTTGG AACAGCAGCT GGTCATAAAG AAGGAAACTG GATTTTGGAG AGACTTTGGA  1260
TTTGGGATGA CGTGTCAGTA TCGGTCAGAC TTCATCAATA TAGGTGGGTT TGATCTGGAC  1320
ATCAAAGGCT GGGGCGGAGA GGATGTGCAC CTTTATCGCA AGTATCTCCA CAGCAACCTC  1380
ATAGTGGTAC GGACGCCTGT GCGAGGACTC TTCCACCTCT GGCATGAGAA GCGCTGCATG  1440
GACGAGCTGA CCCCCGAGCA GTACAAGATG TGCATGCAGT CCAAGGCCAT GAACGAGGCA  1500
TCCCACGGCC AGCTGGGCAT GCTGGTGTTC AGGCACGAGA TAGAGGCTCA CCTTCGCAAA  1560
CAGAAACAGA AGACAAGTAG CAAAAAAACA TGA
```

A186 Protein sequence:

Gene name: ESTs
Unigene number: Hs.11260
Probeset Accession #: R73640
Protein Accession #: NP_060841
Signal sequence: 1-26
Transmembrane domains: none found
Cellular Localization: not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MVRRGLLAWI SRVVVLLVLL CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ    60
EWEEQHRNYV SSLKRQIAQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTQADLLA   120
FLHSQVDKAE VNAGVKLATE YAAVPFDSFT LQKVYQLETG LTRHPEEKPV RKDKRDELVE   180
AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILF   240
RPFGPIMKVK NEKLNMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG   300
KEEINEVKGI LENTSKAANF RNFTFIQLNG EFSRGKGLDV GARFWKGSNV LLFFCDVDIY   360
FTSEFLNTCR LNTQPGKKVF YPVLFSQYNP GIIYGHHDAV PPLEQQLVIK KETGFWRDFG   420
FGMTCQYRSD FINIGGFDLD IKGWGGEDVH LYRKYLHSNL IVVRTPVRGL FHLWHEKRCM   480
DELTPEQYKM CMQSKAMNEA SHGQLGMLVF RHEIEAHLRK QKQKTSSKKT
```

A187 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Nucleic Acid Accession #: AF189723
Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC    60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC   120
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT   180
TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTTTTA   240
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTACAGTT   300
GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA   360
CCAGAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT   420
CCAGGTGATA CAGTTTGCCT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTT   480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTCT   540
AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT   600
GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCAT TGGAACAGGA   660
GAAAATTCTG AATTTGGGGA GGTTTTTAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC   720
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACTTT CCTTTTACTC CTTTGGTATA   780
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT   840
ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTCACAGTG   900
ACGCTAGCTC TTGGTGTTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT   960
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTCAG ATAAAACTGG AACACTGACG  1020
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT  1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTC  1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT  1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCCT TAATTGCTCT TGCAATGAAG  1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT  1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT  1380
TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA  1440
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC  1500
ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCCTGAACT GGGACAGCTG  1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT  1620
ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTC ACAGGAGACT  1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCCAAAA CTTCCCAGTC AGTCTCAGGA  1740
GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTGCAGTA  1800
TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT  1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC  1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC  1980
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT  2040
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AATAACATTA AAAATTTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACTTTA  2100
ATCTCATTGG CTACATTAAT GAACTTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG  2160
ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA  2220
GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACTTGATA  2280
CTTAAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTTTGT CTTCTGGCGT  2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG  2400
TTTTTTGACA TGTTCAATGC ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT  2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA  2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG  2580
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG  2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT  2700
CTTGAAGTAT GA
```

A188 Protein sequence:

Gene name:	ATPase, Ca++ transporting, type 2C, member 1
Unigene number:	Hs.106778
Probeset Accession #:	N51919
Protein Accession #:	AAF27813
Signal sequence:	none found
Transmembrane domains:	60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
Pfam domains:	Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization:	not determined

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1          11         21         31         41         51
|          |          |          |          |          |
MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI    60
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP   120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS   180
KVTAPQPAAT NGDLASRSNI AFMGTLVRCG KAKGVVIGTG ENSEFGEVFK MMQAEEAPKT   240
PLQKSMDLLG KQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPIVVTV   300
TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT   360
GVGYNQFGEV IVDGDVVHGF YNPAVSRIVE AGCVCNDAVI RNNTLMGKPT EGALIALAMK   420
MGLDGLQQDY IRKAEYPFSS EQKWMAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK   480
GQTLTLTQQQ RDVYQQEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTGVKEAV   540
TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV   600
FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEAADMI   660
LVDDDFQTIM SAIEEGKGIY NNIKNFVRFQ LSTSIAALTL ISLATLMNFP NPLNAMQILW   720
INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR   780
ELRDNVITPR DTTMTFTCFV FFDMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL   840
LVIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIIK KVERSREKIQ KHVSSTSSSF   900
LEV
```

A189 DNA SEQUENCE

Gene name:	ESTs
Unigene number:	Hs.293185
Probeset Accession #:	N62096
Nucleic Acid Accession #:	N62096
Coding sequence:	1-1284 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGGATTGCC TTATTCAATG    60
AAGCAAGCTG GGTTTCCTTT GGGAATATTG CTTTTATTCT GGGTTTCATA TGTTACAGAC   120
TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCAGTCT   180
TTGGTCAATA AAACTTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTTTG   240
TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT   300
TTTCAAAGAA TCCCAGGAGT TGATCCTGAA AACGTGTTTA TTGGTCGCCA CTTCATTATT   360
GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT   420
GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAAT TGTAATGGCA   480
AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG   540
CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC   600
 TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT   660
 ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA   720
 TTTACTGGCT TCACCCAAGG GGACTTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA   780
 ACATTTGGAA GATTTTGTTA TCGTGTCACT GTCATTTTGA CATACCCTAT GGAATGCTTT   840
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC   900
 ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC   960
 CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCCCTCAT TTTTATCATT  1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG  1080
 TCTTGTGTCA TGCTTCCCAT TGGTGCTGTG GTGATGGTTT TTGGATTCGT CATGGCTATT  1140
 ACAAATACTC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAATTTC  1200
 TCTCTCACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACTTTC TACTTTAAAT  1260
 ATTAGTATCT TTCAACTCGA GTAA
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A190 Protein sequence:

Gene name:	ESTs
Unigene number:	Hs.293185
Probeset Accession #:	N62096
Protein Accession #:	none found
Signal sequence:	none found
Transmembrane domains:	28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVSYVTD FSLVLLIKGG ALSGTDTYQS    60
LVNKTFGFPG YLLLSVLQFL YPFIAMISYN IIAGDTLSKV FQRIPGVDPE NVFIGRHFII   120
GLSTVTFTLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGPHIP KTEDAWVFAK   180
PNAIQAVGVM SFAFICHHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT   240
FTGFTQGDLF ENYCRNDDLV TFGRFCYGVT VILTYPMECF VTREVIANVF FGGNLSSVFH   300
IVVTVMVITV ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM   360
SCVMLPIGAV VMVFGFVMAI TNTQDCTHGQ EMFYCFPDNF SLTNTSESHV QQTTQLSTLN   420
ISIFQLE
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A191 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGT TTTCCCTTGT TTTATTGATA    60
AAAGGAGGGG CCCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCGGC   120
TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA   180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT   240
GATCCTGAAA ACGTGTTTAT TGGTCGCCAC TTCATTATTG GACTTTCCAC AGTTACCTTT   300
ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT   360
ACAGGTTTAA CAACTCTGAT TCTTGGAATT GTAATGGCAA GGGCAATTTC ACTGGGTCCA   420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC   480
GGGGTTATGT CTTTTGCATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA   540
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCATCGT GATTTCTGTA   600
TTTATCTGTA TATTCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG   660
GACTTATTTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTTGGAAG ATTTTGTTAT   720
GGTGTCACTG TCATTTTGAC ATACCCTATG GAATGCTTTG TGACAAGAGA GGTAATTGCC   780
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC   840
ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC   900
AATGGTGTGC TCTGTGCAAC TCCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA   960
CTGTCTGAAG AACCAAGGAC ACACTCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCATT  1020
GGTGCTGTGG TGATGGTTTT TGGATTCGTC ATGGCTATTA CAAATACTCA AGACTGCACC  1080
CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTTCT CTCTCACAAA TACCTCAGAG  1140
TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG  1200
TAA
```

A192 Protein sequence:

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: 1-26
Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI    60
SYNIIAGDTL SKVFQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLIS   120
TGLTTLILGI VMARAISLGP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL   180
EEPTVAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY   240
GVTVILTYPM ECFVTREVIA NVFFGGNLSS VFHIVVTVMV ITVATLVSLL IDCLGIVLEL   300
NGVLCATPLI FIIPSACYLK LSEEPRTHSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT   360
HGQEMFYCFP DNFSLTNTSE SHVQQTTQLS TLNISIFQLE
```

A193 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT    60
CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTTGTATC CTTTTATAGC AATGATAAGT   120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT   180
CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT   240
CTGCCTTTAT CCTTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA   300
GGTTTAACAA CTCTGATTCT TGGAATTGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC   360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCGGG   420
```

```
GTTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA   480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT   540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC   600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT   660
GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT   720
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC   780
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT   840
GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG   900
TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGTCTT GTGTCATGCT TCCCATTGGT   960
GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT  1020
GGGCAGGAAA TGTTCTACTG CTTTCCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT  1080
CATGTTCAGC AGACAACACA ACTTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA
```

A194 Protein sequence:

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQVNKTFGF PGYLLLSVLQ PLYPFIAMIS YNIIAGDTLS KVFQRIPGVD    60
PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLGKVSLIST GLTTLILGIV MARAISLGPH   120
IPKTEDAWVF AKPNAIQAVG VMSFAFICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF   180
ICIFFATCGY LTFTGFTQGD LFENYCRNDD LVTFGRFCYG VTVILTYPME CFVTREVIAN   240
VFFGGNLSSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL   300
SEEPRTHSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES   360
HVQQTTQLST LNISIFQLE
```

A195 DNA SEQUENCE:

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGATTTAGA TGACAGAGAA    60
ACCCTTGTTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTTAAT   120
GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT   180
GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACAGA CTTTTCCCTT   240
GTTTTATTGA TAAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAGTC TTTCGTCAAT   300
AAAACTTTCG GCTTTCCAGG GTATCTGCTC CTCTCTGTTC TTCAGTTTTT GTATCCTTTT   360
ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAGT TTTTCAAAGA   420
ATCCCAGGAG TTGATCCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC   480
ACAGTTACCT TTACTCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC   540
TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT   600
TCACTGGGTC CACACATACC AAAAACAGAA GACGCTTGGG TATTTGCAAA GCCCAATGCC   660
ATTCAAGCGG TCGGGGTTAT GTCTTTTGCA TTTATTTGCC ACCATAACTC CTTCTTAGTT   720
TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC   780
GTGATTTCTG TATTTATCTG TATATTCTTT GCTACATGTG GATACTTGAC ATTTACTGGC   840
TTCACCCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTTGGA   900
AGATTTTGTT ATGGTGTCAC TGTCATTTTG ACATACCCTA TGGAATGCTT TGTGACAAGA   960
GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCA CATTGTTGTA  1020
ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCATTGC TGATTGATTG CCTCGGGATA  1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCCTCA TTTTTATCAT TCCATCAGCC  1140
TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC  1200
ATGCTTCCCA TTGGTGCTGT GGTGATGGTT TTTGGATTCG TCATGGCTAT TACAAATACT  1260
CAAGACTGCA CCCATGGGCA GGAAATGTTC TACTGCTTTC CTGACAATTT CTCTCTCACA  1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC  1380
TTTCAATGA
```

A196 Protein sequence:

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA    60
```

```
GFPLGILLLF WVSYVTDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF   120
IAMISYNIIA GDTLSKVFQR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIAKLGKV   180
SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPNA IQAVGVMSFA FICHHNSFLV   240
YSSLEEPTVA KWSRLIHMSI VISVFICIFF ATCGYLTFTG FTQGDLFENY CRNDDLVTFG   300
RFCYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIVV TVMVITVATL VSLLIDCLGI   360
VLELNGVLCA TPLIFIIPSA CYLKLSEEPR THSDKIMSCV MLPIGAVVMV FGFVMAITNT   420
QDCTHGQEMF YCFPDNFSLT NTSESHVQQT TQLSTLNISI FQ
```

A197 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.31608
Probeset Accession #: H18836
Nucleic Acid Accession #: NM_017636
Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCACG    60
GAGAAGCCCA CCGATGCCTA CGGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC   120
AATTTCCTCC GGCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTCACACGC   180
ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCAGTGC TGGGGGGATC GGGGGGCCCC   240
GTCCTCCAGA CCTGGCTGCA GGACCTGCTG CGTCGTGGGC TGGTGCGGGC TGCCCAGAGC   300
ACAGGAGCCT GGATTGTCAC TGGGGGTCTG CACACGGGCA TCGGCCGGCA TGTTGGTGTG   360
GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGCACCA AGGTGGTGGC CATGGGTGTG   420
GCCCCCTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCCAAGGG CTCGTTCCCT   480
GCGAGGTACC GGTGGCGCGG TGACCCGGAG GACGGGGTCC AGTTTCCCCT GGACTACAAC   540
TACTCGGCCT TCTTCCTGGT GGACGACGGC ACACACGGCT GCCTGGGGGG CGAGAACCGC   600
TTCCGCTTGC GCCTGGAGTC CTACATCTCA CAGCAGAAGA CGGGCGTGGG AGGGACTGGA   660
ATTGACATCC CTGTCCTGCT CCTCCTGATT GATGGTGATG AGAAGATGTT GACGCGAATA   720
GAGAACGCCA CCCAGGCTCA GCTCCCATGT CTCCTCGTGG CTGGCTCAGG GGGAGCTGCG   780
GACTGCCTGG CGGAGACCCT GGAAGACACT CTGGCCCCAG GGAGTGGGGG AGCCAGGCAA   840
GGCGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCCAAAG GGGACCTTGA GGTCCTGCAG   900
GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCCTGA CAGTCTATTC TTCTGAGGAT   960
GGGTCTGAGG AATTCGAGAC CATAGTTTTG AAGGCCCTTG TGAAGGCCTG TGGGAGCTCG  1020
GAGGCCTCAG CCTACCTGGA TGAGCTGCGT TTGGCTGTGG CTTGGAACCG CGTGGACATT  1080
GCCCAGAGTG AACTCTTTCG GGGGGACATC CAATGGCGGT CCTTCCATCT CGAAGCTTCC  1140
CTCATGGACG CCCTGCTGAA TGACCGGCCT GAGTTCGTGC GCTTGCTCAT TTCCCACGGC  1200
CTCAGCCTGG GCCACTTCCT GACCCCGATG CGCCTGGCCC AACTCTACAG CGCGGCGCCC  1260
TCCAACTCGC TCATCCGCAA CCTTTTGGAC CAGGCGTCCC ACAGCGCAGG CACCAAAGCC  1320
CCAGCCCTAA AAGGGGGAGC TGCGGAGCTC CGGCCCCCTG ACGTGGGGCA TGTGCTGAGG  1380
ATGCTGCTGG GGAAGATGTG CGCGCCGAGG TACCCCTCCG GGGGCGCCTG GGACCCTCAC  1440
CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTCGCCGCTC  1500
TCGCTGGATG CTGGCCTCGG GCAGGCCCCC TGGAGCGACC TGCTTCTTTG GGCACTGTTG  1560
CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCCTCA  1620
GCTCTTGGGG CCTGTTTGCT GCTCCGGGTG ATGGCACGCC TGGAGCCTGA CGCTGAGGAG  1680
GCAGCACGGA GGAAAGACCT GGCGTTCAAG TTTGAGGGGA TGGGCGTTGA CCTCTTTGGC  1740
GAGTGCTATC GCAGCAGTGA GGTGAGGGCT GCCCGCCTCC TCCTCCGTCG CTGCCCGCTC  1800
TGGGGGGATG CCACTTGCCT CCAGCTGGCC ATGCAAGCTG ACGCCCGTGC CTTCTTTGCC  1860
CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA  1920
CCCATCTGGG CCCTGGTTCT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CCGCCTCATC  1980
ACCTTCAGGA AATCAGAAGA GGAGCCCACA CGGGAGGAGC TAGAGTTTGA CATGGATAGT  2040
GTCATTAATG GGGAAGGGCC TGTCGGGACG GCGGACCCAG CCGAGAAGAC GCCGCTGGGG  2100
GTCCCGCGCC AGTCGGGCCG TCCGGGTTGC TGCGGGGGCC GCTGCGGGGG GCGCCGGTGC  2160
CTACGCCGCT GGTTCCACTT CTGGGGCGCG CCGGTGACCA TCTTCATGGG CAACGTGGTC  2220
AGCTACCTGC TGTTCCTGCT GCTTTTCTCG CGGGTGCTGC TCGTGGATTT CCAGCCGGCG  2280
CCGCCCGGCT CCCTGGAGCT GCTGCTCTAT TTCTGGGCTT TCACGCTGCT GTGCGAGGAA  2340
CTGCGCCAGG GCCTGAGCGG AGGCGGGGGC AGCCTCGCCA GCGGGGGCCC CGGGCCTGGC  2400
CATGCCTCAC TGAGCCAGCG CCTGCGCCTC TACCTCGCCG ACAGCTGGAA CCAGTGCGAC  2460
CTAGTGGCTC TCACCTGCTT CCTCCTGGGC GTGGGCTGCC GGCTGACCCC GGGTTTGTAC  2520
CACCTGGGCC GCACTGTCCT CTGCATCGAC TTCATGGTTT TCACGGTGCG GCTGCTTCAC  2580
ATCTTCACGG TCAACAAACA GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG  2640
GACGTGTTCT TCTTCCTCTT CTTCCTCGGC GTGTGGCTGG TAGCCTATGG CGTGGCCACG  2700
GAGGGGCTCC TGAGGCCACG GGACAGTGAC TTCCCAAGTA TCCTGCGCCG CGTCTTCTAC  2760
CGTCCCTACC TGCAGATCTT CGGGCAGATT CCCCAGGAGG ACATGGACGT GGCCCTCATG  2820
GAGCACAGCA ACTGCTCGTC GGAGCCCGGC TTCTGGGCAC ACCCTCCTGG GGCCCAGGCG  2880
GGCACCTGCG TCTCCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCCTCGT CATCTTCCTG  2940
CTCGTGGCCA ACATCCTGCT GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTCGGC  3000
AAAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCGCCT CATCCGGGAA  3060
TTCCACTCTC GGCCCGCGCT GGCCCCGCCC TTTATCGTCA TCTCCCACTT GCGCCTCCTG  3120
CTCAGGCAAT TGTGCAGGCG ACCCCGGAGC CCCCAGCCGT CCTCCCCGGC CCTCGAGCAT  3180
TTCCGGGTTT ACCTTTCTAA GGAAGCCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT  3240
AAGGAGAACT TTCTGCTGGC ACGCGCTAGG GACAAGCGGG AGAGCGACTC CGAGCGTCTG  3300
AAGCGCACGT CCCAGAAGGT GGACTTGGCA CTGAAACAGC TGGGACACAT CCGCGAGTAC  3360
GAACAGCGCC TGAAAGTGCT GGAGCGGGAG GTCCAGCAGT GTAGCCGCGT CCTGGGGTGG  3420
GTGGCCGAGG CCCTGAGCCG CTCTGCCTTG CTGCCCCCAG GTGGGCCGCC ACCCCCTGAC  3480
CTGCCTGGGT CCAAAGACTG A
```

A198 Protein sequence:

Gene name: ESTs
Unigene number: Hs.31608
Probeset Accession #: H18836
Protein Accession #: none found

Signal sequence: none found
Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MEDAFGAAVV TVWDSDAHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR    60
TWGFRAPNLV VSVLGGSGGP VLQTWLQDLL RRGLVRAAQS TGAWIVTGGL HTGIGRHVGV   120
AVRDHQMAST GGTKVVAMGV APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVQFPLDYN   180
YSAFFLVDDG THGCLGGENR FRLRLESYIS QQKTGVGGTG IDIPVLLLLI DGDEKMLTRI   240
ENATQAQLPC LLVAGSGGAA DCLAETLEDT LAPGSGGARQ GEARDRIRRF FPKGDLEVLQ   300
AQVERIMTRK ELLTVYSSED GSEEFETIVL KALVKACGSS EASAYLDELR LAVAWNRVDI   360
AQSELFRGDI QWRSFHLEAS LMDALLNDRP EFVRLLISHG LSLGHFLTPM RLAQLYSAAP   420
SNSLIRNLLD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH   480
PGQGFGESMY LLSDKATSPL SLDAGLGQAP WSDLLLWALL LNRAQMAMYF WEMGSNAVSS   540
ALGACLLLRV MARLEPDAEE AARRKDLAFK FEGMGVDLFG ECYRSSEVRA ARLLLRRCPL   600
WGDATCLQLA MQADARAFFA QDGVQSLLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI   660
TFRKSEEEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCGGRRC   720
LRRWFHFWGA PVTIFMGNVV SYLLFLLLFS RVLLVDFQPA PPGSLELLLY FWAFTLLCEE   780
LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY   840
HLGRTVLCID FMVFTVRLLH IFTVNKQLGP KIVIVSKMMK DVFFFLFFLG VWLVAYGVAT   900
EGLLRPRDSD FPSILRRVFY RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPPGAQA   960
GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQGNSDLYW KAQRYRLIRE  1020
FHSRPALAPP FIVISHLRLL LRQLCRRPRS PQPSSPALEH FRVYLSKEAE RKLLTWESVH  1080
KENFLLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQQCSRVLGW  1140
VAEALSRSAL LPPGGPPPPD LPGSKD
```

A199 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.40808
Probeset Accession #: AA054237
Nucleic Acid Accession #: AA054237
Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCCTGGGG    60
CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTACGAGA CCGACCCCCG GCGCCACAAG   120
GAGAGCTGCG AGCGCAGCCG CGCGGGCGCC GACCCCCCGG ACCAGAAGAA CCGCCTGATG   180
CCGCTGTCGC ACCTGCCGCT GCGGGACTCG CCCCCGCTGG GGCGCCGGCT GCTCCCGGGC   240
GGCCCGGGGC GCGCCGACCC CGAGTCCTGG CGCTCGCTCC TGGGGCTCGG CGGGCTGGAC   300
GCCGAGTGCG GCCGGCCCCT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC   360
CTGGGCATCG ACCGGGACAT CGACACCCTC ATCCTGAAAG GTATTGCGCA GCGATGCACG   420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCCTTT TAATTTAACC   480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC   540
CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC   600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT   660
TGCACCATTT CCCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTTGAA CCGGCTCCCA   720
AAGCTAATTT ATAGCCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC   780
GCCTGGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT   840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA
```

A200 Protein sequence:
Gene name: ESTs
Unigene number: Hs.40808
Probeset Accession #: AA054237
Protein Accession #: none found
Signal sequence: 1-18
Transmembrane domains: 179-201, 209-231, 257-279
Cellular Localization: plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM    60
PLSHLPLRDS PPLGRRLLPG GPGRADPESW RSLLGLGGLD AECGRPLFAT YSGLWRKCYF   120
LGIDRDIDTL ILKGIAQRCT AIKYHFSQPI RLRNIPFNLT KTIQQDEWHL LHLRRITAGF   180
LGMAVAVLLC GCIVATVSFF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP   240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV
```

A201 DNA SEQUENCE
Gene name: CDA14
Unigene number: Hs.26813
Probeset Accession #: N32912
Nucleic Acid Accession #: NM_016570
Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG    60
AAGGTTCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA   120
```

```
TTTACAACTA TGGCTTTATT AACCATAATG GAATTCTCAG TATATCAAGA TACATGGATG   180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT   240
ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTTAGC AGAAACAATG   300
GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG   360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT   420
CAAGATGTGA TATTTAAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA   480
GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA   540
GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA   600
CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTTT CTCATAGAAT AGATCATTTG   660
TCTTTTGGAG AGCTTGTTCC AGCAATTATT AATCCTTTAG ATGGAACTGA AAAAATTGCT   720
ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA   780
TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAC   840
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT   900
ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTTGTAAG ACTCTGTGGT   960
ATTGTTGGAG GAATCTTTTC AACAACAGGC ATGTTACATG GAATTGGAAA ATTTATAGTT  1020
GAAATAATTT GCTGTCGTTT CAGACTTGGA TCCTATAAAC CTGTCAATTC TGTTCCTTTT  1080
GAGGATGGCC ACACAGACAA CCACTTACCT CTTTTAGAAA ATAATACACA TTGA
```

A202 Protein sequence:

Gene name: CDA14
Unigene number: Hs.26813
Probeset Accession #: N32912
Protein Accession #: NP_057654
Signal sequence: none found
Transmembrane domains: none found
Cellular Localization: nuclear

```
1          11         21         31         41         51
|          |          |          |          |          |
MRRLNRKKTL SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM    60
KYEYEVDKDF SSKLRINIDI TVAMKCQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ   120
KEWQRMLQLI QSRLQEEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK   180
VAGNFHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SFGELVPAII NPLDGTEKIA   240
IDHNQMFQYF ITVVPTKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL   300
MVTVTEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKFIV EIICCRFRLG SYKPVNSVPF   360
EDGHTDNHLP LLENNTH
```

A203 DNA SEQUENCE

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
Unigene number: Hs.44926
Probeset Accession #: S79876
Nucleic Acid Accession #: NM_001935.1
Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGCGCGTCTC CGCCGCCCGC GTGACTTCTG CCTGCGCTCC TTCTCTGAAC GCTCACTTCC    60
GAGGAGACGC CGACGATGAA GACACCGTGG AAGATTCTTC TGGGACTGCT GGGTGCTGCT   120
GCGCTTGTCA CCATCATCAC CGTGCCCGTG GTTCTGCTGA ACAAAGGCAC AGATGATGCT   180
ACAGCTGACA GTCGCAAAAC TTACACTCTA ACTGATTACT TAAAAAATAC TTATAGACTG   240
AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAATAAT   300
ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT   360
GATGAGTTTG GACATTCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC   420
TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCCTACA CAGCTTCATA TGACATTTAT   480
GATTTAAATA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC   540
ACATGGTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGGA ACAATGACAT TTATGTTAAA   600
ATTGAACCAA ATTTACCAAG TTACAGAATC ACATGGACGG GGAAAGAAGA TATAATATAT   660
AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCCTACTC TGCTCTGTGG   720
TGGTCTCCAA ACGGCACTTT TTTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT   780
ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCA   840
TATCCAAAGG CAGGAGCTGT GAATCCAACT GTAAAGTTCT TTGTTGTAAA TACAGACTCT   900
CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCCTGCTTC TATGTTGATA   960
GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAAGAATTTC TTTGCAGTGG  1020
CTCAGGAGGA TTCAGAACTA TTCGGTCATG GATATTTGTG ACTATGATGA ATCCAGTGGA  1080
AGATGGAACT GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA  1140
AGATTTAGGC CTTCAGAACC TCATTTTACC CTTGATGGTA ATAGCTTCTA CAAGATCATC  1200
AGCAATGAAG AAGGTTACAG ACACATTTGC TATTTCCAAA TAGATAAAAA AGACTGCACA  1260
TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACCAG TGATTATCTA  1320
TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAAATCCAA  1380
CTTATTGACT ATACAAAAGT GACATGCCTC AGTTGTGAGC TGAATCCGGA AAGGTGTCAG  1440
TACTATTCTG TGTCATTCAG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCCT  1500
GGTCTGCCCC TCTATACTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCCTGGAA  1560
GACAATTCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAAACTGGAC  1620
TTCATTATTT TGAATGAAAC AAAATTTTGG TATCAGATGA TCTTGCCTCC TCATTTTGAT  1680
AAATCCAAGA AATATCCTCT ACTATTAGAT GTGTATGCAG GCCCATGTAG TCAAAAAGCA  1740
GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA  1800
GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC  1860
AGAAGACTGG GAACATTTGA AGTTGAAGAT CAAATTGAAG CAGCCAGACA ATTTTCAAAA  1920
ATGGGATTTG TGGACAACAA ACGAATTGCA ATTTGGGGCT GGTCATATGG AGGGTACGTA  1980
ACCTCAATGG TCCTGGGATC GGGAAGTGGC GTGTTCAAGT GTGGAATAGC CGTGGCGCCT  2040
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GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT  2100
CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAAAATTTT  2160
AAACAAGTTG AGTACCTCCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG  2220
TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT  2280
ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG  2340
AGCCACTTCA TAAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA  2400
AAGCTTATTA AAACTCATTT TTGTTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA  2460
TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTC  2520
ATACCTATCA TCTTAAGTAG GGACTTCTGT CTTCACAACA GATTATTACC TTACAGAAGT  2580
TTGAATTATC CGGTCGGGTT TTATTGTTTA AAATCATTTC TGCATCAGCT GCTGAAACAA  2640
CAAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT  2700
TTTCTAACTG GACTGGTTCA AATGTTGTTC TCTTCTTTAA AGGGATGGCA AGATGTGGGC  2760
AGTGATGTCA CTAGGGCAGG GACAGCATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA  2820
TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTCAG CTCCCCTCGG  2880
AGAAGAGCTG TTCACCACGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAAACAGTCT  2940
CAGGAAATCA AATATCGAAA GCACTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC  3000
AAAGAAATGT AAGGGAAACT GCCAGCAACG CAGCCCCCAG GTGCCAGTTA TGGCTATAGG  3060
TGCTACAAAA ACACAGCAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAAAAA  3120
TACTGATGTT CCTAGTGAAA GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC  3180
CTGTTAAAAG ATGAAAATAT TTGTATCACA AATCTTAACT TGAAGGAGTC CTTGCATCAA  3240
TTTTTCTTAT TTCATTTCTT TGAGTGTCTT AATTAAAAGA ATATTTTAAC TTCCTTGGAC  3300
TCATTTTAAA AAATGGAACA TAAAATACAA TGTTATGTAT TATTATTCCC ATTCTACATA  3360
CTATGGAATT TCTCCCAGTC ATTTAATAAA TGTGCCTTCA TTTTTTC
```

A204 Protein sequence:

Gene name:	dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
Unigene number:	Hs.44926
Probeset Accession #:	S79876
Protein Accession #:	NP_001926.1
Signal sequence:	none found
Transmembrane domains:	6-28
DPPIV_N_term domain:	43-557
Peptidase_S9 domain:	558-635
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MKTPWKILLG LLGAAALVTI ITVPVVLLNK GTDDATADSR KTYTLTDYLK NTYRLKLYSL    60
RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFGH SINDYSISPD GQFILLEYNY   120
VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSPV GHKLAYVWNN DIYVKIEPNL   180
PSYRITWTGK EDIIYNGITD WVYEEEVFSA YSALWWSPNG TFLAYAQFND TEVPLIEYSF   240
YSDESLQYPK TVRVPYPKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL   300
CDVTWATQER ISLQWLRRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS   360
EPHFTLDGNS FYKIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN   420
EYKGMPGGRN LYKIQLIDYT KVTCLSCELN PERCQYYSVS FSKEAKYYQL RCSGPGLPLY   480
TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDFIILN ETKFWYQMIL PPHFDKSKKY   540
PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RGSGYQGDKI MHAINRRLGT   600
FEVEDQIEAA RQFSKMGFVD NKRIAIWGWS YGGYVTSMVL GSGSGVFKCG IAVAPVSRWE   660
YYDSVYTERY MGLPTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQQSAQIS   720
KALVDVGVDF QAMWYTDEDH GIASSTAHQH IYTHMSHFIK QCFSLP
```

A205 DNA SEQUENCE

Gene name:	predicted exon
Unigene number:	none found
Probeset Accession #:	none found
Nucleic Acid Accession #:	none found
Coding sequence:	1-261 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAAATGACA ATGCCATCAG AGTTGACAAC    60
AGAAGTGTGA TTAAAGTGCG TGCTAACCAG TGTTCCCTGC ATGAGGCAGA AAGTGAATCC   120
AGAAACCCTC AGGAGCTCTG GATGGGCCTG CTCCTCTTGA TGGGGGTCCT AGAAGCATGT   180
GTGGAAATGA GGCCTCTGTC AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC   240
CAGCCCACAC TGGATGTCTA A
```

A206 Protein sequence:

Gene name:	predicted exon
Unigene number:	none found
Probeset Accession #:	none found
Protein Accession #:	none found
Signal sequence:	none found
Transmembrane domains:	46-68
Cellular Localization:	not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MALAKVREPN ANDNAIRVDN RSVIKVRANQ CSLHEAESES RNPQELWMGL LLLMGVLEAC    60
VEMRPLSVWS LRDDKEQSPH QPTLDV
```

A207 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.222886
Probeset Accession #: AI672225
Nucleic Acid Accession #: none found
Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAACTGCT    60
CTCATACTTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT   120
ATTGATGTAT CTTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC   180
ATCATGTGGA CCAGTTTTGT GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT   240
TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTCATGTGGG ATTCCCAGAA   300
AACCTGACTA ATGGTGCCGC TGCTGGCAAT GGTGATGATG GATTAATTCC TCCAAGGAAG   360
AGCAGAACAC CTGAAAGCCA GCAATTTCCT GACACTGAGA ATGAAGAGTA TCACAGGTTT   420
GTCAAAGATC AGATAGTTGT AGATATGCGG CGTTATTTCT GA
```

A208 Protein sequence:
Gene name: ESTs
Unigene number: Hs.222886
Probeset Accession #: AI672225
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 16-38
Cellular Localization: not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPLLEQN IDVSSQDLDR RPESMLFLVI    60
IMWTSFVEDN LSMGWGKLED FMAIEEEMKK HGSTHVGFPE NLTNGAAAGN GDDGLIPPRK   120
SRTPESQQFP DTENEEYHRF VKDQIVVDMR RYF
```

A209 DNA SEQUENCE
Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
Unigene number: Hs.23796
Probeset Accession #: NM_014253
Nucleic Acid Accession #: NM_014253
Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GACTGCTTGC ATTAAAGGAC TTCCTCATCC TTTTTTTCAT GAAACTGAGC TTGCTTAATC    60
AGAGATGGAG CAAACTGACT GCAAACCCTA CCAGCCTCTA CCAAAAGTCA AGCATGAAAT   120
GGATCTAGCT TACACCAGTT CTTCTGATGA GAGTGAAGAT GGAAGAAAAC CAAGACAGTC   180
ATACAACTCC AGGGAGACCC TGCACGAGTA TAACCAGGAG CTGAGGATGA ATTACAATAG   240
CCAGAGTAGA AAGAGGAAAG AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAAC   300
CTCTCACACT CTGTGCTCTG GCTACCAAAC AGACATGCAC AGCGTTTCTC GGCATGGCTA   360
CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA   420
TGCACTAAGA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCCTGTT TGTCCAGCCG   480
GGCCAACTCT GCATTATCCT TGACTGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA   540
TGGTTTCAAA TTCTCTCCTG TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA   600
TGTGCAGAGC AGCCCACACA ACCAGTTCAC CTTCAGACCC CTCCCACCGC CACCTCCGCC   660
TCCTCATGCC TGCACCTGTG CCAGGAAGCC ACCCCCTGCA GCGGACTCTC TTCAGAGGAG   720
ATCAATGACT ACCCGCAGCC AGCCCAGCCC AGCTGCTCCA GCTCCCCCAA CCAGCACGCA   780
GGATTCAGTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCAG   840
GCATTCCCTG TTCAAACATG GATCTGGTTC CTCTGCGATC TTCAGTGCAG CCAGTCAGAA   900
CTACCCTCTG ACATCCAATA CCGTGTACTC GCCCCCTCCC AGGCCTCTTC CTCGAAGCAC   960
CTTTTCCCGA CCTGCCTTTA CCTTTAACAA ACCTTACAGG TGCTGCAACT GGAAGTGCAC  1020
AGCATTGAGC GCCACTGCAA TCACAGTGAC TTTGGCCTTG TTACTAGCCT ATGTGATTGC  1080
AGTGCATTTG TTCGGCCTGA CTTGGCAGTT GCAACCAGTT GAAGGAGAGC TGTATGCAAA  1140
TGGAGTTAGC AAAGGGAACA GGGGGACCGA GTCCATGGAC ACTACTTACT CTCCAATTGG  1200
AGGAAAAGTT TCTGATAAAT CAGAGAAAAA AGTGTTTCAG AAGGGACGGG CGATAGACAC  1260
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TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTTCTT TAGCCAAGGA  1380
CTCTCTGCTG GGAATTTATG GCAGAAGAAA CATTCCACCT ACACATACTC AGTTTGATTT  1440
TGTAAAACTA ATGGATGGCA AACAGCTGGT CAAGCAGGAC TCCAAGGGCT CTGATGATAC  1500
ACAGCACTCC CCTCGGAACC TGATCTTAAC TTCGCTTCAG GAGACAGGTT TCATAGAGTA  1560
TATGGATCAA GGACCTTGGT ATCTGGCGTT TTACAATGAT GGAAAAAAGA TGGAGCAAGT  1620
ATTCGTGTTA ACTACAGCAA TTGAAATAAT GGATGACTGT TCAACCAATT GCAATGGAAA  1680
TGGAGAGTGT ATCTCTGGCC ATTGTCATTG TTTCCCAGGA TTCCTTGGAC CTGACTGTGC  1740
TAGAGATTCC TGCCCTGTGC TGTGTGGTGG GAATGGAGAA TACGAGAAAG GACACTGTGT  1800
CTGCCGGCAT GGCTGGAAGG GGCCAGAGTG TGACGTTCCG GAAGAACAAT GCATTGATCC  1860
AACATGCTTT GGCCACGGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA  1920
AGGAGAAATA TGCGAGGAAG AGGACTGCCT AGACCCAATG TGTTCCAACC ATGGCATCTG  1980
TGTAAAAGGA GAATGTCACT GTTCTACTGG CTGGGGAGGA GTTAACTGTG AAACACCACT  2040
TCCTGTATGT CAAGAGCAGT GCTCAGGACA CGGAACTTTT CTTCTGGACG CTGGAGTATG  2100
CAGCTGTGAT CCCAAGTGGA CAGGATCTGA CTGCTCAACA GAGCTGTGTA CCATGGAGTG  2160
TGGTAGCCAT GGAGTCTGCT CAAGAGGAAT TTGCCAGTGT GAAGAAGGCT GGGTAGGACC  2220
AACATGTGAG GAACGCTCCT GTCATTCTCA TTGTACTGAG CATGGCCAAT GCAAAGATGG  2280
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AAAATGTGAG TGTAGCCCTG GATGGGAGGG CGACCACTGC ACAATTGCTC ACTACTTAGA 2340
TGCTGTCCGA GATGGCTGCC CAGGGCTCTG CTTTGGAAAT GGACGATGTA CCCTGGATCA 2400
AAATGGTTGG CACTGTGTGT GTCAGGTGGG TTGGAGTGGG ACAGGCTGCA ATGTTGTCAT 2460
GGAAATGCTT TGTGGAGATA ACTTGGACAA TGATGGAGAT GGTTTAACCG ACTGTGTGGA 2520
TCCTGACTGT TGTCAACAAA GCAACTGTTA TATAAGTCCT CTCTGCCAGG GCTCACCAGA 2580
TCCTCTTGAC CTCATTCAGC AAAGCCAAAC TCTCTTCTCT CAGCACACTT CAAGACTTTT 2640
TTATGATCGA ATCAAATTCC TCATTGGCAA GGACAGTACT CATGTCATTC CTCCTGAGGT 2700
GTCATTTGAC AGCAGGCGTG CCTGTGTGAT TCGAGGCCAA GTGGTGGCCA TAGATGGAAC 2760
TCCTCTAGTG GGAGTGAATG TCAGTTTCTT GCACCACAGT GATTATGGGT TTACCATCAG 2820
CCGGCAAGAT GGAAGCTTTG ACCTCGTGGC CATCGGTGGC ATCTCTGTCA TCTTAATCTT 2880
CGACCGATCC CCTTTCCTGC CTGAGAAGAG AACACTCTGG TTGCCTTGGA ATCAGTTTAT 2940
TGTGGTAGAG AAAGTCACCA TGCAGAGAGT TGTATCAGAC CCGCCATCCT GCGATATCTC 3000
CAACTTTATC AGCCCAAACC CTATTGTGCT TCCTTCACCG CTCACATCAT TTGGAGGGTC 3060
CTGTCCAGAG AGGGGAACTA TTGTTCCTGA GCTGCAGGTT GTACAGGAGG AAATTCCCAT 3120
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CACATTTGCT TGGAACAAGA CCGATATCTA TGGACAGAAG GTTTGGGGCC TGGCAGAGGC 3360
TTTGGTATCT GTGGGATATG AATATGAAAC GTGCCCTGAC TTTATTCTCT GGGAGCAAAG 3420
GACAGTCGTT TTACAAGGTT TTGAGATGGA TGCTTCTAAC CTAGGAGACT GGTCTTTGAA 3480
TAAGCATCAC ATTTTGAATC CTCAAAGTGG AATCATACAT AAAGGGAATG GAGAAAATAT 3540
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TGTAGCCTGC ACCAACTGCA ATGGCCCAGC CCACAACAAC AAACTCTTTG CTCCTGTCGC 3660
CTTAGCTTCT GGCCCTGATG GCAGTGTGTA TGTTGGCGAC TTCAATTTTG TAAGGAGAAT 3720
ATTTCCCTCG GGAAACTCCG TTAGTATTTT GGAATTAAGC ACAAGTCCTG CTCACAAATA 3780
CTATCTGGCT ATGGACCCTG TGTCTGAATC ACTCTATCTA TCAGACACCA ATACTCGCAA 3840
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AATCGGCTCA AATGGTCTGA CTTCCACACA ACCACTGAGC TGTGACTCAG GAATGGACAT 4140
CACTCAGGTG CGATTAGAGT GGCCAACAGA CCTTGCAGTA AATCCTATGG ACAATTCATT 4200
GTATGTCTTG GATAACAACA TTGTGCTGCA AATTTCTGAG AACAGGCGTG TTCGGATCAT 4260
CGCAGGACGC CCCATTCACT GCCAGGTGCC AGGCATCGAT CATTTCCTGG TCAGCAAGGT 4320
AGCAATTCAC TCCACTCTAG AGTCAGCGAG GGCCATCAGT GTCTCCCACA GCGGGCTGCT 4380
CTTCATAGCT GAAACAGACG AGAGGAAAGT AAACCGCATT CAGCAAGTAA CCACCAATGG 4440
GGAGATCTAC ATCATCGCTG GTGCCCCCAC TGACTGTGAC TGCAAAATTG ATCCAAACTG 4500
TGACTGTTTT TCAGGTGATG GTGGCTATGC CAAAGATGCA AAGATGAAAG CCCCTTCCTC 4560
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GATAACAAGG GACTATGTTT ATAACTTCAC CTACAATTCT GAAGGTGACT TGGGCGCGAT 4800
TACCAGCAGC AATGGCAATT CAGTGCACAT TCGCCGTGAT GCAGGCGGAA TGCCGCTATG 4860
GCTTGTGGTG CCTGGCGGAC AAGTATACTG GCTGACTATA AGCAGCAATG GAGTCCTGAA 4920
AAGAGTGTCA GCCCAAGGCT ATAATCCGGC CTTAATGACC TATCCAGGAA ACACAGGGCT 4980
TCTGGCTACC AAAAGTAACG AAAATGGATG GACAACCGTT TATGAGTATG ACCCCGAGGG 5040
ACACCTGACC AATGCAACGT TTCCCACTGG AGAGGTCAGC AGCTTCCACA GTGACCTGGA 5100
GAAGCTGACA AAAGTGGAGC TAGATACTTC CAACCGTGAA AATGTCCTCA TGTCAACCAA 5160
CTTGACGGCA ACTAGTACCA TATATATTTT AAAACAAGAA AATACTCAAA GTACCTATCC 5220
GGTGAATCCA GATGGTTCCC TGCGTGTCAC TTTTGCCAGC GGGATGGAGA TCGGCCTCAG 5280
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TCGAATTCTT TATGACCAGA CTGGGCGACC CATTCTGTGG TCTCCTGTAA GCAGATATAA 5580
TGAAGTGAAC ATCACATATT CACCTTCGGG ATTGGTGACG TTTATTCAAA GAGGAACGTG 5640
GAATGAAAAA ATGGAATATG ACCAGAGTGG GAAAATTATT TCAAGAACTT GGGCTGATGG 5700
GAAAATTTGG AGCTATACCT ACTTAGAAAA ATCTGTGATG CTTCTCCTAC ACAGCCAGCG 5760
GCGTTACATC TTTGAGTATG ACCAATCAGA TTGCCTGCTG TCAGTTACCA TGCCTAGCAT 5820
GGTGCGCCAC AGCTTACAAA CCATGCTTTC AGTGGGCTAC TACCGTAATA TCTACACCCC 5880
ACCGGACAGT AGCACTTCTT TTATCCAAGA CTATAGTCGA GATGGCCGAT TGCTACAGAC 5940
CCTGCATCTG GGGACAGGGC GCAGAGTCTT ATACAAGTAC ACCAAGCAAG CAAGGCTTTC 6000
TGAGGTTCTC TATGATACCA CTCAGGTCAC ATTAACATAT GAAGAGTCTT CTGGAGTGAT 6060
TAAGACAATA CACCTGATGC ATGACGGATT CATCTGCACA ATCAGATACA GGCAAACAGG 6120
ACCTCTTATT GGACGCCAGA TTTTCAGATT CAGTGAAGAA GGCCTTGTGA ATGCACGGTT 6180
CGACTACAGC TACAACAATT TCCGAGTCAC AAGCATGCAA GCTGTAATCA ATGAAACCCC 6240
TTTGCCTATA GATCTTTACC GATATGTTGA TGTCTCTGGC AGAACAGAGC AGTTTGGAAA 6300
ATTCAGTGTA ATTAATTACG ATTTAAATCA GGTCATAACT ACTACAGTGA TGAAACACAC 6360
CAAAATCTTC AGTGCCAATG GACAAGTCAT TGAAGTCCAA TATGAAATCC TAAAGGCAAT 6420
TGCCTACTGG ATGACCATTC AATATGATAA TGTGGGCCGA CATGGTAATA TGTGCATAAG 6480
GGTAGGAGTA GATGCCAATA TAACAAGGTA CTTCTATGAA TACGATGCTG ATGGGCAACT 6540
TCAGACTGTT TCTGTAAATG ACAAAACCCA GTGGCGTTAT AGTTACGATC TGAATGGAGA 6600
CATCAACCTC TTAAGCCATG GGAAGAGTGC TCGTCTTACT CCTCTCCGAT ATGACCTCCG 6660
AGACCGCATC ACCAGATTAG GAGAAATTCA GTATAAAATG GATGAAGATG GCTTTCTGAG 6720
GCAGAGGGGA AATGATATTT TTGAATATAA TTCTAATGGC CTGCTGCAGA AAGCCTACAA 6780
TAAGGCTTCT GGCTGGACTG TGCAGTATTA CTATGATGGG CTTGGGCGAC GTGTCGCGAG 6840
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AGGTCACCTT ATTGCCATGG AGTTAAGCAG TGGTGAAGAA TATTATGTAG CCTGTGATAA 7020
TACAGGTACC CCACTAGCTG TGTTCAGCAG CCGAGGTCAG GTCATAAAGG AGATACTATA 7080
CACACCTTAT GGCGATATCT ATCATGACAC TTACCCTGAC TTTCAGGTCA TAATTGGTTT 7140
TCATGGAGGA CTCTATGATT TCCTTACTAA ATTAGTGCAC CTGGGGCAAA GGGATTATGA 7200
TGTTGTTGCT GGCAGATGGA CAACGGCCTA TCATCACATA TGGAAACAGT TGAACCTCCT 7260
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A210 Protein sequence:

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
Unigene number: Hs.23796
Probeset Accession #: NM_014253
Protein Accession #: NP_055068
Signal sequence: none found
Transmembrane domains: 318-340
Cellular Localization: plasma membrane

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LRMWIRGMKS EHSSCLSSRA NSALSLTDTD HERKSDGENG FKFSPVCCDM EAQAGSTQDV   180
QSSPHNQFTF RPLPPPPPPP HACTCARKPP PAADSLQRRS MTTRSQPSPA APAPPTSTQD   240
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SRPAFTFNKP YRCCNWKCTA LSATAITVTL ALLLAYVIAV HLFGLTWQLQ PVEGELYANG   360
VSKGNRGTES MDTTYSPIGG KVSDKSEKKV FQKGRAIDTG EVDIGAQVMQ TIPPGLFWRF   420
QITIHHPIYL KFNISLAKDS LLGIYGRRNI PPTHTQFDFV KLMDGKQLVK QDSKGSDDTQ   480
HSPRNLILTS LQETGFIEYM DQGPWYLAFY NDGKKMEQVF VLTTAIEIMD DCSTNCNGNG   540
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CFGHGTCIMG VCICVPGYKG EICEEEDCLD PMCSNHGICV KGECHCSTGW GGVNCETPLP   660
VCQEQCSGHG TFLLDAGVCS CDPKWTGSDC STELCTMECG SHGVCSRGIC QCEEGWVGPT   720
CEERSCHSHC TEHGQCKDGK CECSPGWEGD HCTIAHYLDA VRDGCPGLCF GNGRCTLDQN   780
GWHCVCQVGW SGTGCNVVME MLCGDNLDND GDGLTDCVDP DCCQQSNCYI SPLCQGSPDP   840
LDLIQQSQTL FSQHTSRLFY DRIKFLIGKD STHVIPPEVS FDSRRACVIR GQVVAIDGTP   900
LVGVNVSFLH HSDYGFTISR QDGSFDLVAI GGISVILIFD RSPFLPEKRT LWLPWNQFIV   960
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FVDGTMIRKI DENAVITTVI GSNGLTSTQP LSCDSGMDIT QVRLEWPTDL AVNPMDNSLY  1380
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LEEDLVLIGN TGGRRILENG VNVTVSQMTS LLNGRTRRFA DIQLQHGALC FNIRYGTTVE  2640
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A211 DNA SEQUENCE:

Gene name: Solute carrier family 26, member 4
Unigene number: Hs.159275
Probeset Accession #: AF030880
Nucleic Acid Accession #: NM_000441
Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

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TTGCTCCGTA AATAAAACGT CCCACTGCCT TCTGAGAGCG CTATAAAGGC AGCGGAAGGG   180
TAGTCCGCGG GGCATTCCGG GCGGGGCGCG AGCAGAGACA GGTCATGGCA GCGCCAGGCG   240
GCAGGTCGGA GCCGCCGCAG CTCCCCGAGT ACAGCTGCAG CTACATGGTG TCGCGGCCGG   300
TCTACAGCGA GCTCGCTTTC CAGCAACAGC ACGAGCGGCG CCTGCAGGAG CGCAAGACGC   360
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CTGAACAAAA

A212 Protein sequence:

Gene name:	Solute carrier family 26, member 4
Unigene number:	Hs.159275
Probeset Accession #:	AF030880
Protein Accession #:	O43511
Signal sequence:	none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317, 347-369, 386-408, 420-442, 448-470, 486-508
Cellular Localization: plasma membrane

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FFPILTYFIF GTSRHISVGP FPVVSLMVGS VVLSMAPDEH FLVSSSNGTV LNTTMIDTAA   180
RDTARVLIAS ALTLLVGIIQ LIFGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSQLKIVL   240
NVSTKNYNGV LSIIYTLVEI FQNIGDTNLA DFTAGLLTIV VCMAVKELND RFRHKIPVPI   300
PIEVIVTIIA TAISYGANLE KNYNAGIVKS IPRGFLPPEL PPVSLFSEML AASFSIAVVA   360
YAIAVSVGKV YATKYDYTID GNQEFIAFGI SNIFSGFFSC FVATTALSRT AVQESTGGKT   420
QVAGIISAAI VMIAILALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV   480
IWVFTCIVSI ILGLDLGLLA GLIFGLLTVV LRVQFPSWNG LGSIPSTDIY KSTKNYKNIE   540
EPQGVKILRF SSPIFYGNVD GFKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT   600
KNGIISDAVS TNNAFEPDED IEDLEELDIP TKEIEIQVDW NSELPVKVNV PKVPIHSLVL   660
DCGAISFLDV VGVRSLRVIV KEFQRIDVNV YFASLQDYVI EKLEQCGFFD DNIRKDTFFL   720
TVHDAILYLQ NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEEELDV QDEAMRTLAS   780
QDEAMRTLAS
```

A213 DNA SEQUENCE:
Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Nucleic Acid Accession #: NM_021614
Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCCGCAGC AGCCCATGCC TCCGGTGCAA CAGCTGCGCC TCCTCCGGTG CCCCGGCGGC    60
GGGGGCGGGA GATAACCTGT CCCTGCTGCT CCGCACCTCC TCGCCCGGCG GCGCCTTCCG   120
GACCCGCACC TCCTCGCCGC TGTCGGGCTC GTCCTGCTGC TGCTGCTGCT GCTCGTCGCG   180
CCGGGGCAGC CAGCTCAATG TGAGCGAGCT GACGCCGTCC AGCCATGCCA GTGCGCTCCG   240
GCAGCAGTAC GCGCAGCAGT CCGCGCAGCA GTCGGCGTCC GCCTCCCAGT ACCACCAGTG   300
CCACAGCCTG CAGCCCGCCG CCAGCCCCAC GGGCAGCCTC GGCAGTCTGG GCTCCGCGCC   360
CCCGCTCTCG CACCACCACC ACCACCCGCA CCCGGCGCAC CACCAGCACC ACCAGCCCCA   420
GGCGCGCCGC GAGAGCAACC CCTTCACCGA AATAGCCATG AGCAGCTGCA GGTACAACGG   480
GGGCGTCATG CGGCCGCTCA GCAACTTGAG CGCGTCCCGC CGGAACCTCC ACGAGATGGA   540
CTCAGAGGCG CAGCCCCTGC AGCCCCCCGC GTCTGTCGGA GGAGGTGGCG GCGCGTCCTC   600
CCCGTCTGCA GACGCTGCCG CCGCCGCCGC TGTTTCGTCC TCAGCCCCCG AGATCGTGGT   660
GTCTAAGCCC GAGCACAACA ACTCCAACAA CCTGGCGCTC TATGGAACCG GCGGCGGAGG   720
CAGCACTGGA GGAGGCGGCG GCGGTGGAGG GAGCGGGCAC GGCAGCAGCA GTGGCACCAA   780
GTCCAGCAAA AAGAAAAACC AGAACATCGG CTACAAGCTG GGCCACCGGC GCGCCCTGTT   840
CGAAAAGCGC AAGCGGCTCA GCGACTACGC GCTCATCTTC GGCATGTTCG GCATCGTGGT   900
CATGGTCATC GAGACCGAGC TGTCGTGGGG CGCCTACGAC AAGGCGTCGC TGTATTCCTT   960
AGCTCTGAAA TGCCTTATCA GTCTCTCCAC GATCATCCTG CTCGGTCTGA TCATCGTGTA  1020
CCACGCCAGG GAAATACAGT TGTTCATGGT GGACAATGGA GCAGATGACT GGAGAATAGC  1080
CATGACTTAT GAGCGTATTT TCTTCATCTG CTTGGAAATA CTGGTGTGTG CTATTCATCC  1140
CATACCTGGG AATTATACAT TCACATGGAC GGCCCGGCTT GCCTTCTCCT ATGCCCCATC  1200
CACAACCACC GCTGATGTGG ATATTATTTT ATCTATACCA ATGTTCTTAA GACTCTATCT  1260
GATTGCCAGA GTCATGCTTT TACATAGCAA ACTTTTCACT GATGCCTCCT CTAGAAGCAT  1320
TGGAGCACTT AATAAGATAA ACTTCAATAC ACGTTTTGTT ATGAAGACTT TAATGACTAT  1380
ATGCCCAGGA ACTGTACTCT TGGTTTTTAG TATCTCATTA TGGATAATTG CCGCATGGAC  1440
TGTCCGAGCT TGTGAAAGGT ACCATGATCA ACAGGATGTT ACTAGCAACT TCCTTGGAGC  1500
GATGTGGTTG ATATCAATAA CTTTTCTCTC CATTGGTTAT GGTGACATGG TACCTAACAC  1560
ATACTGTGGA AAAGGAGTCT GCTTACTTAC TGGAATTATG GGTGCTGGTT GCACAGCCCT  1620
GGTGGTAGCT GTAGTGGCAA GGAAGCTAGA ACTTACCAAA GCAGAAAAAC ACGTGCACAA  1680
TTTCATGATG GATACTCAGC TGACTAAAAG AGTAAAAAAT GCAGCTGCCA ATGTACTCAG  1740
GGAAACATGG CTAATTTACA AAAATACAAA GCTAGTGAAA AAGATAGATC ATGCAAAAGT  1800
AAGAAAACAT CAACGAAAAT TCCTGCAAGC TATTCATCAA TTAAGAAGTG TAAAAATGGA  1860
GCAGAGGAAA CTGAATGACC AAGCAAACAC TTTGGTGGAC TTGGCAAAGA CCCAGAACAT  1920
CATGTATGAT ATGATTTCTG ACTTAAACGA AAGGAGTGAA GACTTCGAGA AGAGGATTGT  1980
TACCCTGGAA ACAAAACTAG AGACTTTGAT TGGTAGCATC CACGCCCTCC CTGGGCTCAT  2040
AAGCCAGACC ATCAGGCAGC AGCAGAGAGA TTTCATTGAG GCTCAGATGG AGAGCTACGA  2100
CAAGCACGTC ACTTACAATG CTGAGCGGTC CCGGTCCTCG TCCAGGAGGC GGCGGTCCTC  2160
TTCCACAGCA CCACCAACTT CATCAGAGAG TAGCTAGAAG AGAATAAGTT AACCACAAAA  2220
TAAGACTTTT TGCCATCATA TGGTCAATAT TTTAGCTTTT ATTGTAAAGC CCCTATGGTT  2280
CTAATCAGCG TTATCCGGGT TCTGATGTCA GAATCCTGGG AACCTGAACA CTAAGTTTTA  2340
GGCCAAAATG AGTGAAAACT CTTTTTTTTT CTTTCAGATG CACAGGGAAT GCACCTATTA  2400
TTGCTATATA GATTGTTCCT CCTGTAATTT CACTAACTTT TTATTCATGC ACTTCAAACA  2460
AACTTTACTA CTACATTATA TGATATATAA TAAAAAAAGT TAATTTCGGA
```

A214 Protein sequence:
Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus
Unigene number: Hs.98280
Probeset Accession #: AA418000
Protein Accession #: NP_067627
Signal sequence: none found
Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

WO03042661 [file://E:/WO03042661.pdf]

Calmodulin binding domain: 412-488
Cellular Localization: plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MSSCRYNGGV MRPLSNLSAS RRNLHEMDSE AQPLQPPASV GGGGGASSPS ADAAAAAAVS    60
SSAPEIVVSK PEHNNSNNLA LYGTGGGGST GGGGGGGGSG HGSSSGTKSS KKKNQNIGYK   120
LGHRRALPEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII   180
LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPIP GNYTFTWTAR   240
LAFSYAPSTT TADVDIILSI PMFLRLYLIA RVMLLHSKLF TDASSRSIGA LNKINFNTRF   300
VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQQD VTSNFLGAMW LISITFLSIG   360
YGDMVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNFM MDTQLTKRVK   420
NAAANVLRET WLIYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV   480
DLAKTQNIMY DMISDLNERS EDFEKRIVTL ETKLETLIGS IHALPGLISQ TIRQQQRDFI   540
EAQMESYDKH VTYNAERSRS SSRRRRSSST APPTSSESS
```

A215 DNA SEQUENCE:
Gene name: CGI-86 protein
Unigene number: Hs.109201
Probeset Accession #: AW161450
Nucleic Acid Accession #: NM_016029
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGCGGGC CGTCTTCTTC CCCCCGAGCT    60
GGGCGTGCGC GGCCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC   120
TGCTCCTGCT CTTGGTGCAG CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC   180
TATGGGCCGA GTGGCAGGGA CGACGCCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG   240
TGACTGGAGC CTCGAGTGGA ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACTAGGAG   300
TTTCTCTTGT GCTGTCAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC   360
TAGAGAATGG CAATTTAAAA GAAAAAGATA TACTTGTTTT GCCCCTTGAC CTGACCGACA   420
CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC   480
TGGTCAACAA TGGTGGAATG TCCCAGCGTT CTCTGTGCAT GGATACCAGC TTGGATGTCT   540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC   600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA   660
TATCTGTACC TCTTTCCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTTTTA   720
ATGGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCCAG   780
GACCTGTGCA ATCAAATATT GTGGAGAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG   840
GCAATAATGG AGACCAGTCC CACAAGATGA CAACCAGTCG TTGTGTGCGG CTGATGTTAA   900
TCAGCATGGC CAATGATTTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA   960
CATATTTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA  1020
AAAGGATTGA GAACTTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA  1080
AGACAAAACA TGACTGAAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA  1140
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT  1200
ACTTTTTAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA  1260
AGATTGCCAT GAATCTTGCA AA
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A216 Protein sequence:
Gene name: CGI-86 protein
Unigene number: Hs.109201
Probeset Accession #: AW161450
Protein Accession #: NP_057113
Signal sequence: 1-26
Transmembrane domains: 183-206, 221-243
Cellular Localization: plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MNWELLLWLL VLCALLLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS    60
GIGEELAYQL SKLGVSLVLS ARRVHELERV KRRCLENGNL KEKDILVLPL DLTDTGSHEA   120
ATKAVLQEFG RIDILVNNGG MSQRSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHMIER   180
KQGKIVTVNS ILGIISVPLS IGYCASKHAL RGFFNGLRTE LATYPGIIVS NICPGPVQSN   240
IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISEQP FLLVTYLWQY   300
MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD
```

A217 DNA SEQUENCE:
Gene name: Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)
Unigene number: Hs.27373
Probeset Accession #: F13036
Nucleic Acid Accession #: AC012478
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCGCGCCG TGCCGCTGCC CGCCCCGCTC CTGCCGCTGC TGCTGCTCGC GCTCCTGGCC    60
GCTCCCGCCG CCCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG   120
CGCGAGTCGC GGCCACCGCC CGGCCCCGGG CCCGGGAACA CCACCCGGTT TGGGTCTGGG   180
GCGGCGGGCG GCAGCGGCAG CTCCAGCTCC AACAGCAGTG GCGACGCCTT GGTGACCCGC   240
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ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGCGTTCGCC   300
TTTACCACCC TCCTCATCGC CTGCCTGCTG CTGCGCCTCT TCAGGTCGGG AAAGAGGTTA   360
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGA AATGGCGCCA   420
CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG   480
TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT   540
GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCCAGCAA GATGCAGTGG AAGGCCTGAT   600
GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAAGTTGG   660
TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCGT CGGAGGTGTT   720
GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC   780
TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC   840
TTTGGGCATC CCTTTAAAGT GCCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG   900
CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCATCT   960
GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT  1020
CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAACCATG  1080
AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGCACCTT TTGTGAAGAC  1140
AGAGCAGTGA CTAAGGTTCT CCAGGGTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA  1200
GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC  1260
ACCCATCCTG TCAGGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG  1320
AGGGTGTTTC GGCGTCCGCG GCAGTCTCTG CATGGCGGAG GGTCAGCGGG TACCGCAACT  1380
TGCCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA  1440
ATCTGTCTCC CCTGCTGTGC CGTGGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT  1500
GTCCTTGCGT CATTTGAGCA GAGCCCACAA AAGGCAGCTG CTGCCCACGG GGAGCCTGTC  1560
AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT  1620
GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCACGTGA GGATGTCACT  1680
CACCCTGGAG GAGACTTGGA TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG  1740
GATGGCAGAT GCCAGAAGAT GGTCCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA  1800
TGTGAGAGGC TCACAGGTTC CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT  1860
TCCCCCCGAC AGCCCCTGTT TCTGTCCAGG CCCTGA
```

A218 Protein sequence:

Gene name:	Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)
Unigene number:	Hs.27373
Probeset Accession #:	F13036
Protein Accession #:	FGENESH predicted
Signal sequence:	1-27
Transmembrane domains:	94-115, 448-469
Cellular Localization:	not determined

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1          11         21         31         41         51
|          |          |          |          |          |
MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG    60
AAGGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAFA FTTLLIACLL LRVFRSGKRL   120
KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGCQTLLTVP   180
VPPPFILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV   240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLLPP FGHPFKVPPT STPHGFRQLQ   300
LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLPN PWWHFSATGS PIKTLYTQTM   360
STLGLDVFCG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHHL RLLRECPPLS   420
THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK   480
ICLPCCAVEH LREAKRSSVT VLASFEQSPQ KAAAAHGEPV KRGPSGQLTR HTCPGWGITH   540
ANLQTIPDTQ GQEGPREDVT HPGGDLDGVA NFYLEEEGFQ DGRCQKMVLM SEEGPPSLTG   600
CERLTGSHHF SSHSKSWSFL SPRQPLFLSR P
```

A219 DNA SEQUENCE

Gene name:	selectin E (endothelial adhesion molecule 1)
Unigene number:	Hs.89546
Probeset Accession #:	M24736
Nucleic Acid Accession #:	NM_000450
Coding sequence:	1-1833 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA    60
GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT   120
CAGCAAAGGT ACACACACCT GGTTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC   180
TCCATATTGA GCTATTCACC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG   240
TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT   300
GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA   360
GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA   420
GCTGCCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT   480
TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAT TGTGAACTGT   540
ACAGCCCTGG AATCCCCTGA GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAAACTTC   600
AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG   660
ACCATGCAGT GTATGTCCTC TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT   720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCCTGGA   780
AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTTGA ACTAATGGGA   840
GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA   900
GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC   960
CCTGCTGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG  1020
TTGCAGGGAC CAGCCCAGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAATCCCA  1080
GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT  1140
CTTCCTAGTG CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG  1200
GGTTTTGTGT TGAAGGGATC CAAAAGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC  1260
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GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG  1320
GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCTTCAGC  1380
TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA  1440
TGGACAGAAG AGGTTCCTTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCCGGGA  1500
AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCCTGT  1560
CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG  1620
TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA  1680
CTTTCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA  1740
TGCTTACGGA AAGCAAAGAA ATTTGTTCCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC  1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA
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A220 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Protein Accession #: NP_000441
Signal sequence: 1-22
Transmembrane domains: 555-573
C-lectin domain: 23-139
Cellular Localization: plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRYTHLVAI QNKEEIEYLN    60
SILSYSPSYY WIGIRKVNNV WVWVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK   120
DVGMWNDERC SKKKLALCVT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC   180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV   240
ECDAVTNPAN GFVECFQNPG SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK   300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPAQVECT TQGQWTQQIP   360
VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN   420
EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ   480
WTEEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW   540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRK CLRKAKKFVP ASSCQSLESD   600
GSYQKPSYIL
```

Taxol Prostate

A221 DNA SEQUENCE

Gene name: ESTs; Liprin A2
Unigene number: Hs.306480
Probeset Accession #: N51002
Nucleic Acid Accession #: N51002
Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC    60
CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT   120
GAAAGGGATC GTCTTCTAGA CACCCTTCGG GAGACCCAGG AAAGCCTCTC ACTTGCCCAG   180
CAAAGACTTC AGGATGTCAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTCAGCC   240
CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA   300
CCGGAATTTG CTGCACTGAC AAAAGAATTA AATGCCTGCA GGGAACAACT TCTAGAAAAG   360
GAAGAAGAAA TCTCTGAACT TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT   420
TTGGAGTGCC TTGTGTCACG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA   480
GCCCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCACT GAAATCTTTG   540
TTTGAGCACC ACAAGGCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA   600
AGAGTCTCTG CACTGGAAGA AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCCTTGCGT   660
GAACAAAATG TTCATATACA AAGAAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA   720
CATCTTGAAG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTC CAATGGTTCT   780
ATAGACTCAA CCGATGAAAC TAGTCAAATA GTTGAACTAC AAGAATTGCT TGAAAAGCAA   840
AACTATGAAA TGGCCCAGAT GAAAGAACGT TTAGCAGCCC TTTCTTCCCG AGTGGGAGAG   900
GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATTA AAACAGAAGA AATGAACACC   960
AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAAGAATT  1020
ACAACCCTTG AAAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG  1080
AATGATAAAC TAGAAAATGA GTTAGCAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG  1140
AAAAACAGAC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG  1200
AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAACTGG CTCAGAGAAT TGCAGCCCTA  1260
ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAACGTA TGAGACATTT AGAGGGTCAA  1320
CTTGAAGAGA AGAATCAAGA ACTTCAAAGA GCTAGGCAAA GAGAGAAAAT GAATGAGGAG  1380
CATAACAAGA GATTATCGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCCTA  1440
CAACTACACT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAAGAA  1500
TCAGAAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAAG ATTAGCAGAA  1560
GAAATTGAAA AGCTGAGATC TGAACTTGAC CAATTGAAAA TGAGAACTGG CTCTTTAATT  1620
GAACCCACAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA  1680
TCCCTAGTGG ACAGCCAGTC TGATTACAGA ACAACTAAAG TAATAAGAAG ACCAAGGAGA  1740
GGCCGCATGG GTGTGCGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG  1800
AATAGAACTC AACAGATTGG AGTACTAAGC AGCCACCCTT TTGAAAGTGA CACTGAAATG  1860
TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTTAGCT CAATGGATCT TCTCTCTCCA  1920
AGTGGTCATT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GGATGCCATC  1980
AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGCG TGCTGAAGAA  2040
ATTGAAAATA GAGTGGCTAG TGTGAGCCTC GAAGGCCTGA ATTTGGCAAG GGTCCACCCA  2100
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GGTACCTCCA TTACTGCCTC TGTTACAGCT TCATCGCTGG CCAGTTCATC TCCCCCCAGT  2160
GGACACTCAA CTCCAAAGCT CACCCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA  2220
GTCATGACAC TGCCAAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCAGT TGTGGAAGAA  2280
GATGGTCGAG AGGACAAAGC AACAATTAAA TGTGAAACTT CTCCTCCTCC TACCCCTAGA  2340
GCCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA  2400
TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTTGGTAGTG CCAACAGCAG CCAAGACTCT  2460
CTTCACAAAG CCCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA  2520
AAAGAAAAAG CTCGACTTGG GCAGCTCCGA GGCTTTATGG AGACTGAAGC TGCAGCTCAG  2580
GAGTCCCTGG GGTTAGGCAA ACTCGGAACT CAAGCTGAGA AGGATCGAAG ACTAAAGAAA  2640
AAGCATGAAC TTCTTGAAGA AGCTCGGAGA AAGGGATTAC CTTTTGCCCA GTGGGATGGG  2700
CCAACTGTGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC  2760
TGCCGAGCCA ACGTGAAGAG TGGTGCCATC ATGTCTGCTT TATCTGACAC TGAGATCCAG  2820
AGAGAAATTG GAATCAGCAA TCCACTGCAT CGCTTAAAAC TTCGATTAGC AATCCAGGAG  2880
ATGGTTTCCC TAACAAGTCC TTCAGCTCCT CCAACATCTC GAACTCCTTC AGGCAACGTT  2940
TGGGTGACTC ATGAAGAAAT GGAAAATCTT GCAGCTCCAG CAAAAACGAA AGAATCTGAG  3000
GAAGGAAGCT GGGCCCAGTG TCCGGTTTTT CTACAGACCC TGGCTTATGG AGATATGAAT  3060
CATGAGTGGA TTGCAAATGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC  3120
TTTATGGAAT GCTTGGTAGA TGCAAGAATG TTAGATCACC TAACAAAAAA AGATCTCCGT  3180
GTCCATTTAA AAATGGTGGA TAGTTTCCAT CGAACAAGTT TACAATATGG AATTATGTGC  3240
TTAAAGAGGT TGAATTATGA CAGAAAAGAA CTAGAAAGAA GACGGGAAGC AAGCCAACAT  3300
GAAATAAAAG ACGTGTTGGT GTGGAGCAAT GACCGAATTA TTCGCTGGAT ACAAGCAATT  3360
GGACTTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC  3420
CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC  3480
ACCCAGGCAA GGCAGATTCT TGAAAGAGAA TACAATAACC TCTTGGCCCT GGGAACTGAA  3540
AGGCGACTGG ATGAAAGTGA TGACAAGAAC TTCAGACGTG GATCAACCTG GAGAAGGCAG  3600
TTTCCTCCTC GTGAAGTACA TGGAATCAGC ATGATGCCTG GGTCCTCAGA AACATTACCA  3660
GCTGGATTTA GGTTAACCAC AACCTCTGGG CAATCAAGAA AAATGACAAC AGATGTTGCT  3720
TCATCAAGAC TGCAGAGGTT AGACAACTCC ACTGTTCGCA CATACTCATG TCTCGAGTAA  3780
GCGGCCGCTT TAA
```

A222 Protein sequence:

Gene name:	ESTs; Liprin A2
Unigene number:	Hs.306480
Probeset Accession #:	N51002
Protein Accession #:	none found
Signal sequence:	none found
Transmembrane domains:	none found
AAA domain:	286-539
SAM domains:	895-964, 1017-1084, 1105-1177
Cellular Localization:	not determined

```
1          11         21         31         41         51
|          |          |          |          |          |
MMCEVMPTIN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLLDTLR ETQESLSLAQ    60
QRLQDVIYDR DSLQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEL NACREQLLEK   120
EEEISELKAE RNNTRLLLEH LECLVSRHER SLRMTVVKRQ AQSPSGVSSE VEVLKALKSL   180
FEHHKALDEK VRERLRVSLE RVSALEEELA AANQEIVALR EQNVHIQRKM ASSEGSTESE   240
HLEGMEPGQK VHEKRLSNGS IDSTDETSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE   300
VEQEAETARK DLIKTEEMNT KYQRDIREAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM   360
NDKLENELAN KEAILRQMEE KNRQLQERLE LAEQKLQQTM RKAETLPEVE AELAQRIAAL   420
TKAEERHGNI EERMRHLEGQ LEEKNQELQR ARQREKMNEE HNKRLSDTVD RLLTESNERL   480
QLHLKERMAA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKLRSELD QLKMRTGSLI   540
EPTIPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRRPRR GRMGVRRDEP KVKSLGDHEW   600
NRTQQIGVLS SHPFESDTEM SDIDDDDRET IFSSMDLLSP SGHSDAQTLA MMLQEQLDAI   660
NKEIRLIQEE KESTELRAEE IENRVASVSL EGLNLARVHP GTSITASVTA SSLASSSPPS   720
GHSTPKLTPR SPAREMDRMG VMTLPSDLRK HRRKIAVVEE DGREDKATIK CETSPPPTPR   780
ALRMTHTLPS SYHNDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKKGI KSSIGRLFGK   840
KEKARLQQLR GFMETEAAAQ ESLGLGKLGT QAEKDRRLKK KHELLEEARR KGLPFAQWDG   900
PTVVAWLELW LGMPAWYVAA CRANVKSGAI MSALSDTEIQ REIGISNPLH RLKLRLAIQE   960
MVSLTSPSAP PTSRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCPVF LQTLAYGDMN  1020
HEWIGNEWLP SLGLPQYRSY FMECLVDARM LDHLTKKDLR VHLKMVDSFH RTSLQYGIMC  1080
LKRLNYDRKE LERRREASQH EIKDVLVWSN DRIIRWIQAI GLREYANNIL ESGVHGSLIA  1140
LDENFDYSSL TLLLQIPTQN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ  1200
FPPREVHGIS MMPGSSETLP AGFRLTTTSG QSRKMTTDVA SSRLQRLDNS TVRTYSCLE
```

A223 DNA SEQUENCE

Gene name:	CDA14
Unigene number:	Hs.26813
Probeset Accession #:	N32912
Nucleic Acid Accession #:	NM_016570
Coding sequence:	1- 1134 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG    60
AAGGTTCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA   120
TTTACAACTA TGGCTTTATT AACCATAATG GAATTCTCAG TATATCAAGA TACATGGATG   180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT   240
ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTTAGC AGAAACAATG   300
GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG   360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT   420
CAAGATGTGA TATTTAAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA   480
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GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA   540
GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA   600
CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTTT CTCATAGAAT AGATCATTTG   660
TCTTTTGGAG AGCTTGTTCC AGCAATTATT AATCCTTTAG ATGGAACTGA AAAAATTGCT   720
ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA   780
TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAC   840
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT   900
ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTTGTAAG ACTCTGTGGT   960
ATTGTTGGAG GAATCTTTTC AACAACAGGC ATGTTACATG GAATTGGAAA ATTTATAGTT  1020
GAAATAATTT GCTGTCGTTT CAGACTTGGA TCCTATAAAC CTGTCAATTC TGTTCCTTTT  1080
GAGGATGGCC ACACAGACAA CCACTTACCT CTTTTAGAAA ATAATACACA TTGA
```

A224 Protein sequence:

Gene name: CDA14
Unigene number: Hs.26813
Probeset Accession #: N32912
Protein Accession #: NP_057654
Signal sequence: none found
Transmembrane domains: none found
Cellular Localization: nuclear

```
1          11         21         31         41         51
|          |          |          |          |          |
MRRLNRKKTL SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM    60
KYEYEVDKDF SSKLRINIDI TVAMKCQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ   120
KEWQRMLQLI QSRLQEEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK   180
VAGNFHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SFGELVPAII NPLDGTEKIA   240
IDHNQMFQYF ITVVPTKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL   300
MVTVTEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKFIV EIICCRFRLG SYKPVNSVPF   360
EDGHTDNHLP LLENNTH
```

Uterine

A225 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG    60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT   120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC   180
ACTTGGGTAC AAACTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA   240
ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC   300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT   360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA   420
GACCCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA   480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT   540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT   600
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAATA   660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAAATAAAT GTTTTTTAAA   720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAA
```

A226 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

```
1          11         21         31         41         51
|          |          |          |          |          |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK    60
PLMVIHHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM   120
FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL
```

A227 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
Unigene number: Hs.285529
Probeset Accession #: AA460530
Nucleic Acid Accession #: NM_003667
Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

```
1          11         21         31         41         51
|          |          |          |          |          |
GTGGCGGCAA CCGGCACCTC AGTCCCCGCC GCGCTTCTCC TCGCCGCCCA CGCCGTGGGG    60
TCAGGAACGC GGCGTCTGGC GCTGCAGACG CCCGCTGAGT TGCAGAAGCC CACGGAGCGG   120
CGCCCGGCGC GCCACGGCCC GTAGCAGTCC GGTGCTGCTC TCCGCCCGCG TCCGGCTCGT   180
GGCCCCCTAC TTCGGGCACC ATGGACACCT CCCGGCTCGG TGTGCTCCTG TCCTTGCCTG   240
TGCTGCTGCA GCTGGCGACC GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT   300
GCCCCACACA CTGTCATTGC GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG   360
ACCTGGGGCT CTCGGAGCTG CCTTCCAACC TCAGCGTCTT CACCTCCTAC CTAGACCTCA   420
GTATGAACAA CATCAGTCAG CTGCTCCCGA ATCCCCTGCC CAGTCTCCGC TTCCTGGAGG   480
AGTTACGTCT TGCGGGAAAC GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT   540
ACAGTCTTAA AGTTCTTATG CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC   600
TGCAGAATTT GCGAAGCCTT CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC   660
CCCCAAGCTG TTTCAGTGGC CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT   720
TAACAGAAAT CCCCGTCCAG GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG   780
CCCTGAACAA AATACACCAC ATACCAGACT ATGCCTTTGG AAACCTCTCC AGCTTGGTAG   840
TTCTACATCT CCATAACAAT AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC   900
ACAGCCTAGA GACTTTAGAT TTAAATTACA ATAACCTTGA TGAATTCCCC ACTGCAATTA   960
GGACACTCTC CAACCTTAAA GAACTAGGAT TTCATAGCAA CAATATCAGG TCGATACCTG  1020
AGAAAGCATT TGTAGGCAAC CCTTCTCTTA TTACAATACA TTTCTATGAC AATCCCATCC  1080
AATTTGTTGG GAGATCTGCT TTTCAACATT TACCTGAACT AAGAACACTG ACTCTGAATG  1140
GTGCCTCACA AATAACTGAA TTTCCTGATT TAACTGGAAC TGCAAACCTG GAGAGTCTGA  1200
CTTTAACTGG AGCACAGATC TCATCTCTTC CTCAAACCGT CTGCAATCAG TTACCTAATC  1260
TCCAAGTGCT AGATCTGTCT TACAACCTAT TAGAAGATTT ACCCAGTTTT TCAGTCTGCC  1320
AAAAGCTTCA GAAAATTGAC CTAAGACATA ATGAAATCTA CGAAATTAAA GTTGACACTT  1380
TCCAGCAGTT GCTTAGCCTC CGATCGCTGA ATTTGGCTTG GAACAAAATT GCTATTATTC  1440
ACCCCAATGC ATTTTCCACT TTGCCATCCC TAATAAAGCT GGACCTATCG TCCAACCTCC  1500
TGTCGTCTTT TCCTATAACT GGGTTACATG GTTTAACTCA CTTAAAATTA ACAGGAAATC  1560
ATGCCTTACA GAGCTTGATA TCATCTGAAA ACTTTCCAGA ACTCAAGGTT ATAGAAATGC  1620
CTTATGCTTA CCAGTGCTGT GCATTTGGAG TGTGTGAGAA TGCCTATAAG ATTTCTAATC  1680
AATGGAATAA AGGTGACAAC AGCAGTATGG ACGACCTTCA TAAGAAAGAT GCTGGAATGT  1740
TTCAGGCTCA AGATGAACGT GACCTTGAAG ATTTCCTGCT TGACTTTGAG GAAGACCTGA  1800
AAGCCCTTCA TTCAGTGCAG TGTTCACCTT CCCCAGGCCC CTTCAAACCC TGTGAACACC  1860
TGCTTGATGG CTGGCTGATC AGAATTGGAG TGTGGACCAT AGCAGTTCTG GCACTTACTT  1920
GTAATGCTTT GGTGACTTCA ACAGTTTTCA GATCCCCTCT GTACATTTCC CCCATTAAAC  1980
TGTTAATTGG GGTCATCGCA GCAGTGAACA TGCTCACGGG AGTCTCCAGT GCCGTGCTGG  2040
CTGGTGTGGA TGCGTTCACT TTTGGCAGCT TTGCACGACA TGGTGCCTGG TGGGAGAATG  2100
GGGTTGGTTG CCATGTCATT GGTTTTTTGT CCATTTTTGC TTCAGAATCA TCTGTTTTCC  2160
TGCTTACTCT GGCAGCCCTG GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTTGAAA  2220
CGAAAGCTCC ATTTTCTAGC CTGAAAGTAA TCATTTTGCT CTGTGCCCTG CTGGCCTTGA  2280
CCATGGCCGC AGTTCCCCTG CTGGGTGGCA GCAAGTATGG CGCCTCCCCT CTCTGCCTGC  2340
CTTTGCCTTT TGCGGAGCCC AGCACCATGG GCTACATGGT CGCTCTCATC TTGCTCAATT  2400
CCCTTTGCTT CCTCATGATG ACCATTGCCT ACACCAAGCT CTACTGCAAT TTGGACAAGG  2460
GAGACCTGGA GAATATTTGG GACTGCTCTA TGGTAAAACA CATTGCCCTG TTGCTCTTCA  2520
CCAACTGCAT CCTAAACTGC CCTGTGGCTT TCTTGTCCTT CTCCTCTTTA ATAAACCTTA  2580
CATTTATCAG TCCTGAAGTA ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTTCCTGCAT  2640
GTCTCAATCC CCTTCTCTAC ATCTTGTTCA ATCCTCACTT TAAGGAGGAT CTGGTGAGCC  2700
TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAACT  2760
CTGATGATGT CGAAAAACAG TCCTGTGACT CAACTCAAGC CTTGGTAACC TTTACCAGCT  2820
CCAGCATCAC TTATGACCTG CCTCCCAGTT CCGTGCCATC ACCAGCTTAT CCAGTGACTG  2880
AGAGCTGCCA TCTTTCCTCT GTGGCATTTG TCCCATGTCT CTAATTAATA TGTGAAGGAA  2940
AATGTTTTCA AAGGTTGAGA ACCTGAAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA  3000
ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA
```

A228 Protein sequence

Gene name:	G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
Unigene number:	Hs.285529
Protein Accession #:	NP_003658.1
Signal sequence:	1-22
Transmembrane domains:	557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
Cellular Localization:	plasma membrane

```
1          11         21         31         41         51
|          |          |          |          |          |
MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL    60
PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLM   120
LQNNQLRHVP TEALQNLRSL QSLRLDANHI SYVPPSCFSG LHSLRHLWLD DNALTEIPVQ   180
AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD   240
LNYNNLDEFP TAIRTLSNLK ELGFHSNNIR SIPEKAFVGN PSLITIHFYD NPIQFVGRSA   300
FQHLPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS   360
YNLLEDLPSF SVCQKLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIIHPNAFST   420
LPSLIKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPELKV IEMPYAYQCC   480
AFGVCENAYK ISNQWNKGDN SSMDDLHKKD AGMFQAQDER DLEDFLLDFE EDLKALHSVQ   540
CSPSPGPFKP CEHLLDGWLI RIGVWTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA   600
AVNMLTGVSS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLLTLAAL   660
ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEP   720
STMGYMVALI LLNSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC   780
PVAFLSFSSL INLTFISPEV IKFILLVVVP LPACLNPLLY ILFNPHFKED LVSLRKQTYV   840
WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS   900
VAFVPCL
```

Table 75: See Table 1

Table 76A depicts Seq ID No; UnigeneID; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in Table 76A is linked by SeqID No to Table 78.

Seq ID No:	Sequence ID No for sequences in table
Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
Pred Subcell Loc:	Predicted sub-cellular localization

Seq ID No	Pkey	ExAccn	UnigeneID	Unigene Title	Pred Subcell Loc
Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	plasma membrane
Seq ID 3 & 4	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	plasma membrane
Seq ID 5 & 6	429423	AI016712	Hs.287797	integrin, beta 1 (fibronectin receptor,	plasma membrane
Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
Seq ID 17 & 18	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	plasma membrane
Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
Seq ID 35 & 36	423961	D13666	Hs.136348	periostin (OSF-2os)	secreted
Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
Seq ID 39 & 40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 41 & 42	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 43 & 44	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	secreted
Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	secreted
Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
Seq ID 57 & 58	411789	AF245505	Hs.72157	Adlican	secreted
Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
Seq ID 63 & 64	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	secreted
Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 73 & 74	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	plasma membrane
Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
Seq ID 115 & 116	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-li	intracell
Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
Seq ID 119 & 120	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 121 & 122	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 123 & 124	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
Seq ID 127 & 128	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	plasma membrane
Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
Seq ID 131 & 132	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	secreted
Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
Seq ID 151 & 152	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	plasma membrane
Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
Seq ID 157 & 158	413324	V00571	Hs.75294	corticotropin releasing hormone	secreted
Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	secreted
Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	secreted
Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
Seq ID 170 & 171	425721	AC002115	Hs.159309	uroplakin 1A	plasma membrane
Seq ID 172 & 173	420370	Y13645	Hs.97234	uroplakin 2	plasma membrane
Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	plasma membrane
Seq ID 176 & 177	402075			ENSP00000251056*:Plasma membrane calcium	secreted
Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
Seq ID 190 & 191	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	plasma membrane
Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
Seq ID 194 & 195	404875			NM_022819*:Homo sapiens phospholipase A2	intracell
Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	plasma membrane
Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
Seq ID 219 & 220	405932			C15000305:gi|3806122|gb|AAC69198.1| (AF0	intracell
Seq ID 221 & 222	405932			C15000305:gi|3806122|gb|AAC69198.1| (AF0	intracell
Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
Seq ID 233 & 234	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	secreted
Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
Seq ID 249 & 250	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	plasma membrane
Seq ID 251	429466	M85835	Hs.12827	ESTs	
Seq ID 252	429466	M85835	Hs.12827	ESTs	
Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
Seq ID 255 & 256	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	secreted
Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	plasma membrane
Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
Seq ID 265 & 266	444471	AB020684	Hs.11217	KIAA0877 protein	plasma membrane
Seq ID 267 & 268	409395	U46745	Hs.336678	dystrobrevin, alpha	secreted
Seq ID 269 & 270	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
Seq ID 271 & 272	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	plasma membrane
Seq ID 273	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
Seq ID 274	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
Seq ID 275 & 276	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	plasma membrane
Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	secreted
Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	plasma membrane
Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	plasma membrane
Seq ID 283 & 284	404049			NM_018937*:Homo sapiens protocadherin be	plasma membrane
Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
Seq ID 287 & 288	404029			NM_018936*:Homo sapiens protocadherin be	plasma membrane
Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospha	plasma membrane

Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	plasma membrane
Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
Seq ID 311 & 312	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	secreted
Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
Seq ID 345 & 346	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	secreted
Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
Seq ID 349 & 350	417542	J04129	Hs.82269	progestagen-associated endometrial prote	secreted
Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
Seq ID 359 & 360	418462	BE001596	Hs.85266	integrin, beta 4	plasma membrane
Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	secreted
Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
Seq ID 429 & 430	404682			C9001188*:gi|12738842|ref|NP_073725.1| p	secreted
Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	plasma membrane
Seq ID 435 & 436	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
Seq ID 437 & 438	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
Seq ID 439 & 440	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
Seq ID 445 & 446	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrimin	plasma membrane
Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	secreted
Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
Seq ID 469 & 470	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10???	plasma membrane
Seq ID 471 & 472	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10???	plasma membrane
Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
Seq ID 479 & 480	448243	AW369771	Hs.52620	integrin, beta 8	plasma membrane
Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
Seq ID 483 & 484	428187	AI687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	secreted
Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	secreted
Seq ID 499 & 500	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	secreted
Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
Seq ID 507 & 508	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	secreted
Seq ID 511 & 512	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	intracell
Seq ID 513	431989	AW972870	Hs.291069	ESTs	
Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (	secreted
Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	secreted
Seq ID 541 & 542	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	secreted
Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	plasma membrane
Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
Seq ID 547 & 548	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	plasma membrane
Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
Seq ID 561 & 562	418396	AI765805	Hs.26691	ESTs	plasma membrane
Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
Seq ID 565 & 566	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
Seq ID 569 & 570	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
Seq ID 571 & 572	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
Seq ID 575 & 576	413435	X51405	Hs.75360	carboxypeptidase E	secreted
Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	plasma membrane
Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
Seq ID 585 & 586	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
Seq ID 587 & 588	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	plasma membrane
Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	intracell
Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 617 & 618	422424	AI186431	Hs.296638	prostate differentiation factor	secreted
Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
Seq ID 621 & 622	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	secreted
Seq ID 623 & 624	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	plasma membrane
Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
Seq ID 627 & 628	425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

Table 76C:

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59968
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 77 provides Pkey; Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

Seq ID No:	Sequence ID No for sequences in table
Pkey:	Unique Eos probeset identifier number
Disease Indications:	Diseases designated for coverage as described in Table 1
Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)

Seq ID No	Pkey	Disease Indications	PreferredUtility
Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung	Ab, sm, imaging
Seq ID 5 & 6	429423	angiogenesis	Ab, sm
Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
Seq ID 15 & 16	407836	angiogenesis	CTL
Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab,CTL, imaging
Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab,CTL, imaging
Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab,sm, CTL, imaging
Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab,sm, CTL, imaging
Seq ID 69 & 70	416636	breast, pancreas, uterine	Ab,sm, CTL, imaging
Seq ID 71 & 72	416636	breast, pancreas, uterine	Ab,sm, CTL, imaging
Seq ID 73 & 74	409079	breast, prostate	Ab,sm, CTL, imaging
Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab,sm, CTL, imaging
Seq ID 79 & 80	451398	breast, ovarian	CTL
Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
Seq ID 83 & 84	421524	breast	Ab,sm, CTL, imaging
Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
Seq ID 95 & 96	325372	breast	CTL
Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab,sm, CTL, imaging
Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
Seq ID 115 & 116	428179	breast	sm, CTL
Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab,CTL, imaging
Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

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Seq ID 149 & 150	104888	colon, stomach, uterine	Ab, imaging
Seq ID 151 & 152	420159	bladder, stomach	Ab, sm, CTL, imaging
Seq ID 153 & 154	422330	pancreas, colon, bladder	Ab,sm, CTL, imaging, diagnostic
Seq ID 155 & 156	452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
Seq ID 157 & 158	413324	bladder	Ab, sm, CTL, diagnostic
Seq ID 159 & 160	412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
Seq ID 161 & 162	416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
Seq ID 163 & 164	407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
Seq ID 165	402230	bladder	sm, CTL
Seq ID 166 & 167	402230	bladder	sm, CTL
Seq ID 168 & 169	432829	bladder	CTL
Seq ID 170 & 171	425721	bladder	Ab, imaging
Seq ID 172 & 173	420370	bladder	Ab, CTL, imaging
Seq ID 174 & 175	437852	bladder, lung	Ab, sm, CTL, imaging
Seq ID 176 & 177	402075	bladder, lung, head & neck, cervical	diagnostic
Seq ID 178 & 179	421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
Seq ID 180 & 181	451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
Seq ID 182 & 183	451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
Seq ID 184 & 185	451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
Seq ID 186 & 187	408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
Seq ID 188 & 189	422282	bladder, lung, head & neck	CTL, diagnostic
Seq ID 190 & 191	425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
Seq ID 192 & 193	439738	bladder, lung, cervical	Ab, sm, CTL, imaging
Seq ID 194 & 195	404875	bladder	sm, CTL
Seq ID 196 & 197	425883	bladder, pancreas	Ab,CTL, imaging
Seq ID 198 & 199	404977	bladder, ovarian	Ab, sm, CTL, diagnostic
Seq ID 200 & 201	420876	pancreas, bladder	Ab,sm, CTL, imaging
Seq ID 202 & 203	427747	bladder, lung, ovarian, stomach	sm, CTL
Seq ID 204 & 205	420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
Seq ID 206 & 207	446673	bladder	sm, CTL
Seq ID 208	437553	bladder	Ab,CTL, imaging
Seq ID 209 & 210	437553	bladder	Ab,CTL, imaging
Seq ID 211 & 212	437553	bladder	Ab,CTL, imaging
Seq ID 213 & 214	426900	bladder, prostate	Ab,CTL, imaging
Seq ID 215 & 216	426900	bladder, prostate	Ab,CTL, imaging
Seq ID 217 & 218	426900	bladder, prostate	Ab,CTL, imaging
Seq ID 219 & 220	405932	bladder, lung, head & neck, cervical	sm
Seq ID 221 & 222	405932	bladder, lung, head & neck, cervical	sm
Seq ID 223 & 224	424008	bladder, head & neck, stomach, cervical	Ab,sm, CTL, imaging
Seq ID 225 & 226	424008	bladder, head & neck, stomach, cervical	Ab,sm, CTL, imaging
Seq ID 227 & 228	424008	bladder, head & neck, stomach, cervical	Ab,sm, CTL, imaging
Seq ID 229 & 230	444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
Seq ID 231 & 232	421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, CTL, diagnostic
Seq ID 233 & 234	417079	bladder, lung, head & neck, cervical	Ab, diagnostic
Seq ID 235 & 236	412986	glioblastoma	Ab,sm, CTL, imaging
Seq ID 237 & 238	412986	glioblastoma	Ab,sm, CTL, imaging
Seq ID 239 & 240	412986	glioblastoma	Ab,sm, CTL, imaging
Seq ID 241 & 242	447072	glioblastoma, pancreas	sm, CTL
Seq ID 243 & 244	419723	glioblastoma	Ab, CTL, diagnostic
Seq ID 245 & 246	419723	glioblastoma	Ab,sm, CTL, imaging
Seq ID 247 & 248	430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
Seq ID 249 & 250	456759	glioblastoma	Ab,sm, CTL, imaging
Seq ID 251	429466	glioblastoma, uterine	
Seq ID 252	429466	glioblastoma, uterine	
Seq ID 253 & 254	419721	glioblastoma, lung	Ab,sm, CTL, imaging
Seq ID 255 & 256	407034	glioblastoma	Ab, CTL, diagnostic
Seq ID 257 & 258	413472	glioblastoma	Ab,sm, CTL, imaging
Seq ID 259 & 260	438380	glioblastoma	Ab, CTL, diagnostic, imaging
Seq ID 261 & 262	425271	glioblastoma	Ab, CTL, diagnostic
Seq ID 263 & 264	419704	glioblastoma	sm, CTL
Seq ID 265 & 266	444471	glioblastoma, lung, colon	Ab,sm, CTL, imaging
Seq ID 267 & 268	409395	glioblastoma	Ab, CTL, diagnostic
Seq ID 269 & 270	413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
Seq ID 271 & 272	433800	glioblastoma, lung	Ab, CTL, imaging
Seq ID 273	458435	glioblastoma	
Seq ID 274	458435	glioblastoma	
Seq ID 275 & 276	424343	glioblastoma, ovarian, uterine	Ab,sm, CTL, imaging
Seq ID 277 & 278	424998	glioblastoma	Ab, CTL, diagnostic
Seq ID 279 & 280	412709	glioblastoma	Ab,sm, CTL, imaging
Seq ID 281 & 282	435615	glioblastoma	Ab,sm, CTL, imaging
Seq ID 283 & 284	404049	glioblastoma	Ab,sm, CTL, imaging
Seq ID 285 & 286	418932	glioblastoma	Ab,sm, CTL, imaging
Seq ID 287 & 288	404029	glioblastoma	Ab,sm, CTL, imaging
Seq ID 289 & 290	436480	glioblastoma	sm, CTL
Seq ID 291 & 292	452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
Seq ID 293 & 294	452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
Seq ID 295 & 296	436895	breast, renal, ovarian, glioblastoma	Ab,sm, imaging
Seq ID 297 & 298	421471	renal	Ab,sm, CTL, imaging
Seq ID 299 & 300	428296	renal	Ab,sm, CTL, imaging
Seq ID 301 & 302	423508	renal, colon	Ab, CTL, imaging
Seq ID 303 & 304	450001	renal, lung	Ab,sm, CTL, imaging
Seq ID 305 & 306	410407	renal, lung, colon, stomach, ovarian, uterine	Ab,sm, CTL, imaging
Seq ID 307 & 308	453496	renal, prostate	Ab,sm, CTL, imaging

Seq ID 309 & 310	420737	renal	Ab,sm, CTL, imaging
Seq ID 311 & 312	309931	lung	Ab,sm, CTL, imaging
Seq ID 313 & 314	412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
Seq ID 315 & 316	417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
Seq ID 317 & 318	430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
Seq ID 319 & 320	413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
Seq ID 321 & 322	425650	lung, head & neck, cervical, bladder	Ab, imaging
Seq ID 323 & 324	423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
Seq ID 325 & 326	418663	lung, bladder, head & neck, cervical	Ab, imaging
Seq ID 327 & 328	418663	lung, bladder, head & neck, cervical	Ab, imaging
Seq ID 329 & 330	429610	lung	CTL, diagnostic
Seq ID 331 & 332	406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
Seq ID 333 & 334	431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
Seq ID 335 & 336	422158	head & neck, bladder, lung, cervical, stomach	diagnostic
Seq ID 337 & 338	431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
Seq ID 339 & 340	437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
Seq ID 341 & 342	428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
Seq ID 343 & 344	429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
Seq ID 345 & 346	417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
Seq ID 347 & 348	431009	lung, bladder, head & neck	Ab, sm, imaging
Seq ID 349 & 350	417542	lung	CTL, diagnostic
Seq ID 351 & 352	449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
Seq ID 353 & 354	410555	lung	Ab, sm, imaging
Seq ID 355 & 356	410555	lung	Ab, sm, imaging
Seq ID 357 & 358	424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
Seq ID 359 & 360	418462	lung, bladder	Ab, imaging
Seq ID 361 & 362	410274	lung, renal	diagnostic
Seq ID 363 & 364	439606	lung, bladder, head & neck, cervical .	Ab,sm, imaging
Seq ID 365 & 366	404877	lung, bladder	CTL
Seq ID 367 & 368	444781	lung, bladder, head & neck, cervical	Ab, imaging
Seq ID 369 & 370	109424	bladder, lung	Ab, sm, CTL, imaging
Seq ID 371 & 372	415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
Seq ID 373 & 374	415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
Seq ID 375 & 376	415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
Seq ID 377 & 378	415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
Seq ID 379 & 380	415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
Seq ID 381 & 382	415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
Seq ID 383 & 384	421817	lung, cervical, head & neck & bladder	Ab,sm, CTL, imaging
Seq ID 385 & 386	418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
Seq ID 387 & 388	418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
Seq ID 389 & 390	409420	lung, head & neck, pancreas, stomach, cervical, bladder	CTL, diagnostic
Seq ID 391 & 392	332180	lung	Ab, sm, imaging
Seq ID 393 & 394	408790	lung	Ab,sm, CTL, imaging
Seq ID 395 & 396	408790	lung	Ab,sm, CTL, imaging
Seq ID 397 & 398	439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, imaging
Seq ID 399 & 400	409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
Seq ID 401 & 402	428969	lung, cervical	Ab, CTL, diagnostic
Seq ID 403 & 404	428969	lung, cervical	Ab, CTL, diagnostic
Seq ID 405 & 406	428969	lung, cervical	Ab, CTL, diagnostic
Seq ID 407 & 408	428969	lung, cervical	Ab, CTL, diagnostic
Seq ID 409 & 410	450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
Seq ID 411 & 412	450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
Seq ID 413 & 414	414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
Seq ID 415 & 416	407944	lung, head & neck	Ab, sm, imaging
Seq ID 417 & 418	407944	lung, head & neck	Ab, sm, imaging
Seq ID 419 & 420	428486	pancreas	Ab, CTL, diagnostic
Seq ID 421 & 422	457489	pancreas, prostate, lung	Ab, CTL, diagnostic
Seq ID 423 & 424	432874	pancreas, stomach	Ab, CTL, diagnostic
Seq ID 425 & 426	445891	stomach, pancreas, ovarian	Ab, CTL, imaging
Seq ID 427 & 428	445891	stomach, pancreas, ovarian	Ab, CTL, Imaging
Seq ID 429 & 430	404682	pancreas	Ab, CTL, diagnostic
Seq ID 431 & 432	429547	pancreas, head & neck, lung, ovarian	Ab, CTL, diagnostic
Seq ID 433 & 434	425921	stomach, pancreas	Ab,sm, CTL, imaging
Seq ID 435 & 436	407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
Seq ID 437 & 438	407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
Seq ID 439 & 440	407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
Seq ID 441 & 442	432596	pancreas, breast	CTL
Seq ID 443 & 444	444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
Seq ID 445 & 446	423685	pancreas, uterine, colon	CTL
Seq ID 447 & 448	428392	pancreas	Ab, CTL, diagnostic
Seq ID 449 & 450	429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
Seq ID 451 & 452	448030	pancreas, renal and stomach,	Ab,sm, Imaging
Seq ID 453 & 454	422109	pancreas, lung, colon	Ab, CTL, diagnostic
Seq ID 455 & 456	419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
Seq ID 457 & 458	449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
Seq ID 459 & 460	427333	pancreas, colon	Ab, sm, imaging
Seq ID 461 & 462	417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
Seq ID 463 & 464	419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
Seq ID 465 & 466	431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
Seq ID 467 & 468	413554	pancreas, glioblastoma	Ab, CTL, diagnostic
Seq ID 469 & 470	452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
Seq ID 471 & 472	452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
Seq ID 473 & 474	426322	pancreas, bladder, stomach	Ab, diagnostic

Seq ID 475 & 476	429010	pancreas	sm, CTL
Seq ID 477 & 478	431462	pancreas, lung, glioblastoma	Ab, diagnostic
Seq ID 479 & 480	448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab,sm, imaging
Seq ID 481 & 482	426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
Seq ID 483 & 484	428187	ovarian, uterine, colon, stomach	Ab,sm, CTL, imaging
Seq ID 485 & 486	428579	ovarian, Ewing, uterine, pancreas	Ab,sm, CTL, imaging
Seq ID 487 & 488	428579	ovarian, Ewing, uterine, pancreas	Ab,sm, CTL, imaging
Seq ID 489 & 490	428579	ovarian, Ewing, uterine, pancreas	Ab,sm, CTL, imaging
Seq ID 491 & 492	428579	ovarian, Ewing, uterine, pancreas	Ab,sm, CTL, imaging
Seq ID 493 & 494	445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
Seq ID 495 & 496	422278	ovarian, head & neck, bladder, cervical, lung	Ab,sm, imaging
Seq ID 497 & 498	424620	ovarian	Ab, CTL, diagnostic
Seq ID 499 & 500	406400	ovarian, uterine	Ab, CTL, diagnostic
Seq ID 501 & 502	431130	ovarian, uterine	Ab, CTL, diagnostic
Seq ID 503 & 504	420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
Seq ID 505 & 506	428450	ovarian, cervical, pancreas, lung	sm
Seq ID 507 & 508	446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
Seq ID 509 & 510	436982	ovarian, fibrosis	Ab, CTL, diagnostic
Seq ID 511 & 512	453392	ovarian, lung, glioblastoma	CTL
Seq ID 513	431989	ovarian	
Seq ID 514	439820	ovarian, uterine, cervical, breast, prostate	
Seq ID 515 & 516	409178	ovarian, breast	Ab, CTL, diagnostic
Seq ID 517 & 518	426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
Seq ID 519 & 520	421478	ovarian, bladder	Ab, CTL, imaging
Seq ID 521 & 522	421478	ovarian, bladder	Ab, CTL, imaging
Seq ID 523 & 524	425776	ovarian, uterine, lung	Ab,sm, CTL, imaging
Seq ID 525 & 526	425776	ovarian, uterine, lung	Ab,sm, CTL, imaging
Seq ID 527 & 528	452097	ovarian	Ab, sm, diagnostic
Seq ID 529 & 530	416530	ovarian, uterine	Ab, CTL, diagnostic
Seq ID 531 & 532	431515	ovarian, prostate, lung	Ab,sm, CTL, imaging
Seq ID 533 & 534	419452	ovarian, prostate, lung, breast, uterine	Ab,sm, CTL, imaging
Seq ID 535 & 536	412078	ovarian	CTL
Seq ID 537 & 538	412078	ovarian	CTL
Seq ID 539 & 540	411773	ovarian	Ab, sm, CTL, diagnostic
Seq ID 541 & 542	407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
Seq ID 543 & 544	431616	prostate, pancreas, colon	Ab,sm, CTL, imaging
Seq ID 545 & 546	452792	prostate, uterine, breast	Ab, CTL, imaging
Seq ID 547 & 548	400294	prostate, taxol prostate	Ab,sm, CTL, imaging
Seq ID 549 & 550	432653	prostate, lung	Ab,sm, CTL, imaging
Seq ID 551 & 552	432653	prostate, lung	Ab,sm, CTL, imaging
Seq ID 553 & 554	432653	prostate, lung	Ab,sm, CTL, imaging
Seq ID 555 & 556	432653	prostate, lung	Ab,sm, CTL, imaging
Seq ID 557 & 558	400290	prostate, colon	Ab,sm, CTL, imaging
Seq ID 559 & 560	410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
Seq ID 561 & 562	418396	prostate	Ab,sm, CTL, imaging
Seq ID 563 & 564	451027	prostate, uterine, glioblastoma	Ab,sm, CTL, imaging
Seq ID 565 & 566	446057	prostate	Ab,sm, CTL, imaging
Seq ID 567 & 568	433466	prostate	Ab, CTL, diagnostic
Seq ID 569 & 570	453370	prostate	Ab,sm, CTL, imaging
Seq ID 571 & 572	453370	prostate	Ab,sm, CTL, imaging
Seq ID 573 & 574	414569	prostate	Ab,sm, CTL, imaging
Seq ID 575 & 576	413435	prostate, glioblastoma, pancreas	Ab, sm, diagnostic
Seq ID 577 & 578	426501	prostate, breast, glioblastoma, lung	Ab, CTL, imaging
Seq ID 579 & 580	448999	prostate, glioblastoma	Ab,sm, CTL, imaging
Seq ID 581 & 582	408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab,sm, CTL, imaging
Seq ID 583 & 584	412628	prostate	Ab, CTL, diagnostic
Seq ID 585 & 586	403047	prostate, bladder, colon	Ab,sm, CTL, imaging
Seq ID 587 & 588	403047	prostate, bladder, colon	Ab,sm, CTL, imaging
Seq ID 589 & 590	408430	prostate	Ab,sm, CTL, imaging
Seq ID 591 & 592	445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
Seq ID 593 & 594	451982	prostate, bladder	CTL
Seq ID 595 & 596	427958	prostate, glioblastoma	Ab,sm, CTL, imaging
Seq ID 597 & 598	421887	prostate	Ab, CTL, imaging
Seq ID 599 & 600	425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
Seq ID 601 & 602	432101	prostate, pancreas	Ab,sm, imaging
Seq ID 603 & 604	407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab,sm, imaging
Seq ID 605 & 606	416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
Seq ID 607 & 608	416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
Seq ID 609 & 610	131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
Seq ID 611 & 612	131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
Seq ID 613 & 614	131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
Seq ID 615 & 616	131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
Seq ID 617 & 618	422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, CTL, diagnostic
Seq ID 619 & 620	428970	stomach, pancreas, colon	Ab,sm, imaging
Seq ID 621 & 622	428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, diagnostic
Seq ID 623 & 624	439018	uterine, stomach, prostate	Ab,sm, CTL, imaging
Seq ID 625 & 626	420610	uterine, ovarian endometrioid, lung	CTL
Seq ID 627 & 628	425723	ovarian endometrioid, uterine, colon	Ab, CTL, diagnostic
Seq ID 629 & 630	456652	uterine, ovarian	CTL
Seq ID 631 & 632	418281	uterine, ovarian	Ab, CTL, diagnostic
Seq ID 633 & 634	429903	lung	sm

Table 78

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001400
Coding sequence: 251..1399

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AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT  180
CTCGCCTCGC CCTCTAGCGT TCGTCTGGAG TAGCGCCACC CCGGCTTCCT GGGGACACAG  240
GGTTGGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCCACCGCA GCTCGGTCTC  300
TGACTACGTC AACTATGATA TCATCGTCCG GCATTACAAC TACACGGGAA AGCTGAATAT  360
CAGCGCGGAC AAGGAGAACA GCATTAAACT GACCTCGGTG GTGTTCATTC TCATCTGCTG  420
CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCCA  480
CCGACCCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTTGG CAGGAGTAGC  540
CTACACAGCT AACCTGCTCT TGTCTGGGGC CACCACCTAC AAGCTCACTC CCGCCCAGTG  600
GTTTCTGCGG GAAGGGAGTA TGTTTGTGGC CCTGTCAGCC TCCGTGTTCA GTCTCCTCGC  660
CATCGCCATT GAGCGCTATA TCACAATGCT GAAAATGAAA CTCCACAACG GGAGCAATAA  720
CTTCCGCCTC TTCCTGCTAA TCAGCGCCTG CTGGGTCATC TCCCTCATCC TGGGTGGCCT  780
GCCTATCATG GGCTGGAACT GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCCGCT  840
CTACCACAAG CACTATATCC TCTTCTGCAC CACGGTCTTC ACTCTGCTTC TGCTCTCCAT  900
CGTCATTCTG TACTGCAGAA TCTACTCCTT GGTCAGGACT CGGAGCCGCC GCCTGACGTT  960
CCGCAAGAAC ATTTCCAAGG CCAGCCGCAG CTCTGAGAAG TCGCTGGCGC TGCTCAAGAC 1020
CGTAATTATC GTCCTGAGCG TCTTCATCGC CTGCTGGGCA CCGCTCTTCA TCCTGCTCCT 1080
GCTGGATGTG GGCTGCAAGG TGAAGACCTG TGACATCCTC TTCAGAGCGG AGTACTTCCT 1140
GGTGTTAGCT GTGCTCAACT CCGGCACCAA CCCCATCATT TACACTCTGA CCAACAAGGA 1200
GATGCGTCGG GCCTTCATCC GGATCATGTC CTGCTGCAAG TGCCCGAGCG GAGACTCTGC 1260
TGGCAAATTC AAGCGACCCA TCATCGCCGG CATGGAATTC AGCCGCAGCA AATCGGACAA 1320
TTCCTCCCAC CCCCAGAAAG ACGAAGGGGA CAACCCAGAG ACCATTATGT CTTCTGGAAA 1380
CGTCAACTCT TCTTCCTAGA ACTGGAAGCT GTCCACCCAC CGGAAGCGCT CTTTACTTGG 1440
TCGCTGGCCA CCCCAGTGTT TGGAAAAAAA TCTCTGGGCT TCGACTGCTG CCAGGGAGGA 1500
GCTGCTGCAA GCCAGAGGGA GGAAGGGGGA GAATACGAAC AGCCTGGTGG TGTCGGGTGT 1560
TGGTGGGTAG AGTTAGTTCC TGTGAACAAT GCACTGGGAA GGGTGGAGAT CAGGTCCCGG 1620
CCTGGAATAT ATATTCTACC CCCCTGGAGC TTTGATTTTG CACTGAGCCA AAGGTCTAGC 1680
ATTGTCAAGC TCCTAAAGGG TTCATTTGGC CCCTCCTCAA AGACTAATGT CCCCATGTGA 1740
AAGCGTCTCT TTGTCTGGAG CTTTGAGGAG ATGTTTTCCT TCACTTTAGT TTCAAACCCA 1800
AGTGAGTGTG TGCACTTCTG CTTCTTTAGG GATGCCCTGT ACATCCCACA CCCCACCCTC 1860
CCTTCCCTTC ATACCCCTCC TCAACGTTCT TTTACTTTAT ACTTTAACTA CCTGAGAGTT 1920
ATCAGAGCTG GGGTTGTGGA ATGATCGATC ATCTATAGCA AATAGGCTAT GTTGAGTACG 1980
TAGGCTGTGG GAAGATGAAG ATGGTTTGGA GGTGTAAAAC AATGTCCTTC GCTGAGGCCA 2040
AAGTTTCCAT GTAAGCGGGA TCCGTTTTTT GGAATTTGGT TGAAGTCACT TTGATTTCTT 2100
TAAAAAACAT CTTTTCAATG AAATGTGTTA CCATTTCATA TCCATTGAAG CCGAAATCTG 2160
CATAAGGAAG CCCACTTTAT CTAAATGATA TTAGCCAGGA TCCTTGGTGT CCTAGGAGAA 2220
ACAGACAAGC AAAACAAAGT GAAAACCGAA TGGATTAACT TTTGCAAACC AAGGGAGATT 2280
TCTTAGCAAA TGAGTCTAAC AAATATGACA TCCGTCTTTC CCACTTTTGT TGATGTTTAT 2340
TTCAGAATCT TGTGTGATTC ATTTCAAGCA ACAACATGTT GTATTTTGTT GTGTTAAAAG 2400
TACTTTTCTT GATTTTTGAA TGTATTTGTT TCAGGAAGAA GTCATTTTAT GGATTTTTCT 2460
AACCCGTGTT AACTTTTCTA GAATCCACCC TCTTGTGCCC TTAAGCATTA CTTTAACTGG 2520
TAGGGAACGC CAGAACTTTT AAGTCCAGCT ATTCATTAGA TAGTAATTGA AGATATGTAT 2580
AAATATTACA AAGAATAAAA ATATATTACT GTCTCTTTAG TATGGTTTTC AGTGCAATTA 2640
AACCGAGAGA TGTCTTGTTT TTTTAAAAAG AATAGTATTT AATAGGTTTC TGACTTTTGT 2700
GGATCATTTT GCACATAGCT TTATCAACTT TTAAACATTA ATAAACTGAT TTTTTTAAAG
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Seq ID NO: 2 Protein sequence
Protein Accession #: NP_001391

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MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSV VFILICCFII   60
LENIFVLLTI WKTKKFHRPM YYFIGNLALS DLLAGVAYTA NLLLSGATTY KLTPAQWFLR  120
EGSMFVALSA SVFSLLAIAI ERYITMLKMK LHNGSNNFRL FLLISACWVI SLILGGLPIM  180
GWNCISALSS CSTVLPLYHK HYILFCTTVF TLLLLSIVIL YCRIYSLVRT RSRRLTFRKN  240
ISKASRSSEK SLALLKTVII VLSVFIACWA PLFILLLLDV GCKVKTCDIL FRAEYFLVLA  300
VLNSGTNPII YTLTNKEMRR AFIRIMSCCK CPSGDSAGKF KRPIIAGMEF SRSKSDNSSH  360
PQKDEGDNPE TIMSSGNVNS SS
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Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: NM_002205.1
Coding sequence: 1..3149

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1          11         21         31         41         51
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CGCCGACCCC CGCTSSTGCC GCTGCTGTTG CTGCTSSTGC CGCCGCCACC CAGGGTCGGG  120
GGCTTCAACT TAGACGCGGA GGCCCCAGCA GTACTCTCGG GGCCCCCGGG CTCCTTCTTC  180
GGATTCTCAG TGGAGTTTTA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA  240
CCCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCCT  300
TGGGGTGCCA GCCCCACACA GTGCACCCCC ATTGAATTTG ACAGCAAAGG CTCTCGGCTC  360
CTGGAGTCCT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCCTTGCAG  420
TGGTTCGGGG CAACAGTTCG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC  480
AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA  540
GATAACTTCA CCCGAATTCT GGAGTATGCA CCCTGCCGCT CAGATTTCAG CTGGGCAGCA  600
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GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT   660
TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG   720
ATTGCAGAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT   780
CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTTGGTGAA   840
TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAAGGGAA CCTCACTTAC   900
GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACTT CTCAGGGGAA   960
CAGATGGCCT CCTACTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GGACGGGCTG  1020
GATGACTTGC TGGTGGGGGC ACCCCTGCTC ATGGATCGGA CCCCTGACGG GCGGCCTCAG  1080
GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCCACC  1140
CTTACCCTCA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCCTGGGG  1200
GACCTGGACC AGGATGGCTA CAÀTGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC  1260
CAGCAGGGAG TAGTGTTTGT ATTTCCTGGG GGCCCAGGAG GGCTGGGCTC TAAGCCTTCC  1320
CAGGTTCTGC AGCCCCTGTG GGCAGCCAGC CACACCCCAG ACTTCTTTGG CTCTGCCCTT  1380
CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCTTTGGT  1440
GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CCGCTAGTGC CTCCCTCACC  1500
ATCTTCCCCG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCCTGTG  1560
GCCTGCATCA ACCTTAGCTT CTGCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT  1620
GGTTTCACAG TGGAACTTCA GCTGCACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA  1680
CTGTTCCTGG CCTCCAGGCA GGCAACCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT  1740
CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA  1800
CTCTCGCCGA TTCACATCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC  1860
CACGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG  1920
ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCCTG ACCTGCAGCT GGAAGTGTTT  1980
GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCCATGCC  2040
CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG  2100
GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC  2160
TTTGCCGTGA ACCAGAGCCG CCTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA  2220
GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC  2280
ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGTT  2340
TCCTTTCGGC TCTCCGTGGA GGCTCAGGCC CAGGTCACCC TGAACGGTGT CTCCAAGCCT  2400
GAGGCAGTGC TATTCCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG  2460
GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT  2520
AGCCAGGGTG TGCTGGAACT CAGCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCCTATAT  2580
GTGACCAGAG TTACGGGACT CAACTGCACC ACCAATCACC CCATTAACCC AAAGGGCCTG  2640
GAGTTGGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAAC GGGAAGCTCC AAGCCGCAGC  2700
TCTGCTTCCT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTTT CAGGCTGCGC  2760
TGTGAGCTCG GGCCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAGTTGCA TTTCCGAGTC  2820
TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG  2880
TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCCTCGGC AGCTGCCCCA AAAAGAGCGT  2940
CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTGG  3000
ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC  3060
TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG  3120
CTCAAGCCTC CAGCCACCTC TGATGCCTGA
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Seq ID NO: 4 Protein sequence
Protein Accession #: NP_002196.1

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GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL   120
LESSLSSSEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCYLST   180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ   240
IAESYYPEYL INLVQGQLQT RQASSIYDDS YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY   300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ   360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET   420
QQGVVFVFPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRDLDGNG YPDLIVGSFG   480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI   540
GFTVELQLDW QKQKGGVRRA LFLASRQATL TQTLLIQNGA REDCREMKIY LRNESEFRDK   600
LSPIHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF   660
GEQNHVYLGD KNALNLTFHA QNVGEGGAYE AELRVTAPPE AEYSGLVRHP GNFSSLSCDY   720
FAVNQSRLLV CDLGNPMKAG ASLWGGLRFT VPHLRDTKKT IQFDFQILSK NLNNSQSDVV   780
SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPQKEE DLGPAVHHVY ELINQGPSSI   840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLHH QQKREAPSRS   900
SASSGPQILK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV   960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IIILAILFGL LLLGLLIYIL  1020
YKLGFFKRSL PYGTAMEKAQ LKPPATSDA
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Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: NM_002211.1
Coding sequence: 1..2397

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ATGAATTTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTTGCT    60
CAAACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA   120
GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT   180
TCTGCACGAT GTGATGATTT AGAAGCCTTA AAAAAGAAGG GTTGCCCTCC AGATGACATA   240
GAAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAACCAA CCGTAGCAAA   300
GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCACA GCAGTTGGTT   360
TTGCGATTAA GATCAGGGGA GCCACAGACA TTTACATTAA AATTCAAGAG AGCTGAAGAC   420
TATCCCATTG ACCTCTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTTGGAG   480
AATGTAAAAA GTCTTGGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCGGACTTC   540
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AGAATTGGAT TTGGCTCATT TGTGGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA   600
GCTAAGCTCA GGAACCCTTG CACAAGTGAA CAGAACTGCA CCAGCCCATT TAGCTACAAA   660
AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTTGG AAAACAGCGC   720
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TGTCACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT   960
CACCTTGTCC AGAAACTGAG TGAAAATAAT ATTCAGACAA TTTTTGCAGT TACTGAAGAA  1020
TTTCAGCCTG TTTACAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA  1080
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TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTTCTT TGGATACTAG TACTTGTGAA  1800
GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT  1860
ACAGATCCGA AGTTTCAAGG GCAAACGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT  1920
GCTGAGCATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA  1980
TGCACACAGG AATGTTCCTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC  2040
CAGCCGGTCC AACCTGATCC TGTGTCCCAT TGTAAGGAGA AGGATGTTGA CGACTGTTGG  2100
TTCTATTTTA CGTATTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT  2160
CCAGAGTGTC CCACTGGTCC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAATT  2220
GTTCTTATTG GCCTTGCATT ACTGCTGATA TGGAAGCTTT TAATGATAAT TCATGACAGA  2280
AGGGAGTTTG CTAAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAT  2340
CCTATTTATA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGGG AAAATGA
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Seq ID NO: 6 Protein sequence
Protein Accession #: NP_002202.1

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SARCDDLEAL KKKGCPPDDI ENPRGSKDIK KNKNVTNRSK GTAEKLKPED ITQIQPQQLV   120
LRLRSGEPQT FTLKFKRAED YPIDLYYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF   180
RIGFGSFVEK TVMPYISTTP AKLRNPCTSE QNCTSPPSYK NVLSLTNKGE VFNELVGKQR   240
ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFSTDA GFHFAGDGKL GGIVLPNDGQ   300
CHLENNMYTM SHYYDYPSIA HLVQKLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGTL   360
SANSSNVIQL IIDAYNSLSS EVILENGKLS EGVTISYKSY CKNGVNGTGE NGRKCSNISI   420
GDEVQFEISI TSNKCPKKDS DSFKIRPLGF TEEVEVILQY ICECECQSEG IPESPKCHEG   480
NGTFECGACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVCRK   540
RDNTNEIYSG KFCECDNFNC DRSNGLICGG NGVCKCRVCE CNPNYTGSAC DCSLDTSTCE   600
ASNGQICNGR GICECGVCKC TDPKFQGQTC EMCQTCLGVC AEHKECVQCR AFNKGEKKDT   660
CTQECSYFNI TKVESRDKLP QPVQPDPVSH CKEKDVDDCW FYFTYSVNGN NEVMVHVVEN   720
PECPTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIIHDR REFAKFEKEK MNAKWDTGEN   780
PIYKSAVTTV VNPKYEGK
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Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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1          11         21         31         41         51
|          |          |          |          |          |
AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCATTC CTTGTGCTGT TGTGTCTGCC    60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT   120
TGCCCAGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTCAAAC AGTTTAGAAG   180
AAAGGACAGT AATCTCATTG TTAAAAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA   240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT   300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT   360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT   420
TGAGAAAGCT CTGAAAGTCT GGGAAGAGGT GACTCCACTC ACATTCTCCA GGCTGTATGA   480
AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT   540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA   600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCCT   660
CGTTGCTGCT CATGAACTTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACTGAAGC   720
TTTGATGTAC CCACTCTACA ACTCATTCAC AGAGCTCGCC CAGTTCCGCC TTTCGCAAGA   780
TGATGTGAAT GGCATTCAGT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT   840
GGTGCCCACA AAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT   900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT   960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTCAT TTGATTTCTG CATTTTGGCC  1020
CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTTTAT  1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG  1140
AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA  1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTGC AGCGGACAAA TACTGGAGAT TTGATGAAAA  1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA  1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGGATCATC  1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG  1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTTAAT AAATCTAATA  1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT  1560
```

GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC 1620
ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
CTT

Seq ID NO: 8 Protein sequence
Protein Accession #: NP_002416

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1          11         21         31         41         51
|          |          |          |          |          |
MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVKQF RRKDSNLIVK   60
KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTYRIVNYT  120
PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS FAVKEHGDFY SFDGPGHSLA  180
HAYPPGPGLY GDIHFDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLYNS  240
FTELAQFRLS QDDVNGIQSL YGPPPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL  300
RGEYLFFKDR YFWRRSHWNP EPEFHLISAF WPSLPSYLDA AYEVNSRDTV FIFKGNEFWA  360
IRGNEVQAGY PRGIHTLGFP PTIRKIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF  420
PRLIADDFPG VEPKVDAVLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC
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Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: XM_058189.2
Coding sequence: 169..774

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1          11         21         31         41         51
|          |          |          |          |          |
GAAGACCAGC TCAGCTCTTC AGTTGTTGAT CATTGTCTAT TGTTCTCCAA ACAGTAAACC   60
AGTATTTCAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATTCCCCGTC TCCTCATGAA  120
TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTTCTAAGC AGGGCAAAAT GGGGTCTCGG  180
AAGTGTGGAG GCTGCCTAAG TTGTTTGCTG ATTCCGCTTG CACTTTGGAG TATAATCGTG  240
AACATATTAT TGTATTTCCC GAATGGGCAA ACTTCCTATG CATCCAGCAA TAAACTCACC  300
AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA  360
ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAAACTGC  420
AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTTCT  480
GGATACTGCC TGGTCATCTC TGCCTTGGGT CTTGTCCAAG GGCCATATTG CCGCACCCTT  540
GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA  600
TGGATTCAGT GCCTGGAACC TGCACATGTT GTGGAGTGGA ACATCATTTT ATTTTCCATT  660
CTCATAACCC TCAGTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA  720
TCCAAGATAC TGTGTGGAAG CTATTCAGTG ATCTTCCAGC CTGGAATCAT TTGAATAAGG  780
ACAAAATGTT TTCCATTATC AAGACATGGC CATCTATCTA AATATTATAT CAACTGTGTA  840
GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCATT TGGTGTTTAT TTGTAAAAAA  900
TTTGCAGTCC TCACTGCACA TGCAAGTATA CCACCCTTCC ATTTAGTATG TTTTTTAAGT  960
AATATGCATC AGAAACTTCA GAAATACTTC TGCCCTTTGA TCAAACAAAT CCATTTCCAA 1020
GAATCTGTAC TAGGGAAGTA AATAAGAATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080
TGCAACATTA TTTAATATTC TGGAAAATTG GAAACACCCC AAAATTCTAA ACTCAGAGGA 1140
AGGATTAAGT AAAGAGTGGT ACATACTGTA AATGTTTTCT GATATTAAAA AAAAAATTAA 1200
ATAAAAAATA AAGAGTACTA CATGGTTGTA AAA
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Seq ID NO: 10 Protein sequence
Protein Accession #: XP_058189.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGSRKCGGCL SCLLIPLALW SIIVNILLYF PNGQTSYASS NKLTNYVWYF EGICFSGIMM   60
LIVTTVLLVL ENNNNYKCCQ SENCSKKYVT LLSIIFSSLG IAFSGYCLVI SALGLVQGPY  120
CRTLDGWEYA FEGTAGRFLT DSSIWIQCLE PAHVVEWNII LFSILITLSG LQVIICLIRV  180
VMQLSKILCG SYSVIFQPGI I
```

Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC   60
CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA  120
TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCAGTG  180
GTTGAAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT  240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT  300
GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT  360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC  420
TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG  480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT  540
CTTGCTCATG CTTTTCAACC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT  600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC  660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC  720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT  780
GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCACAAA CCCCAAAAGC ATGTGACAGT  840
AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA  900
TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC  960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260
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GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTCAT  1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT  1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG
```

Seq ID NO: 12 Protein sequence
Protein Accession #: NP_002412.1

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1          11         21         31         41         51
|          |          |          |          |          |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV    60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN   120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGQADIM ISFVRGDHRD NSPFDGPGGN   180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSLGLSHST DIGALMYPSY   240
TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR   300
FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFADRDEV RFFKGNKYWA VQGQNVLHGY   360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDPG YPKMIAHDFP   420
GIGHKVDAVF MKDGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN
```

Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1409

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC    60
CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA   120
TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCAGTG   180
GTTGAAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT   240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT   300
GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT   360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC   420
TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG   480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT   540
CTTGCTCATG CTTTTCAACC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT   600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC   660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC   720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT   780
GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCACAAA CCCCAAAAGC ATGTGACAGT   840
AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA   900
TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC   960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC  1020
CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC  1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT  1140
CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT  1200
GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT  1260
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTCAT  1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT  1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG
```

Seq ID NO: 14 Protein sequence
Protein Accession #: NP_002412.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV    60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN   120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGQADIM ISFVRGDHRD NSPFDGPGGN   180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSLGLSHST DIGALMYPSY   240
TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR   300
FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFADRDEV RFFKGNKYWA VQGQNVLHGY   360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDPG YPKMIAHDFP   420
GIGHKVDAVF MKDGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN
```

Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 141..1580

```
1          11         21         31         41         51
|          |          |          |          |          |
TCTGCGTGTG CCGGGGCTAG GGGCTGGAAG TCCTGGCTCT AGTTGCACCT CGGAAGGAAA    60
AGGCAAACAG AGGAGGGAAG GCGTCTTAGG ACTGCCTGGA TCCAGAGCAC TTTCCTCGGC   120
CTCTACAGGC CTGTGTCGCT ATGGGTTCCC CCGCCGCCCC GGAGGGAGCG CTGGGCTACG   180
TCCGCGAGTT CACTCGCCAC TCCTCCGACG TGCTGGGCAA CCTCAACGAG CTGCGCCTGC   240
GCGGGATCCT CACTGACGTC ACGCTGCTGG TTGGCGGGCA ACCCCTCAGA GCACACAAGG   300
CAGTTCTCAT CGCCTGCAGT GGCTTCTTCT ATTCAATTTT CCGGGGCCGT GCGGGAGTCG   360
GGGTGGACGT GCTCTCTCTG CCCGGGGGTC CCGAAGCGAG AGGCTTCGCC CCTCTATTGG   420
ACTTCATGTA CACTTCGCGC CTGCGCCTCT CTCCAGCCAC TGCACCAGCA GTCCTAGCGG   480
CCGCCACCTA TTTGCAGATG GAGCACGTGG TCCAGGCATC CCACCGCTTC ATCCAGGCCA   540
GCTATGAACC TCTGGGCATC TCCCTGCGCC CCCTGGAAGC AGAACCCCCA ACACCCCCAA   600
CGGCCCCTCC ACCAGGTAGT CCCAGGCGCT CCGAAGGACA CCCAGACCCA CCTACTGAAT   660
CTCGAAGCTG CAGTCAAGGC CCCCCCAGTC CAGCCAGCCC TGACCCCAAG GCCTGCAACT   720
GGAAAAAGTA CAAGTACATC GTGCTAAACT CTCAGGCCTC CCAAGCAGGG AGCCTGGTCG   780
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GGGAGAGAAG TTCTGGTCAA CCTTGCCCCC AAGCCAGGCT CCCCAGTGGA GACGAGGCCT   840
CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTCCT GGTCCCCAGA   900
GCAGGCTCTC TCCAACTGCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC   960
CCTACCTCCT CACATCCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC  1020
CACTACCGGG AAGTGAATTT TTCAGCTGCC AGAACTGTGA GGCTGTGGCA GGGTGCTCAT  1080
CGGGGCTGGA CTCCTTGGTT CCTGGGGACG AAGACAAACC CTATAAGTGT CAGCTGTGCC  1140
GGTCTTCGTT CCGCTACAAG GGCAACCTTG CCAGTCATCG TACAGTGCAC ACAGGGGAAA  1200
AGCCTTACCA CTGCTCAATC TGCGGAGCCC GTTTTAACCG GCCAGCAAAC CTGAAAACGC  1260
ACAGCCGCAT CCATTCGGGA GAGAAGCCGT ATAAGTGTGA GACGTGCGGC TCGCGCTTTG  1320
TACAGGTGGC ACATCTGCGG GCGCACGTGC TGATCCACAC CGGGGAGAAG CCCTACCCTT  1380
GCCCTACCTG CGGAACCCGC TTCCGCCACC TGCAGACCCT CAAGAGCCAC GTTCGCATCC  1440
ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGGCCT GCATTTCCGG CACAAGAGTC  1500
AACTGCGGCT GCATCTGCGC CAGAAACACG GAGCTGCTAC CAACACCAAA GTGCACTACC  1560
ACATTCTCGG GGGGCCCTAG CTGAGCCCAG GCCCAGGCCC CACTTGCTTC CTGCCGGTGG  1620
GAAAGCTGCA GGCCCAGGCC TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGGC  1680
CACTTTGGTA TCAGAAATTG CCACCCTCTT AATTTCTCAC TGGGGAGAGC AGGGGTGGCA  1740
GATCCTGGCT AGATCTGCCT CTGTTTTGCT GGTCAAAACC TCTTCCCCAC AAGCCAGATT  1800
GTTTCTGAGG AGAGAGCTAG CTAGGGGCTG GGAAAGGGGA GAGATTGGAG TCCTGGTCTC  1860
CCTAAGGGAA TAGCCCTCCA CCTGTGGCCC CCATTGCATT CAGTTTATCT GTAAATATAA  1920
TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTCATTCGA TTGCATTTCC CACTCCCCTC  1980
TTCCACAAGT GTGATTAAAA GTGACCAGAA ACACAGAAGG TGAGATCACA GCTCTGCTGG  2040
CAGAGATTAC TAGCCCTTGG CTCTCTCGTT TGGCTTGGGT ATTTTATATT ATTTCTGTCA  2100
TAACTTTTAT CTTTAGAATT GTTCTTTCTC CTGTTTGTTT GCTTGTTAGT TTGTTTAAAA  2160
TGGAAAAAGG GGTTCTCTGT GTTCTGCCCC TGTAATTCTA GGTCTGGAAC CTTTATTTGT  2220
TCTAGGGCAG CTCTGGGAAC ATGCGGGATT GTGGAATTGG GTCAGGAACC CTCTCTGGTA  2280
TTCTGGATGT TGTAGGTTCT CTAGCAGTCT AGAAATGGAT ACAGACATTT CTCTGTTCTT  2340
CAAGGGTGAT AGGAACCATT ATGTTGAGCC CAAAATGGAA GTAATAATAA ATGCCTCCTG  2400
GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCCGTA TCACTCCAAC TGGAGGCTGT  2460
GGGTGTGGGG GATTCTGTAT CTGGATTCCG TATCACTCCA AGTGGAGGCT GGCAGGTTTT  2520
TCTGCAAGAT GGTCCAGAAT CTAAAATGTC CCATTAATCT GGTCACTTGG GTTTGGCTCT  2580
GCTGTATCCA TCTATAGTGG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCCTCC  2640
CACGGGGGCC TGTTCTTAGC ACTGAGTTGA TCGCTCCATG GGGGAGAGAT CAGACATTCC  2700
TTATCAGAGA TGATGTGACC TTTTCTGACT CTGCCCAGTC TCTATGAATG TTATGGCCTA  2760
GGGAAGAATC ATGAAACTCT TTAGCTTGAT TAGATGGTAA ACAGTGTTAA CCCATCCTTT  2820
ACTACAGAGG CATATGGGTT TGAATGTTAC CTGGGGTTCT CTCTATTGAG TTGAGCCCCT  2880
TCTTCCTTTA GTGGGTTTTG GACATCTTCT GGCAAGTGTC CAGATGCCAG AACCTTCTTT  2940
TCCTCTAGAA GGGATGGTGC TTGGTAACCT TACCTTTTAA AAGCTGGGTC TGTGACCTGG  3000
TCTTCCCATC CCTGCATTCC TGTCTGGAAC CAGTGAATGC ATTAGAACCT TCCATAGGAA  3060
AAGAAAAGGG GCTGAGTTCC ATTCTGGGTT TGCTGTAGTT TGGTTGGGAT TATTGTTGGC  3120
ATTACAGATG TAAAAGATTG ACTAGCCCAT AGGCCAAAGG CCTGTTCTAG TTGACCAAGT  3180
TTCAAGTAGG ATTAAGAGGT TGGTTGAGGG GTGCAGTTTC TGGTGTAGGC CAGGTAGGTA  3240
GAAAGTGAGG AACAGGGTTG CCTCTTGGCT GGGTGGAGTC TCTGAAATGT TAGAAGAAGC  3300
GCTGAAGCCT TGATTGATAG TTCTGCCCCT TGTTGCCCTG GGGCTTATCT GATTATGGGA  3360
CGAGGGTAGA AAGTAAGAAG CACTTTTGAA TTTGTGGGGT AGAACTTCAA CAATAAGTCA  3420
GTTCTAGTGG CTGTCGCCTG GGGACTAGTG AGAAAGCTAC TCTTCTCCCT CTTCCCTCTT  3480
TCTCCCCATG GCCCCACTGC AGAATTAAAG AAGGAAGAAG GGAAGGCGGA GGAGTCTATA  3540
AGAAGGAATC ATGATTTCTA TTTAGCAGAT TGGATGGGCA GGTGGAGAAT GCCTGGGGGT  3600
AGAAATGTTA GATCTTGCAA CATCAGATCC TTGGAATAAA GAAGCCTCTC TGYGCWRAAA  3660
AAAAAAAAAA AAAAAA
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Seq ID NO: 16 Protein sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
MGSPAAPEGA LGYVREFTRH SSDVLGNLNE LRLRGILTDV TLLVGGQPLR AHKAVLIACS    60
GFFYSIFRGR AGVGVDVLSL PGGPEARGFA PLLDFMYTSR LRLSPATAPA VLAAATYLQM   120
EHVVQACHRF IQASYEPLGI SLRPLEAEPP TPPTAPPPGS PRRSEGHPDP PTESRSCSQG   180
PPSPASPDPK ACNWKKYKYI VLNSQASQAG SLVGERSSGQ PCPQARLPSG DEASSSSSSS   240
SSSSEEGPIP GPQSRLSPTA ATVQFKCGAP ASTPYLLTSQ AQDTSGSPSE RARPLPGSEF   300
FSCQNCEAVA GCSSGLDSLV PGDEDKPYKC QLCRSSFRYK GNLASHRTVH TGEKPYHCSI   360
CGARFNRPAN LKTHSRIHSG EKPYKCETCG SRFVQVAHLR AHVLIHTGEK PYPCPTCGTR   420
FRHLQTLKSH VRIHTGEKPY HCDPCGLHFR HKSQLRLHLR QKHGAATNTK VHYHILGGP
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Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: XM_039209
Coding sequence: 1..2049

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCTGAAGA TGCTCTCCTT TAAGCTGCTG CTGCTGGCCG TGGCTCTGGG CTTCTTTGAA    60
GGAGATGCTA AGTTTGGGGA AAGAAACGAA GGGAGCGGAG CAAGGAGGAG AAGGTGCCTG   120
AATGGGAACC CCCCGAAGCG CCTGAAAAGG AGAGACAGGA GGATGATGTC CCAGCTGGAG   180
CTGCTGAGTG GGGGAGAGAT GCTGTGCGGT GGCTTCTACC CTCGGCTGTC CTGCTGCCTG   240
CGGAGTGACA GCCCGGGGCT AGGGCGCCTG GAGAATAAGA TATTTTCTGT TACCAACAAC   300
ACAGAATGTG GGAAGTTACT GGAGGAAATC AAATGTGCAC TTTGCTCTCC ACATTCTCAA   360
AGCCTGTTCC ACTCACCTGA GAGAGAAGTC TTGGAAAGAG ACCTAGTACT TCCTCTGCTC   420
TGCAAAGACT ATTGCAAAGA ATTCTTTTAC ACTTGCCGAG GCCATATTCC AGGTTTCCTT   480
CAAACAACTG CGGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGGTGG GTTGTGCTTT   540
CCAGATTTTC CAAGAAAACA AGTCAGAGGA CCAGCATCTA ACTACTTGGA CCAGATGGAA   600
GAATATGACA AAGTGGAAGA GATCAGCAGA AAGCACAAAC ACAACTGCTT CTGTATTCAG   660
GAGGTTGTGA GTGGGCTGCG GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTCGCAA   720
CGTCTCTTCA TTCTGGAAAA AGAAGGTTAT GTGAAGATAC TTACCCCTGA AGGAGAAATT   780
TTCAAGGAGC CTTATTTGGA CATTCACAAA CTTGTTCAAA GTGGAATAAA GGGAGGAGAT   840
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GAAAGAGGAC TGCTAAGCCT CGCATTCCAT CCCAATTACA AGAAAAATGG AAAGTTGTAT   900
GTGTCCTATA CCACCAACCA AGAACGGTGG GCTATCGGGC CTCATGACCA CATTCTTAGG   960
GTTGTGGAAT ACACAGTATC CAGAAAAAAT CCACACCAAG TTGATTTGAG AACAGCCAGA  1020
GTCTTTCTTG AAGTTGCAGA ACTCCACAGA AAGCATCTGG GAGGACAACT GCTCTTTGGC  1080
CCTGACGGCT TTTTGTACAT CATTCTTGGT GATGGGATGA TTACACTGGA TGATATGGAA  1140
GAAATGGATG GGTTAAGTGA TTTCACAGGC TCAGTGCTAC GGCTGGATGT GGACACAGAC  1200
ATGTGTAACG TGCCTTATTC CATACCAAGG AGCAACCCAC ACTTCAACAG CACCAACCAG  1260
CCCCCCGAAG TGTTTGCTCA TGGGCTCCAC GATCCAGGCA GATGTGCTGT GGATAGACAT  1320
CCCACTGATA TAAACATCAA TTTAACGATA CTGTGTTCAG ACTCCAATGG AAAAAACAGA  1380
TCATCAGCCA GAATTCTACA GATAATAAAG GGGAAAGATT ATGAAAGTGA GCCATCACTT  1440
TTAGAATTCA AGCCATTCAG TAATGGTCCT TTGGTTGGTG GATTTGTATA CCGGGGCTGC  1500
CAGTCAGAAA GATTGTATGG AAGCTACGTG TTTGGAGATC GTAATGGGAA TTTCCTAACT  1560
CTCCAGCAAA GTCCTGTGAC AAAGCAGTGG CAAGAAAAAC CACTCTGTCT CGGCACTAGT  1620
GGGTCCTGTA GAGGCTACTT TTCCGGTCAC ATCTTGGGAT TTGGAGAAGA TGAACTAGGT  1680
GAAGTTTACA TTTTATCAAG CAGTAAAAGT ATGACCCAGA CTCACAATGG AAAACTCTAC  1740
AAAATTGTAG ATCCCAAAAG ACCTTTAATG CCTGAGGAAT GCAGAGCCAC GGTACAACCT  1800
GCACAGACAC TGACTTCAGA GTGCTCCAGG CTCTGTCGAA ACGGCTACTG CACCCCCACG  1860
GGAAAGTGCT GCTGCAGTCC AGGCTGGGAG GGGGACTTCT GCAGAACTGC AAAATGTGAG  1920
CCAGCATGTC GTCATGGAGG TGTCTGTGTT AGACCGAACA AGTGCCTCTG TAAAAAAGGA  1980
TATCTTGGTC CTCAATGTGA ACAAGTGGAC AGAAACATCC GCAGAGTGAC CAGGGCAGAC  2040
ATCACCTAG
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Seq ID NO: 18 Protein sequence
Protein Accession #: XP_039209

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1          11         21         31         41         51
|          |          |          |          |          |
MLKMLSFKLL LLAVALGFFE GDAKFGERNE GSGARRRRCL NGNPPKRLKR RDRRMMSQLE    60
LLSGGEMLCG GFYPRLSCCL RSDSPGLGRL ENKIFSVTNN TECGKLLEEI KCALCSPHSQ   120
SLFHSPEREV LERDLVLPLL CKDYCKEFFY TCRGHIPGFL QTTADEFCFY YARKDGGLCF   180
PDFPRKQVRG PASNYLDQME EYDKVEEISR KHKHNCFCIQ EVVSGLRQPV GALHSGDGSQ   240
RLFILEKEGY VKILTPEGEI FKEPYLDIHK LVQSGIKGGD ERGLLSLAFH PNYKKNGKLY   300
VSYTTNQERW AIGPHDHILR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG   360
PDGFLYIILG DGMITLDDME EMDGLSDFTG SVLRLDVDTD MCNVPYSIPR SNPHFNSTNQ   420
PPEVFAHGLH DPGRCAVDRH PTDININLTI LCSDSNGKNR SSARILQIIK GKDYESEPSL   480
LEFKPFSNGP LVGGFVYRGC QSERLYGSYV FGDRNGNFLT LQQSPVTKQW QEKPLCLGTS   540
GSCRGYFSGH ILGFGEDELG EVYILSSSKS MTQTHNGKLY KIVDPKRPLM PEECRATVQP   600
AQTLTSECSR LCRNGYCTPT GKCCCSPGWE GDFCRTAKCE PACRHGGVCV RPNKCLCKKG   660
YLGPQCEQVD RNIRRVTRAD IT
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Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_014331.2
Coding sequence: 1..1506

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1          11         21         31         41         51
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ATGGTCAGAA AGCCTGTTGT GTCCACCATC TCCAAAGGAG GTTACCTGCA GGGAAATGTT    60
AACGGGAGGC TGCCTTCCCT GGGCAACAAG GAGCCACCTG GGCAGGAGAA AGTGCAGCTG   120
AAGAGGAAAG TCACTTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA   180
GGAATCTTCA TCTCTCCTAA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCTCTG   240
ACCATCTGGA CGGTGTGTGG GGTCCTGTCA CTATTTGGAG CTTTGTCTTA TGCTGAATTG   300
GGAACAACTA TAAAGAAATC TGGAGGTCAT TACACATATA TTTTGGAAGT CTTTGGTCCA   360
TTACCAGCTT TTGTACGAGT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT   420
GTGATATCCC TGGCATTTGG ACGCTACATT CTGGAACCAT TTTTTATTCA ATGTGAAATC   480
CCTGAACTTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCCTAAAT   540
AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA   600
GCAATTCTGA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAAGGTCA AACGCAGAAC   660
TTTAAAGACG CGTTTTCAGG AAGAGATTCA AGTATTACGC GGTTGCCACT GGCTTTTTAT   720
TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA   780
AACCCTGAAA AAACCATTCC CCTTGCAATA TGTATATCCA TGGCCATTGT CACCATTGGC   840
TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTTCA   900
AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG   960
ATCTTTGTTG CCCTCTCCTG CTTTGGCTCC ATGAACGGTG GTGTGTTTGC TGTCTCCAGG  1020
TTATTCTATG TTGCGTCTCG AGAGGGTCAC CTTCCAGAAA TCCTCTCCAT GATTCATGTC  1080
CGCAAGCACA CTCCTCTACC AGCTGTTATT GTTTTGCACC CTTTGACAAT GATAATGCTC  1140
TTCTCTGGAG ACCTCGACAG TCTTTTGAAT TTCCTCAGTT TTGCCAGGTG GCTTTTTATT  1200
GGGCTGGCAG TTGCTGGGCT GATTTATCTT CGATACAAAT GCCCAGATAT GCATCGTCCT  1260
TTCAAGGTGC CACTGTTCAT CCCAGCTTTG TTTTCCTTCA CATGCCTCTT CATGGTTGCC  1320
CTTTCCCTCT ATTCGGACCC ATTTAGTACA GGGATTGGCT TCGTCATCAC TCTGACTGGA  1380
GTCCCTGCGT ATTATCTCTT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG  1440
TCAGAGAAAA TAACCAGAAC ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG  1500
TTATGAACTA ATGGACTTGA GATCTTGGCA ATCTGCCCAA GGGGAGACAC AAAATAGGGA  1560
TTTTTACTTC ATTTTCTGAA AGTCTAGAGA ATTACAACTT TGGTGATAAA CAAAAGGAGT  1620
CAGTTATTTT TATTCATATA TTTTAGCATA TTCGAACTAA TTTCTAAGAA ATTTAGTTAT  1680
AACTCTATGT AGTTATAGAA AGTGAATATG CAGTTATTCT ATGAGTCGCA CAATTCTTGA  1740
GTCTCTGATA CCTACCTATT GGGGTTAGGA GAAAAGACTA GACAATTACT ATGTGGTCAT  1800
TCTCTACAAC ATATGTTAGC ACGGCAAAGA ACCTTCAAAT TGAAGACTGA GATTTTTCTG  1860
TATATATGGG TTTTGTAAAG ATGGTTTTAC ACACTACAGA TGTCTATACT GTGAAAAGTG  1920
TTTTCAATTC TGAAAAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT  1980
ATTTTACATT GACATTGCAT TGCTTCCCCT TAGATACCAA TTTAGATAAC AAACACTCAT  2040
GCTTTAATGG ATTATACCCA GAGCACTTTG AACAAAGGTC AGTGGGGATT GTTGAATACA  2100
TTAAAGAAGA GTTTCTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAAGT  2160
AAAAATCCTT GAGAATTTAT TATGTCAGAT GTTTTTTCAT TCATTATCAG GAAGTTTTAG  2220
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TTATCTGTCA TTTTTTTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG  2280
AGCAAGAGTT AGTTTGGTAT TAAATCCTCA TTAGAACAAC CACCTGTTTC ACTAATAACT  2340
TACCCCTGAT GAGTCTATCT AAACATATGC ATTTTAAGCC TTCAAATTAC ATTATCAACA  2400
TGAGAGAAAT AACCAACAAA GAAGATGTTC AAAATAATAG TCCCATATCT GTAATCATAT  2460
CTACATGCAA TGTTAGTAAT TCTGAAGTTT TTTAAATTTA TGGCTATTTT TACACGATGA  2520
TGAATTTTGA CAGTTTGTGC ATTTTCTTTA TACATTTTAT ATTCTTCTGT TAAAATATCT  2580
CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATTGCAA  2640
AAGAAATGTC GCTGTAAATA AGATTTACAA CTGATGTTTC TAGAAAATTT CCACTTCTAT  2700
ATCTAGGCTT TGTCAGTAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA  2760
CTGATAAGAA GAAAATTGAA ATGAGAATCT GTGGATAAGT GTTTGTGTTC AGAAGATGTT  2820
GTTTTGCCAG TATTAGAAAA TACTGTGAGC CGGGCATGGT GGCTTACATC TGTAATCCCA  2880
GCACTTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCGG GAGTTCTAGA CCAGCCTGAC  2940
CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT  3000
GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG  3060
GAGGTTGCAG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT  3120
CCATCTCCAA AAAAAAAAAA AAAA
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Seq ID NO: 20 Protein sequence
Protein Accession #: NP_055146.1

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1          11         21         31         41         51
|          |          |          |          |          |
MVRKPVVSTI SKGGYLQGNV NGRLPSLGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA   60
GIFISPKGVL QNTGSVGMSL TIWTVCGVLS LPGALSYAEL GTTIKKSGGH YTYILEVPGP  120
LPAFVRVWVE LLIIRPAATA VISLAFGRYI LEPFFIQCEI PELAIKLITA VGITVVMVLN  180
SMSVSWSARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY  240
YGMYAYAGWF YLNFVTEEVE NPEKTIPLAI CISMAITIGV YVLTNVAYFT TINAEELLLS  300
NAVAVTPSER LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV  360
RKHTPLPAVI VLHPLTMIML FSGDLDSLLN FLSFARWLFI GLAVAGLIYL RYKCPDMHRP  420
FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM  480
SEKITRTLQI ILEVVPEEDK L
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Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: NM_002422.2
Coding sequence: 64..1497

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1          11         21         31         41         51
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ACAAGGAGGC AGGCAAGACA GCAAGGCATA GAGACAACAT AGAGCTAAGT AAAGCCAGTG   60
GAAATGAAGA GTCTTCCAAT CCTACTGTTG CTGTGCGTGG CAGTTTGCTC AGCCTATCCA  120
TTGGATGGAG CTGCAAGGGG TGAGGACACC AGCATGAACC TTGTTCAGAA ATATCTAGAA  180
AACTACTACG ACCTCAAAAA AGATGTGAAA CAGTTTGTTA GGAGAAAGGA CAGTGGTCCT  240
GTTGTTAAAA AAATCCGAGA AATGCAGAAG TTCCTTGGAT TGGAGGTGAC GGGGAAGCTG  300
GACTCCGACA CTCTGGAGGT GATGCGCAAG CCCAGGTGTG GAGTTCCTGA TGTTGGTCAC  360
TTCAGAACCT TTCCTGGCAT CCCGAAGTGG AGGAAAACCC ACCTTACATA CAGGATTGTG  420
AATTATACAC CAGATTTGCC AAAAGATGCT GTTGATTCTG CTGTTGAGAA AGCTCTGAAA  480
GTCTGGGAAG AGGTGACTCC ACTCACATTC TCCAGGCTGT ATGAAGGAGA GGCTGATATA  540
ATGATCTCTT TTGCAGTTAG AGAACATGGA GACTTTTACC CTTTTGATGG ACCTGGAAAT  600
GTTTTGGCCC ATGCCTATGC CCCTGGGCCA GGGATTAATG GAGATGCCCA CTTTGATGAT  660
GATGAACAAT GGACAAAGGA TACAACAGGG ACCAATTTAT TTCTCGTTGC TGCTCATGAA  720
ATTGGCCACT CCCTGGGTCT CTTTCACTCA GCCAACACTG AAGCTTTGAT GTACCCACTC  780
TATCACTCAC TCACAGACCT GACTCGGTTC CGCCTGTCTC AAGATGATAT AAATGGCATT  840
CAGTCCCTCT ATGGACCTCC CCCTGACTCC CCTGAGACCC CCCTGGTACC CACGGAACCT  900
GTCCCTCCAG AACCTGGGAC GCCAGCCAAC TGTGATCCTG CTTTGTCCTT TGATGCTGTC  960
AGCACTCTGA GGGGAGAAAT CCTGATCTTT AAAGACAGGC ACTTTTGGCG CAAATCCCTC 1020
AGGAAGCTTG AACCTGAATT GCATTTGATC TCTTCATTTT GGCCATCTCT TCCTTCAGGC 1080
GTGGATGCCG CATATGAAGT TACTAGCAAG GACCTCGTTT TCATTTTTAA AGGAAATCAA 1140
TTCTGGGCCA TCAGAGGAAA TGAGGTACGA GCTGGATACC CAAGAGGCAT CCACACCCTA 1200
GGTTTCCCTC CAACCGTGAG GAAAATCGAT GCAGCCATTT CTGATAAGGA AAAGAACAAA 1260
ACATATTTCT TTGTAGAGGA CAAATACTGG AGATTTGATG AGAAGAGAAA TTCCATGGAG 1320
CCAGGCTTTC CCAAGCAAAT AGCTGAAGAC TTTCCAGGGA TTGACTCAAA GATTGATGCT 1380
GTTTTTGAAG AATTTGGGTT CTTTTATTTC TTTACTGGAT CTTCACAGTT GGAGTTTGAC 1440
CCAAATGCAA AGAAAGTGAC ACACACTTTG AAGAGTAACA GCTGGCTTAA TTGTTGAAAG 1500
AGATATGTAG AAGGCACAAT ATGGGCACTT TAAATGAAGC TAATAATTCT TCACCTAAGT 1560
CTCTGTGAAT TGAAATGTTC GTTTTCTCCT GCCTGTGCTG TGACTCGAGT CACACTCAAG 1620
GGAACTTGAG CGTGAATCTG TATCTTGCCG GTCATTTTTA TGTTATTACA GGGCATTCAA 1680
ATGGGCTGCT GCTTAGCTTG CACCTTGTCA CATAGAGTGA TCTTTCCCAA GAGAAGGGGA 1740
AGCACTCGTG TGCAACAGAC AAGTGACTGT ATCTGTGTAG ACTATTTGCT TATTTAATAA 1800
AGACGATTTG TCAGTTGTTT T
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Seq ID NO: 22 Protein sequence
Protein Accession #: NP_002413

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1          11         21         31         41         51
|          |          |          |          |          |
MKSLPILLLL CVAVCSAYPL DGAARGEDTS MNLVQKYLEN YYDLEKDVKQ FVRRKDSGPV   60
VKKIREMQKF LGLEVTGKLD SDTLEVMRKP RCGVPDVGHF RTFPGIPKWR KTHLTYRIVN  120
YTPDLPKDAV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYPFDGPGNV  180
LAHAYAPGPG INGDAHFDDD EQWTKDTTGT NLFLVAAHEI GHSLGLFHSA NTEALMYPLY  240
HSLTDLTRFR LSQDDINGIQ SLYGPPPDSP ETPLVPTEPV PPEPGTPANC DPALSFDAVS  300
TLRGEILIFK DRHFWRKSLR KLEPELHLIS SFWPSLPSGV DAAYEVTSKD LVFIFKGNQF  360
WAIRGNEVRA GYPRGIHTLG FPPTVRKIDA AISDKEKNKT YFFVEDKYWR FDEKRNSMEP  420
GFPKQIAEDF PGIDSKIDAV FEEFGFFYFF TGSSQLEFDP NAKKVTHTLK SNSWLNC
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Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

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1          11         21         31         41         51
|          |          |          |          |          |
GCCGCCAGCG GCTTTCTCGG ACGCCTTGCC CAGCGGGCCG CCCGACCCCC TGCACCATGG    60
ACCCCGCTCG CCCCCTGGGG CTGTCGATTC TGCTGCTTTT CCTGACGGAG GCTGCACTGG   120
GCGATGCTGC TCAGGAGCCA ACAGGAAATA ACGCGGAGAT CTGTCTCCTG CCCCTAGACT   180
ACGGACCCTG CCGGGCCCTA CTTCTCCGTT ACTACTACGA CAGGTACACG CAGAGCTGCC   240
GCCAGTTCCT GTACGGGGGC TGCGAGGGCA ACGCCAACAA TTTCTACACC TGGGAGGCTT   300
GCGACGATGC TTGCTGGAGG ATAGAAAAAG TTCCCAAAGT TTGCCGGCTG CAAGTGAGTG   360
TGGACGACCA GTGTGAGGGG TCCACAGAAA AGTATTTCTT TAATCTAAGT TCCATGACAT   420
GTGAAAAATT CTTTTCCGGT GGGTGTCACC GGAACCGGAT TGAGAACAGG TTTCCAGATG   480
AAGCTACTTG TATGGGCTTC TGCGCACCAA AGAAAATTCC ATCATTTTGC TACAGTCCAA   540
AAGATGAGGG ACTGTGCTCT GCCAATGTGA CTCGCTATTA TTTTAATCCA AGATACAGAA   600
CCTGTGATGC TTTCACCTAT ACTGGCTGTG GAGGGAATGA CAATAACTTT GTTAGCAGGG   660
AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGAAAAAGAA AAAGAAGATG CCAAAGCTTC   720
GCTTTGCCAG TAGAATCCGG AAAATTCGGA AGAAGCAATT TTAAACATTC TTAATATGTC   780
ATCTTGTTTG TCTTTATGGC TTATTTGCCT TTATGGTTGT ATCTGAAGAA TAATATGACA   840
GCATGAGGAA ACAAATCATT GGTGATTTAT TCACCAGTTT TTATTAATAC AAGTCACTTT   900
TTCAAAAATT TGGATTTTTT TATATATAAC TAGCTGCTAT TCAAATGTGA GTCTACCATT   960
TTTAATTTAT GGTTCAACTG TTTGTGAGAC GAATTCTTGC AATGCATAAG ATATAAAAGC  1020
AAATATGACT CACTCATTTC TTGGGGTCGT ATTCCTGATT TCAGAAGAGG ATCATAACTG  1080
AAACAACATA AGACAATATA ATCATGTGCT TTTAACATAT TTGAGAATAA AAAGGACTAG  1140
CC
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Seq ID NO: 24 Protein sequence
Protein Accession #: NP_006519

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1          11         21         31         41         51
|          |          |          |          |          |
MDPARPLGLS ILLLFLTEAA LGDAAQEPTG NNAEICLLPL DYGPCRALLL RYYYDRYTQS    60
CRQFLYGGCE GNANNFYTWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM   120
TCEKFFSGGC HRNRIENRFP DEATCMGFCA PKKIPSFCYS PKDEGLCSAN VTRYYFNPRY   180
RTCDAFTYTG CGGNDNNFVS REDCKRACAK ALKKKKKMPK LRFASRIRKI RKKQF
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Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: NM_005458.1
Coding sequence: 1..2825

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGCTTCCC CGCGGAGGTC CGGGCAGCCA GGGCGGCCGC CGCCGCCGCC ACCGCCGCCC    60
GCGCGCCTGC TACTGCTACT GCTGCTGCCG CTGCTGCTGC CTCTGGCGCC CGGGGCCTGG   120
GGCTGGGCGC GGGGCGCCCC CCGGCCGCCG CCCAGCAGCC CGCCGCTCTC CATCATGGGC   180
CTCATGCCGC TCACCAAGGA GGTGGCCAAG GGCAGCATCG GGCGCGGTGT GCTCCCCGCC   240
GTGGAACTGG CCATCGAGCA GATCCGCAAC GAGTCACTCC TGCGCCCCTA CTTCCTCGAC   300
CTGCGGCTCT ATGACACGGA GTGCGACAAC GCAAAAGGGT TGAAAGCCTT CTACGATGCA   360
ATAAAATACG GGCCGAACCA CTTGATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC   420
ATCATTGCAG AGTCCCTCCA AGGCTGGAAT CTGGTGCAGC TTTCTTTTGC TGCAACCACG   480
CCTGTTCTAG CCGATAAGAA AAAATACCCT TATTTCTTTC GGACCGTCCC ATCAGACAAT   540
GCGGTGAATC CAGCCATTCT GAAGTTGCTC AAGCACTACC AGTGGAAGCG CGTGGGCACG   600
CTGACGCAAG ACGTTCAGAG GTTCTCTGAG GTGCGGAATG ACCTGACTGG AGTTCTGTAT   660
GGCGAGGACA TTGAGATTTC AGACACCGAG AGCTTCTCCA ACGATCCCTG TACCAGTGTC   720
AAAAAGCTGA AGGGGAATGA TGTGCGGATC ATCCTTGGCC AGTTTGACCA GAATATGGCA   780
GCAAAAGTGT TCTGTTGTGC ATACGAGGAG AACATGTATG GTAGTAAATA TCAGTGGATC   840
ATTCCGGGCT GGTACGAGCC TTCTTGGTGG GAGCAGGTGC ACACGGAAGC CAACTCATCC   900
CGCTGCCTCC GGAAGAATCT GCTTGCTGCC ATGGAGGGCT ACATTGGCGT GGATTTCGAG   960
CCCCTGAGCT CCAAGCAGAT CAAGACCATC TCAGGAAAGA CTCCACAGCA GTATGAGAGA  1020
GAGTACAACA ACAAGCGGTC AGGCGTGGGG CCCAGCAAGT TCCACGGGTA CGCCTACGAT  1080
GGCATCTGGG TCATCGCCAA GACACTGCAG AGGGCCATGG AGACACTGCA TGCCAGCAGC  1140
CGGCACCAGC GGATCCAGGA CTTCAACTAC ACGGACCACA CGCTGGGCAG GATCATCCTC  1200
AATGCCATGA ACGAGACCAA CTTCTTCGGG GTCACGGGTC AAGTTGTATT CCGGAATGGG  1260
GAGAGAATGG GGACCATTAA ATTTACTCAA TTTCAAGACA GCAGGGAGGT GAAGGTGGGA  1320
GAGTACAACG CTGTGGCCGA CACACTGGAG ATCATCAATG ACACCATCAG GTTCCAAGGA  1380
TCCGAACCAC CAAAAGACAA GACCATCATC CTGGAGCAGC TGCGGAAGAT CTCCCTACCT  1440
CTCTACAGCA TCCTCTCTGC CCTCACCATC CTCGGGATGA TCATGGCCAG TGCTTTTCTC  1500
TTCTTCAACA TCAAGAACCG GAATCAGAAG CTCATAAAGA TGTCGAGTCC ATACATGAAC  1560
AACCTTATCA TCCTTGGAGG GATGCTCTCC TATGCTTCCA TATTTCTCTT TGGCCTTGAT  1620
GGATCCTTTG TCTCTGAAAA GACCTTTGAA ACACTTTGCA CCGTCAGGAC CTGGATTCTC  1680
ACCGTGGGCT ACACGACCGC TTTTGGGGCC ATGTTTGCAA AGACCTGGAG AGTCCACGCC  1740
ATCTTCAAAA ATGTGAAAAT GAAGAAGAAG ATCATCAAGG ACCAGAAACT GCTTGTGATC  1800
GTGGGGGGCA TGCTGCTGAT CGACCTGTGT ATCCTGATCT GCTGGCAGGC TGTGGACCCC  1860
CTGCGAAGGA CAGTGGAGAA GTACAGCATG GAGCCGGACC CAGCAGGACG GGATATCTCC  1920
ATCCGCCCTC TCCTGGAGCA CTGTGAGAAC ACCCATATGA CCATCTGGCT TGGCATCGTC  1980
TATGCCTACA AGGGACTTCT CATGTTGTTC GGTTGTTTCT TAGCTTGGGA GACCCGCAAC  2040
GTCAGCATCC CCGCACTCAA CGACAGCAAG TACATCGGGA TGAGTGTCTA CAACGTGGGG  2100
ATCATGTGCA TCATCGGGGC CGCTGTCTCC TTCCTGACCC GGGACCAGCC CAATGTGCAG  2160
TTCTGCATCG TGGCTCTGGT CATCATCTTC TGCAGCACCA TCACCCTCTG CCTGGTATTC  2220
GTGCCGAAGC TCATCACCCT GAGAACAAAC CCAGATGCAG CAACGCAGAA CAGGCGATTC  2280
CAGTTCACTC AGAATCAGAA GAAAGAAGAT TCTAAAACGT CCACCTCGGT CACCAGTGTG  2340
AACCAAGCCA GCACATCCCG CCTGGAGGGC CTACAGTCAG AAAACCATCG CCTGCGAATG  2400
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AAGATCACAG AGCTGGATAA AGACTTGGAA GAGGTCACCA TGCAGCTGCA GGACACACCA  2460
GAAAAGACCA CCTACATTAA ACAGAACCAC TACCAAGAGC TCAATGACAT CCTCAACCTG  2520
GGAAACTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATTT TAAAAAATCA CCTCGATCAA  2580
AATCCCCAGC TACAGTGGAA CACAACAGAG CCCTCTCGAA CATGCAAAGA TCCTATAGAA  2640
GATATAAACT CTCCAGAACA CATCCAGCGT CGGCTGTCCC TCCAGCTCCC CATCCTCCAC  2700
CACGCCTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTCAGCCC CTGCGTCAGC  2760
CCCACCGCCA GCCCCCGCCA CAGACATGTG CCACCCTCCT TCCGAGTCAT GGTCTCGGGC  2820
CTGTAA
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Seq ID NO: 26 Protein sequence
Protein Accession #: NP_005449.1

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1          11         21         31         41         51
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MASPRRSGQP GRPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP PSSPPLSIMG    60
LMPLTKEVAK GSIGRGVLPA VELAIEQIRN ESLLRPYFLD LRLYDTECDN AKGLKAFYDA   120
IKYGPNHLMV FGGVCPSVTS IIAESLQGWN LVQLSFAATT PVLADKKKYP YFFRTVPSDN   180
AVNPAILKLL KHYQWKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV   240
KKLKGNDVRI ILGQFDQNMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS   300
RCLRKNLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQQYER EYNNKRSGVG PSKFHGYAYD   360
GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIIL NAMNETNFFG VTGQVVFRNG   420
ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP   480
LYSILSALTI LGMIMASAFL FFNIKNRNQK LIKMSSPYMN NLIILGGMLS YASIFLFGLD   540
GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKMKKK IIKDQKLLVI   600
VGGMLLIDLC ILICWQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLGIV   660
YAYKGLLMLF GCFLAWETRN VSIPALNDSK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ   720
FCIVALVIIF CSTITLCLVF VPKLITLRTN PDAATQNRRF QFTQNQKKED SKTSTSVTSV   780
NQASTSRLEG LQSENHRLRM KITELDKDLE EVTMQLQDTP EKTTYIKQNH YQELNDILNL   840
GNFTESTDGG KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPILH   900
HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L
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Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: NM_000450.1
Coding sequence: 117..1949

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TTGCTTCACA GTTTCTCTCA GCTCTCACTT TGGTGCTTCT CATTAAAGAG AGTGGAGCCT   180
GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTCAGC   240
AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAAGAAGA GATTGAGTAC CTAAACTCCA   300
TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG   360
TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC   420
CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG   480
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CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA   600
CTTGCAAGTG TGACCCTGGC TTCAGTGGAC TCAAGTGTGA GCAAATTGTG AACTGTACAG   660
CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCAGTCA CCCACTGGGA AACTTCAGCT   720
ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGGAGACCA   780
TGCAGTGTAT GTCCTCTGGA GAATGGAGTG CTCCTATTCC AGCCTGCAAT GTGGTTGAGT   840
GTGATGCTGT GACAAATCCA GCCAATGGGT TCGTGGAATG TTTCCAAAAC CCTGGAAGCT   900
TCCCATGGAA CACAACCTGT ACATTTGACT GTGAAGAAGG ATTTGAACTA ATGGGAGCCC   960
AGAGCCTTCA GTGTACCTCA TCTGGGAATT GGGACAACGA GAAGCCAACG TGTAAAGCTG  1020
TGACATGCAG GGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC CATTCCCCTG  1080
CTGGAGAGTT CACCTTCAAA TCATCCTGCA ACTTCACCTG TGAGGAAGGC TTCATGTTGC  1140
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GTGAAGCTTT CCAGTGCACA GCCTTGTCCA ACCCCGAGCG AGGCTACATG AATTGTCTTC  1260
CTAGTGCTTC TGGCAGTTTC CGTTATGGGT CCAGCTGTGA GTTCTCCTGT GAGCAGGGTT  1320
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AGCCCACATG TGAAGCTGTG AGATGCGATG CTGTCCACCA GCCCCCGAAG GGTTTGGTGA  1440
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GCCTGCTACC TACCTGTGAA GCTCCCACTG AGTCCAACAT TCCCTTGGTA GCTGGACTTT  1800
CTGCTGCTGG ACTCTCCCTC CTGACATTAG CACCATTTCT CCTCTGGCTT CGGAAATGCT  1860
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GCTACCAAAA GCCTTCTTAC ATCCTTTAAG TTCAAAAGAA TCAGAAACAG GTGCATCTGG  1980
GGAACTAGAG GGATACACTG AAGTTAACAG AGACAGATAA CTCTCCTCGG GTCTCTGGCC  2040
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AATAGATCAA AGTCCAGCAG GCAAGGACGG CCTTCAACTG AAAAGACTCA GTGTTCCCTT  2160
TCCTACTCTC AGGATCAAGA AAGTGTTGGC TAATGAAGGG AAAGGATATT TTCTTCCAAG  2220
CAAAGGTGAA GAGACCAAGA CTCTGAAATC TCAGAATTCC TTTTCTAACT CTCCCTTGCT  2280
CGCTGTAAAA TCTTGGCACA GAAACACAAT ATTTTGTGGC TTTCTTTCTT TTGCCCTTCA  2340
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GTTCTTAAGG ATTGTGATAT TTTTACTTGC ATTGAATATA TTATAATCTT CCATACTTCT  2640
TCATTCAATA CAAGTGTGGT AGGGACTTAA AAAACTTGTA AATGCTGTCA ACTATGATAT  2700
GGTAAAAGTT ACTTATTCTA GATTACCCCC TCATTGTTTA TTAACAAATT ATGTTACATC  2760
TGTTTTAAAT TTATTTCAAA AAGGGAAACT ATTGTCCCCT AGCAAGGCAT GATGTTAACC  2820
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CACACAAAGG TATAATTTTA TGAATGTCTT TGTTGGAAAA GAATACAGAA AGATGGATGT  3060
GCTTTGCATT CCTACAAAGA TGTTTGTCAG ATGTGATATG TAAACATAAT TCTTGTATAT  3120
TATGGAAGAT TTTAAATTCA CAATAGAAAC TCACCATGTA AAAGAGTCAT CTGGTAGATT  3180
TTTAACGAAT GAAGATGTCT AATAGTTATT CCCTATTTGT TTTCTTCTGT ATGTTAGGGT  3240
GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTTAT GTTTATTTAT AAGCAGATTT  3300
AACAATTCCA AAGGAATCTC CAGTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC  3360
AGTAATTGCC AAAGCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAAACTC TCCTACACTT  3420
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GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGGTTTGT GTTTGAGTTT TATTGAGAAT  3720
TTTAAATTAT AACTTAAAAT ATTTTATAAT TTTTAAAGTA TATATTTATT TAAGCTTATG  3780
TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT
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Seq ID NO: 28 Protein sequence
Protein Accession #: NP_000441.1

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SILSYSPSYY WIGIRKVNNV WVWVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK   120
DVGMWNDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC   180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV   240
ECDAVTNPAN GFVECFQNPG SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK   300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPAQVECT TQGQWTQQIP   360
VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN   420
EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ   480
WTEEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW   540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRK CLRKAKKFVP ASSCQSLESD   600
GSYQKPSYIL
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Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_007036
Coding sequence: 56..610

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TAATTATGCG GTGGACTGCC CTCAACACTG TGACAGCAGT GAGTGCAAAA GCAGCCCGCG   180
CTGCAAGAGG ACAGTGCTCG ACGACTGTGG CTGCTGCCGA GTGTGCGCTG CAGGGCGGGG   240
AGAAACTTGC TACCGCACAG TCTCAGGCAT GGATGGCATG AAGTGTGGCC CGGGGCTGAC   300
GTGTCAGCCT TCTAATGGGG AGGATCCTTT TGGTGAAGAG TTTGGTATCT GCAAAGACTG   360
TCCCTACGGC ACCTTCGGGA TGGATTGCAG AGAGACCTGC AACTGCCAGT CAGGCATCTG   420
TGACAGGGGG ACGGGAAAAT GCCTGAAATT CCCCTTCTTC CAATATTCAG TAACCAAGTC   480
TTCCAACAGA TTTGTTTCTC TCACGGAGCA TGACATGGCA TCTGGAGATG GCAATATTGT   540
GAGAGAAGAA GTTGTGAAAG AGAATGCTGC CGGGTCTCCC GTAATGAGGA AATGGTTAAA   600
TCCACGCTGA TCCCGGCTGT GATTTCTGAG AGAAGGCTCT ATTTTCGTGA TTGTTCAACA   660
CACAGCCAAC ATTTTAGGAA CTTTCTAGAT ATAGCATAAG TACATGTAAT TTTTGAAGAT   720
CCAAATTGTG ATGCATGGTG GATCCAGAAA ACAAAAAGTA GGATACTTAC AATCCATAAC   780
ATCCATATGA CTGAACACTT GTATGTGTTT GTTAAATATT CGAATGCATG TAGATTTGTT   840
AAATGTGTGT GTATAGTAAC ACTGAAGAAC TAAAAATGCA ATTTAGGTAA TCTTACATGG   900
AGACAGGTCA ACCAAAGAGG GAGCTAGGCA AAGCTGAAGA CCGCAGTGAG TCAAATTAGT   960
TCTTTGACTT TGATGTACAT TAATGTTGGG ATATGGAATG AAGACTTAAG AGCAGGAGAA  1020
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TCTAGAATTT AATTGTGCTT TTTTTTTTTT TTTGGCTTTG GGAAAAGTCA AAATAAAACA  1140
ACCAGAAAAC CCCTGAAGGA AGTAAGATGT TTGAAGCTTA TGGAAATTTG AGTAACAAAC  1200
AGCTTTGAAC TGAGAGCAAT TTCAAAAGGC TGCTGATGTA GTTCCCGGGT TACCTGTATC  1260
TGAAGGACGG TTCTGGGGCA TAGGAAACAC ATACACTTCC ATAAATAGCT TTAACGTATG  1320
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CTTAGGAAAT ATCTCAGAAG TATTTTATTT GAAGTGAAGA ACTTATTTAA GAATTATTTC  1860
AGTATTTACC TGTATTTTAT TCTTGAAGTT GGCCAACAGA GTTGTGAATG TGTGTGGAAG  1920
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Seq ID NO: 30 Protein sequence
Protein Accession #: NP_008967.1

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RGETCYRTVS GMDGMKCGPG LRCQPSNGED PFGEEPGICK DCPYGTFGMD CRETCNCQSG   120
ICDRGTGKCL KFPFFQYSVT KSSNRFVSLT EHDMASGDGN IVREEVVKEN AAGSPVMRKW   180
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LNPR

Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: NM_000963
Coding sequence: 135..1949

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TGCCCGCCGC TCGGATGCTC GCCCGCGCCC TGCTGCTGTG CGCGGTCCTG GCGCTCAGCC   180
ATACAGCAAA TCCTTGCTGT TCCCACCCAT GTCAAAACCG AGGTGTATGT ATGAGTGTGG   240
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CACCGGAATT TTTGACAAGA ATAAAATTAT TTCTGAAACC CACTCCAAAC ACAGTGCACT   360
ACATACTTAC CCACTTCAAG GGATTTTGGA ACGTTGTGAA TAACATTCCC TTCCTTCGAA   420
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ACAATGCTGA CTATGGCTAC AAAAGCTGGG AAGCCTTCTC TAACCTCTCC TATTATACTA   540
GAGCCCTTCC TCCTGTGCCT GATGATTGCC CGACTCCCTT GGGTGTCAAA GGTAAAAAGC   600
AGCTTCCTGA TTCAAATGAG ATTGTGGAAA AATTGCTTCT AAGAAGAAAG TTCATCCCTG   660
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TCAAGACAGA TCATAAGCGA GGGCCAGCTT TCACCAACGG GCTGGGCCAT GGGGTGGACT   780
TAAATCATAT TTACGGTGAA ACTCTGGCTA GACAGCGTAA ACTGCGCCTT TTCAAGGATG   840
GAAAAATGAA ATATCAGATA ATTGATGGAG AGATGTATCC TCCCACAGTC AAAGATACTC   900
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AGACAAGCAG GCTAATACTG ATAGGAGAGA CTATTAAGAT TGTGATTGAA GATTATGTGC  1140
AACACTTGAG TGGCTATCAC TTCAAACTGA AATTTGACCC AGAACTACTT TTCAACAAAC  1200
AATTCCAGTA CCAAAATCGT ATTGCTGCTG AATTTAACAC CCTCTATCAC TGGCATCCCC  1260
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ACAACTCTAT ATTGCTGGAA CATGGAATTA CCCAGTTTGT TGAATCATTC ACCAGGCAAA  1380
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CCTTGAAAGG ACTTATGGGT AATGTTATAT GTTCTCCTGC CTACTGGAAG CCAAGCACTT  1740
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CAGTCACCAT CAATGCAAGT TCTTCCCGCT CCGGACTAGA TGATATCAAT CCCACAGTAC  1920
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GAACCATGTC TATTAATTTA ATTATTTAAT AATATTTATA TTAAACTCCT TATGTTACTT  2040
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ATAACGATAT GTTTTCTCAG ATTTTCTGTT GTACAGTTTA ATTTAGCAGT CCATATCACA  3060
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Seq ID NO: 32 Protein sequence
Protein Accession #: NP_000954

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GYKSWEAFSN LSYYTRALPP VPDDCPTPLG VKGKKQLPDS NEIVEKLLLR RKFIPDPQGS  180
NMMFAFFAQH FTHQFFKTDH KRGPAFTNGL GHGVDLNHIY GETLARQRKL RLFKDGKMKY  240
QIIDGEMYPP TVKDTQAEMI YPPQVPEHLR FAVGQEVFGL VPGLMMYATI WLREHNRVCD  300
VLKQEHPEWG DEQLFQTSRL ILIGETIKIV IEDYVQHLSG YHFKLKFDPE LLFNKQFQYQ  360
NRIAAEFNTL YHWHPLLPDT FQIHDQKYNY QQFIYNNSIL LEHGITQFVE SFTRQIAGRV  420
AGGRNVPPAV QKVSQASIDQ SRQMKYQSFN EYRKRFMLKP YESFEELTGE KEMSAELEAL  480
YGDIDAVELY PALLVEKPRP DAIFGETMVE VGAPFSLKGL MGNVICSPAY WKPSTFGGEV  540
GFQIINTASI QSLICNNVKG CPFTSFSVPD PELIKTVTIN ASSSRSGLDD INPTVLLKER  600
STEL
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Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: NM_001508.1
Coding sequence: 1..1361

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AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC   240
TTGGTGTTCC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC   300
ACGTCCAGCT ACACCCTGTC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC   360
GCTACGCTGC TGCACGTGCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC   420
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GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCCTG   540
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG   600
CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC   660
CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC   720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC   780
ACGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG   840
ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG   900
ATTCGGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGACGAGGTC CTACTTCCGG   960
GCGTACATGA TCCTCCTCCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCATCAAC  1020
CCGCTCCTGT ACACGGTGTC CTCGCAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC  1080
TGCCGCCTGT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC  1140
ACCACCGACA GCGCCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC  1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG  1260
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Seq ID NO: 34 Protein sequence
Protein Accession #: NP_001499.1

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1          11         21         31         41         51
|          |          |          |          |          |
MASPSLPGSD CSQIIDHSHV PEPEVATWIK ITLILVYLII FVMGLLGNSV TIRVTQVLQK    60
KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY   120
ATLLHVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL   180
VNVPSHRGLT CNRSSTRHHE QPETSNMSIC TNLSSRWTVF QSSIFGAFVV YLVVLLSVAF   240
MCWNMMQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ   300
IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC   360
CRLSLQHANH EKRLRVHAHS TTDSAREVQR PLLFASRRQS SARRTEKIFL STFQSEAEPQ   420
SKSQSLSLES LEPNSGAKPA NSAAENGFQE HEV
```

Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: NM_006475.1
Coding sequence: 28..2538

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1          11         21         31         41         51
|          |          |          |          |          |
AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCCATGTT TTCTCTACTA    60
TTGCTGCTTA TTGTTAACCC TATAAACGCC AACAATCATT ATGACAAGAT CTTGGCTCAT   120
AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC   180
ACCAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG   240
AAAACGACTG TTTTATATGA ATGTTGCCCT GGTTATATGA GAATGGAAGG AATGAAAGGC   300
TGCCCAGCAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC   360
ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC   420
TTCACTTACT TTGCACCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCCGTAGA   480
GGTTTGGAGA GCAACGTGAA TGTTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT   540
AAGAGAATGT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT   600
TTGGGGCTTT TCATTAACCA TTATCCTAAT GGGGTTGTCA CTGTTAATTG TGCTCGAATC   660
ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA   720
CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA   780
GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACACTC   840
TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGTCCTAGA AAGGTTCATG   900
GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT   960
TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA  1020
```

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GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT  1080
GTGACAAATA ATGGTGTGAT CCATTTGATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA  1140
CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA  1200
GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT  1260
GCATTTTCTG ATGATACTCT CAGCATGGTT CAGCGCCTCC TTAAATTAAT TCTGCAGAAT  1320
CACATATTGA AAGTAAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAAACC  1380
ATCGGAGGCA AACAGCTCAG AGTCTTCGTA TATCGTACAG CTGTCTGCAT TGAAAATTCA  1440
TGCATGGAGA AAGGGAGTAA GCAAGGGAGA AACGGTGCGA TTCACATATT CCGCGAGATC  1500
ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAAC AAGATAAGCG CTTTAGCACC  1560
TTCCTCAGCC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG  1620
ACATTATTTG TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT  1680
CTGATACGGG ACAAAAATGC TCTTCAAAAC ATCATTCTTT ATCACCTGAC ACCAGGAGTT  1740
TTCATTGGAA AAGGATTTGA ACCTGGTGTT ACTAACATTT TAAAGACCAC ACAAGGAAGC  1800
AAAATCTTTC TGAAAGAAGT AAATGATACA CTTCTGGTGA ATGAATTGAA ATCAAAAGAA  1860
TCTGACATCA TGACAACAAA TGGTGTAATT CATGTTGTAG ATAAACTCCT CTATCCAGCA  1920
GACACACCTG TTGGAAATGA TCAACTGCTG GAAATACTTA ATAAATTAAT CAAATACATC  1980
CAAATTAAGT TTGTTCGTGG TAGCACCTTC AAAGAAATCC CCGTGACTGT CTATACAACT  2040
AAAATTATAA CCAAAGTTGT GGAACCAAAA ATTAAAGTGA TTGAAGGCAG TCTTCAGCCT  2100
ATTATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGGTGA ACCTGAATTC  2160
AGACTGATTA AAGAAGGTGA AACAATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA  2220
AAATACACCA AAATCATTGA TGGAGTGCCT GTGGAAATAA CTGAAAAAGA GACACGAGAA  2280
GAACGAATCA TTACAGGTCC TGAAATAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA  2340
ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCATT  2400
GAAGGTGGTG ATGGTCATTT ATTTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC  2460
ACACCCGTGA GGAAGTTGCA AGCCAACAAA AAAGTTCAAG GTTCTAGAAG ACGATTAAGG  2520
GAAGGTCGTT CTCAGTGAAA ATCCAAAAAC CAGAAAAAAA TGTTTATACA ACCCTAAGTC  2580
AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACTG AAACATCAGC  2640
ACAAAGAAGC AATCATCAAA TAATTCTGAA CACAAATTTA ATATTTTTTT TTCTGAATGA  2700
GAAACATGAG GGAAATTGTG GAGTTAGCCT CCTGTGGTAA AGGAATTGAA GAAAATATAA  2760
CACCTTACAC CCTTTTTCAT CTTGACATTA AAAGTTCTGG CTAACTTTGG AATCCATTAG  2820
AGAAAAATCC TTGTCACCAG ATTCATTACA ATTCAAATCG AAGAGTTGTG AACTGTTATC  2880
CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATAC ATAAAATGCA CGCAAGCCAT  2940
TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA  3000
TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA  3060
CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA  3120
TCTCAAACGT TTCAATAAAA CCATTTTTCA GATATAAAGA GAATTACTTC AAATTGAGTA  3180
ATTCAGAAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA
```

Seq ID NO: 36 Protein sequence
Protein Accession #: NP_006466.1

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1          11         21         31         41         51
|          |          |          |          |          |
MIPFLPMFSL LLLLIVNPIN ANNHYDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC   60
KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTLGIVGA TTTQRYSDAS  120
KLREEIEGKG SPTYFAPSNE AWDNLDSDIR RGLESNVNVE LLNALHSHMI NKRMLTKDLK  180
NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IIHGNQIATN GVVHVIDRVL TQIGTSIQDF  240
IEAEDDLSSF RAAAITSDIL EALGRDGHFT LFAPTNEAFE KLPRGVLERF MGDKVASEAL  300
MKYHILNTLQ CSESIMGGAV FETLEGNTIE IGCDGDSITV NGIKMVNKKD IVTNNGVIHL  360
IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLLAPVN NAFSDDTLSM  420
VQRLLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG  480
RNGAIHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA  540
FKGMTSEEKE ILIRDKNALQ NIILYHLTPG VFIGKGFEPG VTNILKTTQG SKIFLKEVND  600
TLLVNELKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNDQL LEILNKLIKY IQIKFVRGST  660
FKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIIKTEGPTL TKVKIEGEPE FRLIKEGETI  720
TEVIHGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ETEETLKKLL  780
QEEVTKVTKF IEGGDGHLFE DEEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ
```

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40..417

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1          11         21         31         41         51
|          |          |          |          |          |
ATCCAATACA GGAGTGACTT GGAACTCCAT TCTATCACTA TGAAGAAAAG TGGTGTTCTT   60
TTCCTCTTGG GCATCATCTT GCTGGTTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA  120
AAGGGTCGCT GTTCCTGCAT CAGCACCAAC CAAGGGACTA TCCACCTACA ATCCTTGAAA  180
GACCTTAAAC AATTTGCCCC AAGCCCTTCC TGCGAGAAAA TTGAAATCAT TGCTACACTG  240
AAGAATGGAG TTCAAACATG TCTAAACCCA GATTCAGCAG ATGTGAAGGA ACTGATTAAA  300
AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA  360
AAGAAAGTTC TGAAAGTTCG AAAATCTCAA CGTTCTCGTC AAAAGAAGAC TACATAAGAG  420
ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA  480
TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAT TTGACTAGAA AATTTAAAAC  540
ATTACTCTGA AATTGTAACT AAAGTTAGAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA  600
TTGTTAAAGG CTATGATTGT CTTTGTTCTT CTACCACCCA CCAGTTGAAT TTCATCATGC  660
TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCACCCAA CCACATCCCA  720
CTCACAACAG CTGCCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCCAGAGAG  780
TATCTGAGGC ACATGTCAGC AAGTCCTAAG CCTGTTAGCA TGCTGGTGAG CCAAGCAGTT  840
TGAAATTGAG CTGGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC  900
CTACAGGCCT CACACACAAT GTGTCTGAGA GATTCATGCT GATTGTTATT GGGTATCACC  960
ACTGGAGATC ACCAGTGTGT GGCTTTCAGA GCCTCCTTTC TGGCTTTGGA AGCCATGTGA 1020
TTCCATCTTG CCCGCTCAGG CTGACCACTT TATTTCTTTT TGTTCCCCTT TGCTTCATTC 1080
AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCCTTT CTTCTCTCCA GTGCACCTGT 1140
CATATGCTCT GATTTATCTG AGTCAACTCC TTTCTCATCT TGTCCCCAAC ACCCCACAGA 1200
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WO03042661 [file://E:/WO03042661.pcc]


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AGTGCTTTCT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT  1260
AAATAAACCT TTTTGGACAC ACAAATTATC TTAAAACTCC TGTTTCACTT GGTTCAGTAC  1320
CACATGGGTG AACACTCAAT GGTTAACTAA TTCTTGGGTG TTTATCCTAT CTCTCCAACC  1380
AGATTGTCAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC  1440
CTAATAATAC TGTGGAACTA GGTTTTAATA ATTTTTTAAT TGATGTTGTT ATGGGCAGGA  1500
TGGCAACCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG  1560
CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT  1620
GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA  1680
GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG  1740
AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC  1800
CCAACCATAC AAAAATTCCT TTTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT  1860
TCTAAGATCT AACAAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAATATG  1920
AGTTTTATTG TCCGTTTACT TGTTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA  1980
TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT  2040
TAGTGGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAACC TCCTTCCAGG  2100
GGAGGTTCAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA  2160
CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA  2220
TCCCACCCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG  2280
AAAAATCTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG  2340
GTAGACAGTA TATAACTAAC AACCAAAGAC TACATATTGT CACTGACACA CACGTTATAA  2400
TCATTTATCA TATATATACA TACATGCATA CACTCTCAAA GCAAATAATT TTTCACTTCA  2460
AAACAGTATT GACTTGTATA CCTTGTAATT TGAAATATTT TCTTTGTTAA AATAGAATGG  2520
TATCAATAAA TAGACCATTA ATCAG
```

Seq ID NO: 38 Protein sequence
Protein Accession #: NP_002407

```
1          11         21         31         41         51
|          |          |          |          |          |
MKKSGVLFLL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK    60
IEIIATLKNG VQTCLNPDSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR   120
QKKTT
```

Seq ID NO: 39 DNA sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

```
1          11         21         31         41         51
|          |          |          |          |          |
CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCCAGCCC    60
AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCCGGGGCCC CGCCGCCGGG   120
GACGGGCGTC TGCGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCCTCGTCT   180
TCTCCCACCT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCCGCCGTG   240
TCCGCCCAGC CCCCGCTGCC GGACCAGTGC CCCGCGCTGT GCGAGTGCTC CGAGGCAGCG   300
CGCACAGTCA AGTGCGTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCCTAC   360
GTGCGCAACC TCTTCCTTAC CGGCAACCAG CTGGCCGTGC TCCCTGCCGG CGCCTTCGCC   420
CGCCGGCCGC CGCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCAGCCG CCTGGACGAG   480
GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC   540
CCACTGGCCG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC   600
AGTCCCCTTG TGGAACTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC   660
CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCCGTGCACT GCAGGGGCTC   720
CGCCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA   780
CTGCCCAGCC TCAGGCACCT GGACTTAAGT AATAATTCGC TGGTGAGCCT GACCTACGTG   840
TCCTTCCGCA ACCTGACACA TCTAGAAAGC CTCCACCTGG AGGACAATGC CCTCAAGGTC   900
CTTCACAATG GCACCCTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGGT TTTCCTGGAC   960
AACAATCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA  1020
GAGGTAGTGC AGGGCAAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG  1080
GTCCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG  1140
CAAACCTCTT ATGTCTTCCT GGGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCCTCCTG  1200
GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC  1260
AGGGATCACA TGGAAGGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA  1320
AACCTCAGTT CTAACTCGGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG  1380
CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA  1440
TAGATACAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCCTTG TTATGTAAAG  1500
TTTCTCGGTG TGTTCTGTTA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCCTC  1560
TTCTTTTTCT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA  1620
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC  1680
ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTTCGAG AAAAATACTT TATTCATAAA  1740
TATCAGTTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAT AATTGCATCC TATAAACTGC  1800
CTGCAGACGT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA  1860
AGAGCATGCT TACATTTTAC TGTTCTGCAT ATTACAAAAA ATAACTTGCA ACTTCATAAC  1920
TTCTTTGACA AAGTAAATTA CTTTTTTGAT TGCAGTTTAT ATGAAAATGT ACTGATTTTT  1980
TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAAAAA AAAAATAAAG  2040
ATTCTTAAAA GAA
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Seq ID NO: 40 Protein sequence
Protein Accession #: NP_006661

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGGCSRGPA AGDGRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD    60
QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL   120
AALNLSGSRL DEVRAGAFEH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL   180
NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLELASN HFLYLPRDVL AQLPSLRHLD   240
```

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LSNNSLVSLT YVSFRNLTHL ESLHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVCDC   300
HMADMVTWLK ETEVVQGKDR LTCAYPEKMR NRVLLELNSA DLDCDPILPP SLQTSYVFLG   360
IVLALIGAIF LLVLYLNRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV
```

Seq ID NO: 41 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..927

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCTGGGG GGTGCTCCCG GGCCCCCGCC GCCGGGGACG GGCGTCTGCG GCTGGCGCGA    60
CTAGCGCTGG TACTCCTGGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCATCCTCC   120
TTCTCCTCCT CGGCGCCGTT CCTGGCTTCC GCCGTGTCCG CCCAGCCCCC GCTGCCGGAC   180
CAGTGCCCCG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC   240
AATCTGACCG AGGTGCCCAC GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC   300
AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC   360
AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCCTTC   420
CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCCTTCAC   480
AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCCACATTA GGGTTTTCCT GGACAACAAT   540
CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA   600
GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAA AAATGAGGAA TCGGGTCCTC   660
TTGGAACTCA ACAGTGCTGA CCTGGACTGT GACCCGATTC TTCCCCCATC CCTGCAAACC   720
TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCCT CCTGGTTTTG   780
TATTTGAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT   840
CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC   900
AGTTCTAACT CGGATGTCCT CGAGTGA
```

Seq ID NO: 42 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGGCSRGPA AGDGRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD    60
QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLASNHFLY LPRDVLAQLP   120
SLRHLDLSNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELQGL PHIRVFLDNN   180
PWVCDCHMAD MVTWLKETEV VQGKDRLTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT   240
SYVFLGIVLA LIGAIFLLVL YLNRKGIKKW MHNIRDACRD HMEGYHYRYE INADPRLTNL   300
SSNSDVLE
```

Seq ID NO: 43 DNA sequence
Nucleic Acid Accession #: NM_058173
Coding sequence: 68..340

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCGCCTTGC CTTCTCTTAG GCTTTGAAGC ATTTTTGTCT GTGCTCCCTG ATCTTCAGGT    60
CACCACCATG AAGTTCTTAG CAGTCCTGGT ACTCTTGGGA GTTTCCATCT TTCTGGTCTC   120
TGCCCAGAAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCCTGCTGA   180
TGATGAAGCC CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC   240
TACCACTGCA ACCACCGCTG CTTCTACCAC TGCTCGTAAA GACATTCCAG TTTTACCCAA   300
ATGGGTTGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT   360
TCTGCAATTG GGTCACAACT ATTCATGCTT CCTGTGATTT CATCCAACTA CTTACCTTGC   420
CTACGATATC CCCTTTATCT CTAATCAGTT TATTTTCTTT CAAATAAAAA ATAACTATGA   480
GCGAGCTAAC AT
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Seq ID NO: 44 Protein sequence
Protein Accession #: NP_477521

```
1          11         21         31         41         51
|          |          |          |          |          |
MKFLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETTAAA TTATTAAPTT    60
ATTAASTTAR KDIPVLPKWV GDLPNGRVCP
```

Seq ID NO: 45 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

```
1          11         21         31         41         51
|          |          |          |          |          |
CAGCACCCAG CTCCCCGCCA CCGCCATGGT CCCCGACACC GCCTGCGTTC TTCTGCTCAC    60
CCTGGCTGCC CTCGGCGCGT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC   120
GCAGATGCTT CGGGAACTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT   180
GCGGCAGCAG GTCAGGGAGA TCACGTTCCT GAAAAACACG GTGATGGAGT GTGACGCGTG   240
CGGGATGCAG CAGTCAGTAC GCACCGGCCT ACCCAGCGTG CGGCCCCTGC TCCACTGCGC   300
GCCCGGCTTC TGCTTCCCCG GCGTGGCCTG CATCCAGACG GAGAGCGGCG GCCGCTGCGG   360
CCCCTGCCCC GCGGGCTTCA CGGGCAACGG CTCGCACTGC ACCGACGTCA ACGAGTGCAA   420
CGCCCACCCC TGCTTCCCCC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA   480
GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCACCAGGGC GTGGGGCTGG CTTTCGCCAA   540
GGCCAACAAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACTGCGT   600
CCCCAACTCC GTGTGCATCA ACACCCGGGG CTCCTTCCAG TGCGGCCCGT GCCAGCCCGG   660
CTTCGTGGGC GACCAGGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCCGACGG   720
CTCGCCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCCTA GAGCGCGATG GCTCGCGGTC   780
GTGCGTGTGT CGCGTTGGCT GGGCCGGCAA CGGGATCCTC TGTGGTCGCG ACACTGACCT   840
AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCCGGAGCCG CAGTGCCGTA AGGACAACTG   900
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CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCCTG   960
CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGCG  1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG  1080
GTCCCAGAAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA  1140
CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCCGAC AACTGCCCTA GGGTACCCAA  1200
CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA  1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG  1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACTGTC CCACGGTGCC  1380
TAACAGTGCC CAGGAGGACT CAGACCACGA TGGCCAGGGT GATGCCTGCG ACGACGACGA  1440
CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCGC CTGGTGCCTA ACCCCGGCCA  1500
GGAGGACGCG GACAGGGACG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA  1560
GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCACGCTCA CCGACTTCAG  1620
GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT  1680
GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT  1740
GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAC  1800
GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAGGAC AGCTCCAGCT TCTACGTGGT  1860
CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA  1920
GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA  1980
CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG  2040
AAACGTGGGT TGGAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GGCCCCAAGT  2100
GGGCTACATC AGGGTGCGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT  2160
CTTGGACACA ACCATGCGGG GTGGCCGCCT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT  2220
CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA  2280
TCAGCTGCGG CAAGCCTAGG GACCAGGGTG AGGACCCGCC GGATGACAGC CACCCTCACC  2340
GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCCTGAGG GGGAAGTGAG  2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG
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Seq ID NO: 46 Protein sequence
Protein Accession #: NP_000086.1

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1          11         21         31         41         51
|          |          |          |          |          |
MVPDTACVLL LTLAALGASG QGQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT    60
FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG   120
NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD   180
INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH   240
ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ   300
EDVDRDGIGD ACDPDADGDG VPNEKDNCPL VRNPDQRNTD EDKWGDACDN CRSQKNDDQK   360
DTDQDGRGDA CDDDIDGDRI RNQADNCPRV PNSDQKDSDG DGIGDACDNC PQKSNPDQAD   420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPDS   480
RDNCRLVPNP GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD   540
PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI   600
FGYQDSSSFY VVMWKQMEQT YWQANPFRAV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT   660
ESQVRLLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG   720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA
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Seq ID NO: 47 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67..363

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1          11         21         31         41         51
|          |          |          |          |          |
GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC    60
AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC   120
ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA   180
CCTGTTAATC CAAGGTCTTT AGAAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA   240
CGTGTTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA   300
TCGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT   360
TAAAACCAGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG   420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA   480
GTTACACTAA AAGGTGACCA ATGATGGTCA CCAAATCAGC TGCTACTACT CCTGTAGGAA   540
GGTTAATGTT CATCATCCTA AGCTATTCAG TAATAACTCT ACCCTGGCAC TATAATGTAA   600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCTGACC CTGCTTCAAA TATTTCCCTC   660
ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAATTC   720
TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTTTAAAG AATGCTCTTT   780
ACTTCATGGA CTTCCACTGC CATCCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA   840
CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT   900
CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT   960
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA  1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG  1080
TTTTCAAATA AAAATGAGGT ACTCTCCTGG AAATATTAAG
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Seq ID NO: 48 Protein sequence
Protein Accession #: NP_001556.1

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1          11         21         31         41         51
|          |          |          |          |          |
MNQTAILICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV    60
EIIATMKKKG EKRCLNPESK AIKNLLKAVS KEMSKRSP
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Seq ID NO: 49 DNA sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

WO03042661 [file:///E:/WO03042661.pcl]


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1          11         21         31         41         51
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GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG    60
CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG   120
CGCTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCCGCCTCCC CGCAGCGGCT   180
CCGCGGCCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT   240
CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG   300
AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG   360
CATTCCGGGT ACACCTGGGA TCCCAGGTCG GGATGGATTC AAAGGAGAAA AGGGGGAATG   420
TCTGAGGGAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC   480
ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC   540
AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACTTCGG CTAAAATGCA GAAATGCATG   600
CTGTCAGCGT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTGA   660
AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG   720
CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT   780
CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT   840
TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC   900
TTTTTTTATT ATGCCTTGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA   960
CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT  1020
TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTTTTAGT  1080
TGGTTAGAAT ACTTTCTTCA TAGTCACATT CTCTCAACCT ATAATTTGGA ATATTGTTGT  1140
GGTCTTTTGT TTTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT  1200
TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA  1260
CAACCTTAAA AAAAAAAAAA AAAA
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Seq ID NO: 50 Protein sequence
Protein Accession #: XP_057014

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1          11         21         31         41         51
|          |          |          |          |          |
MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA    60
GVPGRDGSPG ANGIPGTPGI PGRDGFKGEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL   120
GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIIYLDQ   180
GSPEMNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIIEE   240
LPK
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Seq ID NO: 51 DNA sequence
Nucleic Acid Accession #: NM_020974
Coding sequence: 81..3080

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1          11         21         31         41         51
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CCGCAACCGC TGAGCCATCC ATGGGGGTCG CGGGCCGCAA CCGTCCCGGG GCGGCCTGGG   120
CGGTGCTGCT GCTGCTGCTG CTGCTGCCGC CACTGCTGCT GCTGGCGGGG GCCGTCCCGC   180
CGGGTCGGGG CCGTGCCGCG GGGCCGCAGG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG   240
ATGACTGCCA TGCCGACGCC CTGTGTCAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA   300
AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC   360
TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT   420
TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG   480
AGAACAATGG CGGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGCTGCT   540
GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG   600
GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCCAAGGG   660
GCAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA   720
TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG   780
GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG   840
AGCGAGAGGA CACTGTCCTG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG   900
ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG   960
ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGTCCTGTT GGATTCACTC  1020
TCCAGTTGGA TGGGAACACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT  1080
GTGATCATTT CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAAGGATTTA  1140
AATTATTAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT  1200
GTGACCACAG CTGCATCAAC CACCCTGGCA CATTTGCTTG TGCTTGCAAC CGAGGGTACA  1260
CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT  1320
GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA  1380
AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT  1440
CACCCCGTGT GTCCCTGCAC TGCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT  1500
GTCACTCTGG CATTCACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA  1560
AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTTCCCGAG GGTCTGCGAC  1620
CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT  1680
GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT  1740
TTATCACTGT TGAGTTTGAG CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTTGTGACC  1800
TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA  1860
AGGCCGTCCA CAGGGAGCAG TTTCACCTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA  1920
AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCCTG TGGAGTGGGC CAGGGTCATG  1980
CAGAAAACCA ATGTGTCAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT  2040
GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT  2100
GCCCAAGACC AGGAAATTCT GGGGCCCTGA AGACCCCAGA AGCTTGGAAT ATGTCTGAAT  2160
GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGCACCT TGCCAGCTCT  2220
GTGCCCTGGG CACGTTCCAG CCTGAAGCTG GTCGAACTTC CTGCTTCCCC TGTGGAGGAG  2280
GCCTTGCCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT  2340
GTTCACCTGG ACATTTCTAC AACACCACCA CTCACCGATG TATTCGTTGC CCAGTGGGAA  2400
CATACCAGCC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG  2460
ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG  2520
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GAGATTTCAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG  2580
AGTGTACGTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATCGTG GTCCCTGAGA  2640
TCTTCCTGCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT  2700
CCAATTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT  2760
CCAGGTCAAA GAAGCTGTGG ATTCAGTTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT  2820
TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCAGGA ACTCATTGAA GACATAGTTC  2880
GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAAACTTA  2940
TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCCAGG  3000
AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT  3060
TTTTGAGACC TTACAAATGA CTCAGCCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG  3120
GGTTGGTGGG ACAGAGCTGT CTTCCTTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCCTC  3180
CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGGTAAATT  3240
GAACTTGGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT  3300
CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGGACT  3360
TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCCTCC TCAAGGAGTC  3420
TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACTTCAGC TTCCTCTAGC  3480
CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG  3540
CAAGAGGGGA GGGAAGGAGA CCCCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG  3600
ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACTTG  3660
AGTTCTAAGC AGTGCTCGTG AAAAAAAAAA GCAGAAAGAA TTAGAAATAA ATAAAAACTA  3720
AGCACTTCTG GAGACAT
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Seq ID NO: 52 Protein sequence
Protein Accession #: NP_066025

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1          11         21         31         41         51
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LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNYR CTCFDGFMLA  120
HDGHNCLDVD ECLENNGGCQ HTCVNVMGSY ECCCKEGFFL SDNQHTCIHR SEEGLSCMNK  180
DHGCSHICKE APRGSVACEC RPGFELAKNQ RDCILTCNHG NGGCQHSCDD TADGPECSCH  240
PQYKMHTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCDRTCKDT  300
STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK  360
SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQQVCVN  420
TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL  480
SSDVTTIRTS VTFKLNEGKC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGKQV  540
PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ  600
FHLQLSGMNL DVAKKPPRTS ERQAESCGVG QGHAENQCVS CRAGTYYDGA RERCILCPNG  660
TFQNEEGQMT CEPCPRPGNS GALKTPEAWN MSECGGLCQP GEYSADGFAP CQLCALGTFQ  720
PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYQPEFG  780
KNNCVSCPGN TTTDFDGSTN ITQCKNRRCG GELGDFTGYI ESPNYPGNYP ANTECTWTIN  840
PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSSNSVTTY ETCQTYERPI AFTSRSKKLW  900
IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLIKALFDV  960
LAHPQNYFKY TAQESREMFP RSFIRLLRSK VSRFLRPYK
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Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_014211
Coding sequence: 157..1479

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GGGACAGGGC TGAGGATGAG GAGAACCCTG GGGACCCAGA AGACCGTGCC TTGCCCGGAA   60
GTCCTGCCTG TAGGCCTGAA GGACTTGCCC TAACAGAGCC TCAACAACTA CCTGGTGATT  120
CCTACTTCAG CCCCTTGGTG TGAGCAGCTT CTCAACATGA ACTACAGCCT CCACTTGGCC  180
TTCGTGTGTC TGAGTCTCTT CACTGAGAGG ATGTGCATCC AGGGGAGTCA GTTCAACGTC  240
GAGGTCGGCA GAAGTGACAA GCTTTCCCTG CCTGGCTTTG AGAACCTCAC AGCAGGATAT  300
AACAAATTTC TCAGGCCCAA TTTTGGTGGA GAACCCGTAC AGATAGCGCT GACTCTGGAC  360
ATTGCAAGTA TCTCTAGCAT TTCAGAGAGT AACATGGACT ACACAGCCAC CATATACCTC  420
CGACAGCGCT GGATGGACCA GCGGCTGGTG TTTGAAGGCA ACAAGAGCTT CACTCTGGAT  480
GCCCGCCTCG TGGAGTTCCT CTGGGTGCCA GATACTTACA TTGTGGAGTC CAAGAAGTCC  540
TTCCTCCATG AAGTCACTGT GGGAAACAGG CTCATCCGCC TCTTCTCCAA TGGCACGGTC  600
CTGTATGCCC TCAGAATCAC GACAACTGTT GCATGTAACA TGGATCTGTC TAAATACCCC  660
ATGGACACAC AGACATGCAA GTTGCAGCTG GAAAGCTGGG GCTATGATGG AAATGATGTG  720
GAGTTCACCT GGCTGAGAGG GAACGACTCT GTGCGTGGAC TGGAACACCT GCGGCTTGCT  780
CAGTACACCA TAGAGCGGTA TTTCACCTTA GTCACCAGAT CGCAGCAGGA GACAGGAAAT  840
TACACTAGAT TGGTCTTACA GTTTGAGCTT CGGAGGAATG TTCTGTATTT CATTTTGGAA  900
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GATTCAGTCC CTGCAAGAAC CTGCATTGGA GTGACGACCG TGTTATCAAT GACCACACTG 1020
ATGATCGGGT CCCGCACTTC TCTTCCCAAC ACCAACTGCT TCATCAAGGC CATCGATGTG 1080
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TACAGTTCCT TACAGCAGAT GGCAGCCAAA GATAGGGGGA CAACAAAGGA AGTAGAAGAA 1200
GTCAGTATTA CTAATATCAT CAACAGCTCC ATCTCCAGCT TTAAACGGAA GATCAGCTTT 1260
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GACAAGTTCA AGTTTGTCTT CCGAGAAAAG ATGGGCAGGA TTGTTGATTA TTTCACAATT 1380
CAAAACCCCA GTAATGTTGA TCACTATTCC AAACTACTGT TTCCTTTGAT TTTTATGCTA 1440
GCCAATGTAT TTTACTGGGC ATACTACATG TATTTTTGAG TCAATGTTAA ATTTCTTGCA 1500
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ACCCACATCC AATGGTGCTA CAAGTGACTG AAATAATATT TGAGTCTTTC TGCTCAAAGA 1620
ATGAAGCTCC AACCATTGTT CTAAGCTGTG TAGAAGTCCT AGCATTATAG GATCTTGTAA 1680
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AAGAATGGGA AGGAGACCAT TGGGTAACCC TCAAGTGTCA GAAGTTGTTT CTAAAGTAAC 1860
TATACATGTT TTTTACTAAA TCTCTGCAGT GCTTATAAAA TACATTGTTG CCTATTTAGG 1920
GAGTAACATT TTCTAGTTTT TGTTTCTGGT TAAAATGAAA TATGGGCTTA TGTCAATTCA 1980
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TTGGAAGTCA ATGCACTAAC TCAATACCAA GATGAGTTTT TAAATAATGA ATATTATTTA  2040
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GGATTCCCCA TACTGGAAGG ACTCTGAGGC TTTATTCCCC CACTATGCAT ATCTTATCAT  2220
TTTATTATTA TACACACATC CATCCTAAAC TATACTAAAG CCCTTTTCCC ATGCATGGAT  2280
GGAAATGGAA GATTTTTTTG TAACTTGTTC TAGAAGTCTT AATATGGGCT GTTGCCATGA  2340
AGGCTTGCAG AATTGAGTCC ATTTTCTAGC TGCCTTTATT CACATAGTGA TGGGGTACTA  2400
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GAGCAACACT CTCCCAGTGG CAGATCCCCT GTATCATTCC AAGAGGAGCA TTCATCCCTT  2520
TGCTCTAATG ATCAGGAATG ATGCTTATTA GAAAACAAAC TGCTTGACCC AGGAACAAGT  2580
GGCTTAGCTT AAGTAAACTT GGCTTTGCTC AGATCCCTGA TCCTTCCAGC TGGTCTGCTC  2640
TGAGTGGCTT ATCCCGCATG AGCAGGAGCG TGCTGGCCCT GAGTACTGAA CTTTCTGAGT  2700
AACAATGAGA CACGTTACAG AACCTATGTT CAGGTTGCGG GTGAGCTGCC CTCTCCAAAT  2760
CCAGCCAGAG ATGCACATTC CTCGGCCAGT CTCAGCCAAC AGTACCAAAA GTGATTTTTG  2820
AGTGTGCCAG GGTAAAGGCT TCCAGTTCAG CCTCAGTTAT TTTAGACAAT CTCGCCATCT  2880
TTAATTTCTT AGCTTCCTGT TCTAATAAAT GCACGGCTTT ACCTTTCCTG TCAGAAATAA  2940
ACCAAGGCTC TAAAAGATGA TTTCCCTTCT GTAACTCCCT AGAGCCACAG GTTCTCATTC  3000
CTTTTCCCAT TATACTTCTC ACAATTCAGT TTCTATGAGT TTGATCACCT GATTTTTTTA  3060
ACAAAATATT TCTAACGGGA ATGGGTGGGA GTGCTGGTGA AAAGAGATGA AATGTGGTTG  3120
TATGAGCCAA TCATATTTGT GATTTTTTAA AAAAAGTTTA AAAGGAAATA TCTGTTCTGA  3180
AACCCCACTT AAGCATTGTT TTTATATAAA AACAATGATA AAGATGTGAA CTGTGAAATA  3240
AATATACCAT ATTAGCTACC CACC
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Seq ID NO: 54 Protein sequence
Protein Accession #: NP_055026

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MNYSLHLAFV CLSLFTERMC IQGSQFNVEV GRSDKLSLPG FENLTAGYNK FLRPNFGGEP   60
VQIALTLDIA SISSISESNM DYTATIYLRQ RWMDQRLVFE GNKSFTLDAR LVEFLWVPDT  120
YIVESKKSFL HEVTVGNRLI RLFSNGTVLY ALRITTTVAC NMDLSKYPMD TQTCKLQLES  180
WGYDGNDVEF TWLRGNDSVR GLEHLRLAQY TIERYFTLVT RSQQETGNYT RLVLQFELRR  240
NVLYFILETY VPSTFLVVLS WVSFWISLDS VPARTCIGVT TVLSMTTLMI GSRTSLPNTN  300
CFIKAIDVYL GICFSFVFGA LLEYAVAHYS SLQQMAAKDR GTTKEVEEVS ITNIINSSIS  360
SFKRKISFAS IEISSDNVDY SDLTMKTSDK FKFVFREKMG RIVDYFTIQN PSNVDHYSKL  420
LFPLIFMLAN VFYWAYYMYF
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Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 138..2405

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Nucleic Acid Accession #: NM_015419.1
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Seq ID NO: 58 Protein sequence
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DGGSQLILEK FQLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHLNQT DPPDIDINAT  360
VALDFECPMT RENYEKLWKL IAYYSEVPVK LHRELMLSKD PRVSYQYRQD ADEEALYYTG  420
VRAQILAEPE WVMQPSIDIQ LNRRQSTAKK VLLSYYTQYS QTISTKDTRQ ARGRSWVMIE  480
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RIKSMEPSDS GLYQCIAQVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN  600
ALAIPEAHLS WILPNRRIIN DLANTSHVYM LPNGTLSIPK VQVSDSGYYR CVAVNQQGAD  660
HFTVGITVTK KGSGLPSKRG RRPGAKALSR VREDIVEDEG GSGMGDEENT SRRLLHPKDQ  720
EVFLKTKDDA INGDKKAKKG RRKLKLWKHS EKEPETNVAE GRRVFESRRR INMANKQINP  780
ERWADILAKV RGKNLPKGTE VPPLIKTTSP PSLSLEVTPP FPAVSPPSAS PVQTVTSAEE  840
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TEGDLKGTAA PTLISEPYEP SPTLHTLDTV YEKPTHEETA TEGWSAADVG SSPEPTSSEY  960
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Seq ID NO: 59 DNA sequence
Nucleic Acid Accession #: Eos sequence
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Seq ID NO: 60 Protein sequence
Protein Accession #: Eos sequence

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Seq ID NO: 62 Protein sequence
Protein Accession #: NP_073580

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CNSFTICNAE MQEVGVGLYP SISLLNHSCD PNCSIVFNGP HLLLRAVRDI EVGEELTICY   180
LDMLMTSEER RKQLRDQYCF ECDCFRCQTQ DKDADMLTGD EQVWKEVQES LKKIEELKAH   240
WKWEQVLAMC QAIISSNSER LPDINIYQLK VLDCAMDACI NLGLLEEALF YGTRTMEPYR   300
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Seq ID NO: 63 DNA sequence
Nucleic Acid Accession #: NM_003014.2
Coding sequence: 238..648

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TCTTGCCAGT GTCCACACAT CCTGCCCCAT CAAGATGTTC TCATCATGTG TTACGAGTGG  1020
CGTTCAAGGA TGATGCTTCT TGAAAATTGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT  1080
AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG  1140
AAGAAAACAG CCGGGCGCAC CAGTCGTAGT AATCCCCCCA AACCAAAGGG AAAGCCTCCT  1200
GCTCCCAAAC CAGCCAGTCC CAAGAAGAAC ATTAAAACTA GGAGTGCCCA GAAGAGAACA  1260
AACCCGAAAA GAGTGTGAGC TAACTAGTTT CCAAAGCGGA GACTTCCGAC TTCCTTACAG  1320
GATGAGGCTG GGCATTGCCT GGGACAGCCT ATGTAAGGCC ATGTGCCCCT TGCCCTAACA  1380
ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCATT TTTCTTAAGG CTATGCTTCA  1440
GTTTTTCTTT GTAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAGGT  1500
GAGTTAAAGC TGGTGGAAAA GGCTTATTGC ATTGCATTCA GAGTAACCTG TGTGCATACT  1560
CTAGAAGAGT AGGGAAAATA ATGCTTGTTA CAATTCGACC TAATATGTGC ATTGTAAAAT  1620
AAATGCCATA TTTCAAACAA AACACGTAAT TTTTTTACAG TATGTTTTAT TACCTTTTGA  1680
TATCTGTTGT TGCAATGTTA GTGATGTTTT AAAATGTGAT GAAAATATAA TGTTTTTAAG  1740
AAGGAACAGT AGTGGAATGA ATGTTAAAAG ATCTTTATGT GTTTATGGTC TGCAGAAGGA  1800
TTTTTGTGAT GAAAGGGGAT TTTTTGAAAA ATTAGAGAAG TAGCATATGG AAAATTATAA  1860
TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTTAGCT AGAAACTTAA AAACAAAAAT  1920
AATAATAAAG AAAAATAAAT AAAAAGGAGA GGCAGACAAT GTCTGGATTC CTGTTTTTTG  1980
GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC CCTCTTAAGC AGCACCAGAA  2040
ACAGTGAGTT TGTCTGTACC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT  2100
ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACTT CCCAGGACAT CCACCCTGAG  2160
AATAATTTGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT  2220
TTAAATATTT TCTTTGCCTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG  2280
AAAGTTGAGT TCCACCTCTG AAATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA  2340
AAAAAGAACT TATTTGCAGC ATTTTATCAA CAAATTTCAT AATTGTGGAC AATTGGAGGC  2400
ATTTATTTTA AAAAACAATT TTATTGGCCT TTTGCTAACA CAGTAAGCAT GTATTTTATA  2460
AGGCATTCAA TAAATGCACA ACGCCCAAAG GAAATAAAAT CCTATCTAAT CCTACTCTCC  2520
ACTACACAGA GGTAATCACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT  2580
GCACTTATAA AATGATTTGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC  2640
CTGCCTCCTT TGCTTGGCCC TTTATTGAGA TAAGTTTTCC TGTCAAGAAA GCAGAAACCA  2700
TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC  2760
TATTGGATAC TTAGGTGGTT TCTTCACTGA CAATACTGAA TAAACATCTC ACCGGAATTC
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Seq ID NO: 64 Protein sequence
Protein Accession #: NP_003005.1

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1          11         21         31         41         51
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|          |          |          |          |          |
MFLSILVALC LWLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ    60
YEELVDVNCS AVLRFFFCAM YAPICTLEFL HDPIKPCKSV CQRARDDCEP LMKMYNHSWP   120
ESLACDELPV YDRGVCISPE AIVTDLPEDV KWIDITPDMM VQERPLDVDC KRLSPDRCKC   180
KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTQVPLITN   240
SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD   300
KKKTAGRTSR SNPPKPKGKP PAPKPASPKK NIKTRSAQKR TNPKRV

Seq ID NO: 65 DNA sequence
Nucleic Acid Accession #:  BC010423
Coding sequence: 248..1780

1          11         21         31         41         51
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AGCTACGGCT GGGTGTGTAG AACGGGGCCG GGGCTGGGGC TGGGTCCCCT AGTGGAGACC   120
CAAGTGCGAG AGGCAAGAAC TCTGCAGCTT CCTGCCTTCT GGGTCAGTTC CTTATTCAAG   180
TCTGCAGCCG GCTCCCAGGG AGATCTCGGT GGAACTTCAG AAACGCTGGG CAGTCTGCCT   240
TTCAACCATG CCCCTGTCCC TGGGAGCCGA GATGTGGGGG CCTGAGGCCT GGCTGCTGCT   300
GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCCGCG GGTGAGCTGG AGACCTCAGA   360
CGTGGTAACT GTGGTGCTGG GCCAGGACGC AAAACTGCCC TGCTTCTACC GAGGGGACTC   420
CGGCGAGCAA GTGGGGCAAG TGGCATGGGC TCGGGTGGAC GCGGGCGAAG GCGCCCAGGA   480
ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC CCGGCTTACG AGGGCCGCGT   540
GGAGCAGCCG CCGCCCCCAC GCAACCCCCT GGACGGCTCA GTGCTCCTGC GCAACGCAGT   600
GCAGGCGGAT GAGGGCGAGT ACGAGTGCCG GGTCAGCACC TTCCCCGCCG GCAGCTTCCA   660
GGCGCGGCTG CGGCTCCGAG TGCTGGTGCC TCCCCTGCCC TCACTGAATC CTGGTCCAGC   720
ACTAGAAGAG GGCCAGGGCC TGACCCTGGC AGCCTCCTGC ACAGCTGAGG GCAGCCCAGC   780
CCCCAGCGTG ACCTGGGACA CGGAGGTCAA AGGCACAACG TCCAGCCGTT CCTTCAAGCA   840
CTCCCGCTCT GCTGCCGTCA CCTCAGAGTT CCACTTGGTG CCTAGCCGCA GCATGAATGG   900
GCAGCCACTG ACTTGTGTGG TGTCCCATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA   960
CATCCTCCAC GTGTCCTTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT  1020
GTGGCACATT GGCAGAGAAG GAGCTATGCT CAAGTGCCTG AGTGAAGGGC AGCCCCCTCC  1080
CTCATACAAC TGGACACGGC TGGATGGGCC TCTGCCCAGT GGGGTACGAG TGGATGGGGA  1140
CACTTTGGGC TTTCCCCCAC TGACCACTGA GCACAGCGGC ATCTACGTCT GCCATGTCAG  1200
CAATGAGTTC TCCTCAAGGG ATTCTCAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA  1260
CTCTGGGAAG CAGGTGGACC TAGTGTCAGC CTCGGTGGTG GTGGTGGGTG TGATCGCCGC  1320
ACTCTTGTTC TGCCTTCTGG TGGTGGTGGT GGTGCTCATG TCCCGATACC ATCGGCGCAA  1380
GGCCCAGCAG ATGACCCAGA AATATGAGGA GGAGCTGACC CTGACCAGGG AGAACTCCAT  1440
CCGGAGGCTG CATTCCCATC ACACGGACCC CAGGAGCCAG CCGGAGGAGA GTGTAGGGCT  1500
GAGAGCCGAG GGCCACCCTG ATAGTCTCAA GGACAACAGT AGCTGCTCTG TGATGAGTGA  1560
AGAGCCCGAG GGCCGCAGTT ACTCCACGCT GACCACGGTG AGGGAGATAG AAACACAGAC  1620
TGAACTGCTG TCTCCAGGCT CTGGGCGGGC CGAGGAGGAG GAAGATCAGG ATGAAGGCAT  1680
CAAACAGGCC ATGAACCATT TTGTTCAGGA GAATGGGACC CTACGGGCCA AGCCCACGGG  1740
CAATGGCATC TACATCAATG GGCGGGGACA CCTGGTCTGA CCCAGGCCTG CCTCCCTTCC  1800
CTAGGCCTGG CTCCTTCTGT TGACATGGGA GATTTTAGCT CATCTTGGGG GCCTCCTTAA  1860
ACACCCCCAT TTCTTGCGGA AGATGCTCCC CATCCCACTG ACTGCTTGAC CTTTACCTCC  1920
AACCCTTCTG TTCATCGGGA GGGCTCCACC AATTGAGTCT CTCCCACCAT GCATGCAGGT  1980
CACTGTGTGT GTGCATGTGT GCCTGTGTGA GTGTTGACTG ACTGTGTGTG TGTGGAGGGG  2040
TGACTGTCCG TGGAGGGGTG ACTGTGTCCG TGGTGTGTAT TATGCTGTCA TATCAGAGTC  2100
AAGTGAACTG TGGTGTATGT GCCACGGGAT TTGAGTGGTT GCGTGGGCAA CACTGTCAGG  2160
GTTTGGCGTG TGTGTCATGT GGCTGTGTGT GACCTCTGCC TGAAAAAGCA GGTATTTTCT  2220
CAGACCCCAG AGCAGTATTA ATGATGCAGA GGTTGGAGGA GAGAGGTGGA GACTGTGGCT  2280
CAGACCCAGG TGTGCGGGCA TAGCTGGAGC TGGAATCTGC CTCCGGTGTG AGGGAACCTG  2340
TCTCCTACCA CTTCGGAGCC ATGGGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA  2400
GAGGCTTGAA CTGTTACAGA AGCCCTCTGC CCTCTGGTGG CCTCTGGGCC TGCTGCATGT  2460
ACATATTTTC TGTAAATATA CATGCGCCGG GAGCTTCTTG CAGGAATACT GCTCCGAATC  2520
ACTTTTAATT TTTTTCTTTT TTTTTTCTTG CCCTTTCCAT TAGTTGTATT TTTTATTTAT  2580
TTTTATTTTT ATTTTTTTTT AGAGTTTGAG TCCAGCCTGG ACGATATAGC CAGACCCTGT  2640
CTGTAAAAAA ACCAAAACCC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 66 Protein sequence
Protein Accession #: AAH10423

1          11         21         31         41         51
|          |          |          |          |          |
MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE    60
QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA   120
DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS   180
VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL   240
HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL   300
GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL   360
FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA   420
EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ   480
AMNHFVQENG TLRAKPTGNG IYINGRGHLV

Seq ID NO: 67 DNA sequence
Nucleic Acid Accession #: NM_001203
Coding sequence: 274..1782

1          11         21         31         41         51
|          |          |          |          |          |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGCGGAGA CCGCGGCGCT    60
GACGACGCGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT   120
GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTTGATAAA GGTTCAGACT TCTGCTGATT   180
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CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC   240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA   300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC   360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA   420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTGCCTGT GGTCACTTCT   480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTCGGG ACACTCCCAT TCCTCATCAA   540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCTACA   600
CTGCCTCCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCTTTACTT   660
ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG   720
TATAAAAGAC AAGAAACCAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC   780
ATTCCTCCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC ACGAAGTGGA   840
TCAGGCCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAAACAG   900
ATTGCAAAAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT   960
GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG  1020
ACAGTGTTGA TGAGGCATGA AAACATTTTG GGTTTCATTG CTGCAGATAT CAAAGGGACA  1080
GGGTCCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT  1140
TATCTGAAGT CCACCACCCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC  1200
AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAACC AGCAATTGCC  1260
CATCGAGATC TGAAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACTTG CTGTATTGCT  1320
GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC  1380
ACTCGAGTTG GCACCAAACG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA  1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG  1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC  1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA  1620
CGCCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACTC  1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA  1740
ACACTTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG  1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA  1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC  1920
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG  1980
TCTGTTTGTA GGCGGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT
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Seq ID NO: 68 Protein sequence
Protein Accession #: NP_001194

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1          11         21         31         41         51
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MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED    60
DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD   120
GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPRYS IGLEQDETYI PPGESLRDLI   180
EQSQSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTEEAS   240
WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS   300
MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILV KKNGTCCIAD LGLAVKFISD   360
TNEVDIPPNT RVGTKRYMPP EVLDESLNRN HFQSYIMADM YSFGLILWEV ARRCVSGGIV   420
EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS   480
RLTALRVKKT LAKMSESQDI KL
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Seq ID NO: 69 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 166..1737

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1          11         21         31         41         51
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AGTGCAGTAG TGTGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCCTCA ACTCAAGCAA   120
TCCTCCCACC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA   180
TTAAAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG   240
GCGGTAGCTG TTTCATTTTT CTTCGTTGAA GTCTTCACCT ACGGCATCAT CAAGACATTT   300
GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG   360
ATAATCTCAA TCTGTGTGTT TGTCTTAACA TTTTCAGCTC CCCTCGCCAC AGTCCTGAGC   420
AATCGTTTCG GACACCGTCT GGTAGTGATG TTGGGGGGGC TACTTGTCAG CACCGGGATG   480
GTGGCCGCCT CCTTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT   540
GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC   600
AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT   660
TTCGCACCAG CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CCTCCTCTTC   720
GTGGGCCTAC TACAGTTAAA CATTGTCATC TTCGGAGCAC TGCTCAGACC CATCTTTATC   780
AGAGGACCAG CGTCACCGAA AATAGTCATC CAGGAAAATC GGAAAGAAGC GCAGTATATG   840
CTTGAAAATG AGAAAACACG AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAACT   900
ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG   960
CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC  1020
TTCTCCATTT TGAAAGAGAA AAGTTTTATT TGTTATGCAT TATTTGGTCT CTTTGCAACA  1080
CTGGGATTCT TTGCACCTTC CTTGTACATC ATTCCTCTGG GCATTAGTCT GGGCATTGAC  1140
CAGGACCGCG CTGCTTTTTT ATTATCTACG ATGGCCATTG CAGAAGTTTT CGGAAGGATC  1200
GGAGCTGGTT TTGTCCTCAA CAGGGAGCCC ATTCGTAAGA TTTACATTGA GCTCATCTGC  1260
GTCATCTTAT TGACTGTGTC TCTGTTTGCC TTTACTTTTG CTACTGAATT CTGGGGTCTA  1320
ATGTCATGCA GCATATTTTT TGGGTTTATG GTTGGAACAA TAGGAGGGAC TCACATTCCA  1380
CTGCTTGCTG AGGATGATGT CGTGGGCATT GAGAAGATGT CTTCTGCAGC TGGGGTCTAC  1440
ATCTTCATTC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC  1500
CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCCTGCGCAG CTGGCATGGC CCTGGCTGCT  1560
GTGTGCCTCG CCCTGGTGAG ACCGTGTAAG ATGGGACTGT GCCAGCATCA TCACTCAGGT  1620
GAAACAAAGG TAGTGAGCCA TCGTGGGAAG ACTTTACAGG ACATACCTGA AGACTTTCTG  1680
GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACGTGC AAATGGAGCC GGTATGACAC  1740
ACTTTCTTAC AACAACAGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAACGGGG  1800
ACACAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAAACTACA TTTTAAAGGG  1860
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AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTTT TGTTTTGTTT TGTTTTAAGC  1920
TTTTTTTTTT TGCTTGTTTT TAAAGCCAAA ACAAAAAACA ACCAAGCACT CTTCCATATA  1980
TAAATCTGGC TGTATTCAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA  2040
TTCCGATATT AAAATAGTGA CATGAACTGG CAAAGTGGTT TTAAAAGCTT TCACGTGGGA  2100
TAAATGATTT TCTTTTTTTC TTTTCTTTCT TCCTATGGTC TTGTCTGAAT AAACTACTCT  2160
CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAAATGAA ATTGGCCAGT C
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Seq ID NO: 70 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MTQNKLKLCS KANVYTEVPD GGWGWAVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESN   60
SRISWIISIC VFVLTFSAPL ATVLSNRFGH RLVVMLGGLL VSTGMVAASF SQEVSHMYVA  120
IGIISGLGYC FSFLPTVTIL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGWR  180
YSLLFVGLLQ LNIVIFGALL RPIFIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS  240
GVELTTSPKN VPTHTNLELE PKADMQQVLV KTSPRPSEKK APLLDFSILK EKSFICYALF  300
GLFATLGFFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY  360
IELICVILLT VSLFAFTFAT EFWGLMSCSI FFGFMVGTIG GTHIPLLAED DVVGIEKMSS  420
AAGVYIFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ  480
HHHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV
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Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: NM_004694
Coding sequence: 166..1737

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1          11         21         31         41         51
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AGTGCAGTAG TGTGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCCTCA ACTCAAGCAA  120
TCCTCCCACC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA  180
TTAAAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG  240
GCGGTAGCTG TTTCATTTTT CTTCGTTGAA GTCTTCACCT ACGGCATCAT CAAGACATTT  300
GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG  360
ATAATCTCAA TCTGTGTGTT TGTCTTAACA TTTTCAGCTC CCCTCGCCAC AGTCCTGAGC  420
AATCGTTTCG GACACCGTCT GGTAGTGATG TTGGGGGGGC TACTTGTCAG CACCGGGATG  480
GTGGCCGCCT CCTTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT  540
GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC  600
AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT  660
TTCGCACCAG CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CCTCCTCTTC  720
GTGGGCCTAC TACAGTTAAA CATTGTCATC TTCGGAGCAC TGCTCAGACC CATCATTATC  780
AGAGGACCAG CGTCACCGAA AATAGTCATC CAGGAAAATC GGAAAGAAGC GCAGTATATG  840
CTTGAAAATG AGAAAACACG AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAACT  900
ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG  960
CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020
TTCTCCATTT TGAAAGAGAA AAGTTTTATT TGTTATGCAT TATTTGGTCT CTTTGCAACA 1080
CTGGGATTCT TTGCACCTTC CTTGTACATC ATTCCTCTGG GCATTAGTCT GGGCATTGAC 1140
CAGGACCGCG CTGCTTTTTT ATTATCTACG ATGGCCATTG CAGAAGTTTT CGGAAGGATC 1200
GGAGCTGGTT TTGTCCTCAA CAGGGAGCCC ATTCGTAAGA TTTACATTGA GCTCATCTGC 1260
GTCATCTTAT TGACTGTGTC TCTGTTTGCC TTTACTTTTG CTACTGAATT CTGGGGTCTA 1320
ATGTCATGCA GCATATTTTT TGGGTTTATG GTTGGAACAA TAGGAGGACT CACATTCCAC 1380
TGCTTGCTGA AGATGATGTC GTGGGCATTG CAGAAGATGT CTTCTGCAGC TGGGGTCTAC 1440
ATCTTCATTC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500
CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCCTGCGCAG CTGGCATGGC CCTGGCTGCT 1560
GTGTGCCTCG CCCTGGTGAG ACCGTGTAAG ATGGGACTGT GCCAGCGTCA TCACTCAGGT 1620
GAAACAAAGG TAGTGAGCCA TCGTGGGAAG ACTTTACAGG ACATACCTGA AGACTTTCTG 1680
GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACGTGC AAATGGAGCC GGTATGACAC 1740
ACTTTCTTAC AACAACAGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAACGGGG 1800
ACACAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAAACTACA TTTTAAAGGG 1860
AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTTT TGTTTTGTTT TGTTTTAAGC 1920
TTTTTTTTTT TGCTTGTTTT TAAAGCCAAA ACAAAAAACA ACCAAGCACT CTTCCATATA 1980
TAAATCTGGC TGTATTCAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA 2040
TTCCGATATT AAAATAGTGA CATGAACTGG CAAAGTGGTT TTAAAAGCTT TCACGTGGGA 2100
TAAATGATTT TCTTTTTTTC TTTTCTTTCT TCCTATGGTC TTGTCTGAAT AAACTACTCT 2160
CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAAATGAA ATTGGCCAGT C
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Seq ID NO: 72 Protein sequence
Protein Accession #: NP_004685

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1          11         21         31         41         51
|          |          |          |          |          |
MTQNKLKLCS KANVYTEVPD GGWGWAVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESN   60
SRISWIISIC VFVLTFSAPL ATVLSNRFGH RLVVMLGGLL VSTGMVAASF SQEVSHMYVA  120
IGIISGLGYC FSFLPTVTIL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGWR  180
YSLLFVGLLQ LNIVIFGALL RPIIIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS  240
GVELTTSPKN VPTHTNLELE PKADMQQVLV KTSPRPSEKK APLLDFSILK EKSFICYALF  300
GLFATLGFFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY  360
IELICVILLT VSLFAFTFAT EFWGLMSCSI FFGFMVGTIG GLTFHCLLKM MSWALQKMSS  420
AAGVYIFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ  480
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Seq ID NO: 73 DNA sequence
Nucleic Acid Accession #: NM_002184.1
Coding sequence: 256..3012

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TAGAAGTAGA AGACTTAGCT TCAAATCCCT ACTCCTTCAC TTACTAATTT TGTGATTTGG   240
AAATATCCGC GCAAGATGTT GACGTTGCAG ACTTGGGTAG TGCAAGCCTT GTTTATTTTC   300
CTCACCACTG AATCTACAGG TGAACTTCTA GATCCATGTG GTTATATCAG TCCTGAATCT   360
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Seq ID NO: 74 Protein sequence
Protein Accession #: NP_002175.1

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SCTVDYSTVY FVNIEVWVEA ENALGKVTSD HINFDPVYKV KPNPPHNLSV INSEELSSIL   240
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YLRGNLAESK CYLITVTPVY ADGPGSPESI KAYLKQAPPS KGPTVRTKKV GKNEAVLEWD   540
QLPVDVQNGF IRNYTIFYRT IIGNETAVNV DSSHTEYTLS SLTSDTLYMV RMAAYTDEGG   600
KDGPEFTFTT PKFAQGEIEA IVVPVCLAFL LTTLLGVLFC FNKRDLIKKH IWPNVPDPSK   660
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ESTQPLLDSE ERPEDLQLVD HVDGGDGILP RQQYFKQNCS QHESSPDISH FERSKQVSSV   840
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Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: NM_022131
Coding sequence: 11..2878

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CACAGTCATT TTGGACCCAC CACTGGTAGC CCTGGATAAA GATGCACCGG TTCCTTTTGC   240
AGGGGAAATC TGTGCGTTCA AGATCCATGG CCAGGAGCTG CCCTTTGAGG CTGTGGTGCT   300
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Seq ID NO: 76 Protein sequence
Protein Accession #: NP_071414

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VEAIDEDCSP QYSQICNYEI VTTDVPFAID RNGNIRNTEK LSYDKQHQYE ILVTAYDCGQ   240
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VCMLVFVVAM GVYRVRIAHQ HFIQETEAAK ESEMDWDDSA LTITVNPMEK HEGPGHGEDE   900
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Seq ID NO: 77 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 482..3007

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Seq ID NO: 78 Protein sequence
Protein Accession #: Eos sequence

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PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TRLQKLYLNG   420
NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNPMPK LKVLYLNNNL LQVLPPHIFS   480
GVPLTKVNLK TNQFTHLPVS NILDDLDLLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV   540
TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTTPATT TNTADTILRS   600
LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM   660
YGHKTTHHTT ERPSASLYEQ HMVSPMVHVY RSPSFGPKHL EEEEERNEKE GSDAKHLQRS   720
LLEQENHSPL TGSNMKYKTT NQSTEFLSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA   780
QLQPDMEAHY PGAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ   840
T
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Seq ID NO: 79 DNA sequence
Nucleic Acid Accession #: NM_016640.2
Coding sequence: 39..1358

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1          11         21         31         41         51
|          |          |          |          |          |
GCTTAAGTTG ACCTCTGGGT CCGGAATCGC GGGCAAAGAT GGCGGCGGCC AGGTGTTGGA    60
GGCCTTTGCT ACGCGGTCCG AGGCTTTCAT TGCACACCGC GGCTAATGCC GCCGCCACGG   120
CTACAGAAAC GACCTCCCAA GACGTCGCGG CGACCCCCGT CGCGCGGTAC CCGCCGATTG   180
TGGCCTCCAT GACAGCCGAC AGCAAAGCTG CACGGCTGCG GCGGATCGAG CGCTGGCAGG   240
CGACGGTGCA CGCTGCGGAG TCGGTAGACG AGAAGCTGCG AATCCTCACC AAGATGCAGT   300
TTATGAAGTA CATGGTTTAC CCGCAGACCT TCGCGCTGAA TGCCGACCGC TGGTACCAGT   360
ACTTCACCAA GACCGTGTTC CTGTCGGGTC TGCCGCCGCC CCCAGCGGAG CCCGAGCCCG   420
AGCCCGAACC CGAACCTGAA CCTGCGCTGG ACCTCGCGGC GCTGCGTGCG GTCGCCTGCG   480
ACTGCCTGCT GCAGGAGCAC TTCTACCTGC GGCGCAGGCG GCGCGTGCAC CGTTACGAGG   540
AGAGCGAGGT CATATCTTTG CCCTTCCTGG ATCAGCTGGT GTCAACCCTC GTGGGCCTCC   600
TCAGCCCACA CAACCCGGCC CTGGCCGCTG CCGCCCTCGA TTATAGATGC CCAGTTCATT   660
TTTACTGGGT GCGTGGTGAA GAAATTATTC CTCGTGGTCA TCGAAGAGGT CGAATTGATG   720
ACTTGCGATA CCAGATAGAT GATAAACCAA ACAACCAGAT TCGAATATCC AAGCAACTCG   780
CAGAGTTTGT GCCATTGGAT TATTCTGTTC CTATAGAAAT CCCCACTATA AAATGTAAAC   840
CAGACAAACT TCCATTATTC AAACGGCAGT ATGAAAACCA CATATTTGTT GGCTCAAAAA   900
CTGCAGATCC TTGCTGTTAC GGTCACACCC AGTTTCATCT GTTACCTGAC AAATTAAGAA   960
GGGAAAGGCT TTTGAGACAA AACTGTGCTG ATCAGATAGA AGTTGTTTTT AGAGCTAATG  1020
CTATTGCAAG CCTTTTTGCT TGGACTGGAG CACAAGCTAT GTATCAAGGA TTCTGGAGTG  1080
AAGCAGATGT TACTCGACCT TTTGTCTCCC AGGCTGTGAT CACAGATGGA AAATACTTTT  1140
CCTTTTTCTG CTACCAGCTA AATACTTTGG CACTGACTAC ACAAGCTGAT CAAAATAACC  1200
CTCGTAAAAA TATATGTTGG GGTACACAAA GTAAGCCTCT TTATGAAACA ATTGAGGATA  1260
ATGATGTGAA AGGTTTTAAT GATGATGTTC TACTTCAGAT AGTTCACTTT CTACTGAATA  1320
GACCAAAAGA AGAAAAATCA CAGCTGTTGG AAAACTGAAA AAGCATATTT GATTGAGAAC  1380
TGTGGGAATA TTTAAATTTT ACTGAAGGAA CAATAATGAT GAGATTTGTA ACTGTCAACT  1440
ATTAAATACA TTGATTTTTG AGACAAAAAA AAAAAAAAAA AA
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Seq ID NO: 80 Protein sequence
Protein Accession #: NP_057724.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAAARCWRPL LRGPRLSLHT AANAAATATE TTSQDVAATP VARYPPIVAS MTADSKAARL    60
RRIERWQATV HAAESVDEKL RILTKMQFMK YMVYPQTFAL NADRWYQYFT KTVFLSGLPP   120
PPAEPEPEPE PEPEPALDLA ALRAVACDCL LQEHFYLRRR RRVHRYEESE VISLPFLDQL   180
VSTLVGLLSP HNPALAAAAL DYRCPVHFYW VRGEEIIPRG HRRGRIDDLR YQIDDKPNNQ   240
IRISKQLAEF VPLDYSVPIE IPTIKCKPDK LPLFKRQYEN HIFVGSKTAD PCCYGHTQFH   300
LLPDKLRRER LLRQNCADQI EVVFRANAIA SLFAWTGAQA MYQGFWSEAD VTRPFVSQAV   360
ITDGKYFSFF CYQLNTLALT TQADQNNPRK NICWGTQSKP LYETIEDNDV KGFNDDVLLQ   420
IVHFLLNRPK EEKSQLLEN
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Seq ID NO: 81 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2070

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCCA GCTCGCCGAC CCCGGGCTCT    60
CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG   120
CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG   180
CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG   240
GAAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCTCCCCA GGCACACTCA   300
ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA   360
GGGGGAACAC AGGACGGGGA GCCCCTCCAG ACTGTCCTTG CCCACCTGGC TGCACTGGCC   420
CCTGTATGCC AACCCAGTGG GTACAGGTTC TGGGGGACCT GGACAGATGC CGCTACCTCT   480
AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCACG TGCTGCTCTC GGGAAGCCCA   540
GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT   600
CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG   660
CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCCTCAC   720
ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG   780
GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCCTGT TTCCTTGCCA CTTGTCCAAG   840
GCACTTCCCC ATCCTGACAG CGCCCCCCAC CCAGCCCAGG ATCCTGGGCT GTGGTCTCAA   900
GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA   960
TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCCAGGGA  1020
GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG  1080
CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCAGTGC TGGGGACGCT  1140
GACAGGACAC GGGAAGAGGC CATGCTTTCC CTCGGGACCT GCTGTTCCAT GTGTCCCAAG  1200
CCCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG  1260
GGCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC  1320
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AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGCG  1380
GGCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG  1440
TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC  1500
TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCCAGA AGGCGGACCT GGAAGAGGAG  1560
CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCCTGGGG TACAAGGGCA GGCCAGAAAG  1620
GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC  1680
AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCCTGC CCCTTCCCCT GCGAAAGCCC  1740
ACCACACTTA GGCAGTGCGA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCAG  1800
ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC  1860
CCGGACGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCCAA GGTCTCCACC  1920
AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA  1980
CTGAAGCAGA CCCCGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG  2040
AAACGGCGCC TGCATCGCTC AGTGCTTTGA
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Seq ID NO: 82 Protein sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL   60
QQQHSEMLAK LHEEIEHLKR ENKGEPARGP RPALPPQAHS TLPLPQHRNT AINSSTRLGS  120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAATS SRGWTMLCSQ AQHVLLSGSP  180
GPEVIAGRQV ATGCSPDLPP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH  240
MLGAQGIWTH SIQGSLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSGPH PAQDPGLWSQ  300
AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVEGGP FPSRCGNSSE  360
LFWAKCGPSR QPQPCSAGDA DRTREEAMLS LGTCCSMCPK PSCFPDGPSG NHLSRASAPL  420
GARWVCINGV WVEPGGPSPA RLKEGSSRTH RPGGKRGRLA GGSADTVRSP ADSLSMSSFQ  480
SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGQARK  540
EKAEASNAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ  600
TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA  660
LKQTPKNNFA ERQKRLQAMQ KRRLHRSVL
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Seq ID NO: 83 DNA sequence
Nucleic Acid Accession #: NM_005264.1
Coding sequence: 557..1954

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1          11         21         31         41         51
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ACCACTAACA TCCCTAACGA GCATCCGAGC CGAGGGCTCT GCTCGGAAAT CGTCCTGGCC   120
CAACTCGGCC CTTCGAGCTC TCGAAGATTA CCGCATCTAT TTTTTTTTTC TTTTTTTCT   180
TTTCCTAGCG CAGATAAAGT GAGCCCGGAA AGGGAAGGAG GGGGCGGGGA CACCATTGCC   240
CTGAAAGAAT AAATAAGTAA ATAAACAAAC TGGCTCCTCG CCGCAGCTGG ACGCGGTCGG   300
TTGAGTCCAG GTTGGGTCGG ACCTGAACCC CTAAAAGCGG AACCGCCTCC CGCCCTCGCC   360
ATCCCGGAGC TGAGTCGCCG GCGGCGGTGG CTGCTGCCAG ACCCGGAGTT TCCTCTTTCA   420
CTGGATGGAG CTGAACTTTG GGCGGCCAGA GCAGCACAGC TGTCCGGGGA TCGCTGCACG   480
CTGAGCTCCC TCGGCAAGAC CCAGCGGCGG CTCGGGATTT TTTTGGGGGG GCGGGGACCA   540
GCCCCGCGCC GGCACCATGT TCCTGGCGAC CCTGTACTTC GCGCTGCCGC TCTTGGACTT   600
GCTCCTGTCG GCCGAAGTGA GCGGCGGAGA CCGCCTGGAT TGCGTGAAAG CCAGTGATCA   660
GTGCCTGAAG GAGCAGAGCT GCAGCACCAA GTACCGCACG CTAAGGCAGT GCGTGGCGGG   720
CAAGGAGACC AACTTCAGCC TGGCATCCGG CCTGGAGGCC AAGGATGAGT GCCGCAGCGC   780
CATGGAGGCC CTGAAGCAGA AGTCGCTCTA CAACTGCCGC TGCAAGCGGG GTATGAAGAA   840
GGAGAAGAAC TGCCTGCGCA TTTACTGGAG CATGTACCAG AGCCTGCAGG GAAATGATCT   900
GCTGGAGGAT TCCCCATATG AACCAGTTAA CAGCAGATTG TCAGATATAT TCCGGGTGGT   960
CCCATTCATA TCAGATGTTT TTCAGCAAGT GGAGCACATT CCCAAAGGGA ACAACTGCCT  1020
GGATGCAGCG AAGGCCTGCA ACCTCGACGA CATTTGCAAG AAGTACAGGT CGGCGTACAT  1080
CACCCCGTGC ACCACCAGCG TGTCCAACGA TGTCTGCAAC CGCCGCAAGT GCCACAAGGC  1140
CCTCCGGCAG TTCTTTGACA AGGTCCCGGC CAAGCACAGC TACGGAATGC TCTTCTGCTC  1200
CTGCCGGGAC ATCGCCTGCA CAGAGCGGAG GCGACAGACC ATCGTGCCTG TGTGCTCCTA  1260
TGAAGAGAGG GAGAAGCCCA ACTGTTTGAA TTTGCAGGAC TCCTGCAAGA CGAATTACAT  1320
CTGCAGATCT CGCCTTGCGG ATTTTTTTAC CAACTGCCAG CCAGAGTCAA GGTCTGTCAG  1380
CAGCTGTCTA AAGGAAAACT ACGCTGACTG CCTCCTCGCC TACTCGGGGC TTATTGGCAC  1440
AGTCATGACC CCCAACTACA TAGACTCCAG TAGCCTCAGT GTGGCCCCAT GGTGTGACTG  1500
CAGCAACAGT GGGAACGACC TAGAAGAGTG CTTGAAATTT TTGAATTTCT TCAAGGACAA  1560
TACATGTCTT AAAAATGCAA TTCAAGCCTT TGGCAATGGC TCCGATGTGA CCGTGTGGCA  1620
GCCAGCCTTC CCAGTACAGA CCACCACTGC CACTACCACC ACTGCCCTCC GGGTTAAGAA  1680
CAAGCCCCTG GGGCCAGCAG GGTCTGAGAA TGAAATTCCC ACTCATGTTT TGCCACCGTG  1740
TGCAAATTTA CAGGCACAGA AGCTGAAATC CAATGTGTCG GGCAATACAC ACCTCTGTAT  1800
TTCCAATGGT AATTATGAAA AAGAAGGTCT CGGTGCTTCC AGCCACATAA CCACAAAATC  1860
AATGGCTGCT CCTCCAAGCT GTGGTCTGAG CCCACTGCTG GTCCTGGTGG TAACCGCTCT  1920
GTCCACCCTA TTATCTTTAA CAGAAACATC ATAGCTGCAT TAAAAAAATA CAATATGGAC  1980
ATGTAAAAAG ACAAAAACCA AGTTATCTGT TTCCTGTTCT CTTGTATAGC TGAAATTCCA  2040
GTTTAGGAGC TCAGTTGAGA AACAGTTCCA TTCAACTGGA ACATTTTTTT TTTTCCTTTT  2100
AAGAAAGCTT CTTGTGATCC TTCGGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC  2160
AAACTCAGAA GGCTTTGGGA TATGCTGTAT TTTAAAGGGA CAGTTTGTAA CTTGGGCTGT  2220
AAAGCAAACT GGGGCTGTGT TTTCGATGAT GATGATCATC ATGATCATGA TGATTTTAAC  2280
AGTTTTACTT CTGGCCTTTC CTAGCTAGAG AAGGAGTTAA TATTTCTAAG GTAACTCCCA  2340
TATCTCCTTT AATGACATTG ATTTCTAATG ATATAAATTT CAGCCTACAT TGATGCCAAG  2400
CTTTTTTGCC ACAAAGAAGA TTCTTACCAA GAGTGGGCTT TGTGGAAACA GCTGGTACTG  2460
ATGTTCACCT TTATATATGT ACTAGCATTT TCCACGCTGA TGTTTATGTA CTGTAAACAG  2520
TTCTGCACTC TTGTACAAAA GAAAAAACCA CCCGGAATTC
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Seq ID NO: 84 Protein sequence
Protein Accession #: NM_005264.1

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1          11         21         31         41         51
|          |          |          |          |          |
MFLATLYFAL PLLDLLLSAE VSGGDRLDCV KASDQCLKEQ SCSTKYRTLR QCVAGKETNF    60
SLASGLEAKD ECRSAMEALK QKSLYNCRCK RGMKKEKNCL RIYWSMYQSL QGNDLLEDSP   120
YEPVNSRLSD IFRVVPFISD VFQQVEHIPK GNNCLDAAKA CNLDDICKKY RSAYITPCTT   180
SVSNDVCNRR KCHKALRQFF DKVPAKHSYG MLFCSCRDIA CTERRRQTIV PVCSYEEREK   240
PNCLNLQDSC KTNYICRSRL ADFFTNCQPE SRSVSSCLKE NYADCLLAYS GLIGTVMTPN   300
YIDSSSLSVA PWCDCSNSGN DLEECLKFLN FFKDNTCLKN AIQAFGNGSD VTVWQPAFPV   360
QTTTATTTTA LRVKNKPLGP AGSENEIPTH VLPPCANLQA QKLKSNVSGN THLCISNGNY   420
EKEGLGASSH ITTKSMAAPP SCGLSPLLVL VVTALSTLLS LTETS
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Seq ID NO: 85 DNA sequence
Nucleic Acid Accession #: XM_027172.1
Coding sequence: 143..1405

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1          11         21         31         41         51
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GGTGGAGACA CCGCCTCAGG GCTCGGTGCA CAGTGGACAT TTGGGGAGCG TTGTGGGTGA    60
CCCCCACACA GGCACTGGGA ATGCAGGGGA GAGGGGCCCA AGGGGGAAAG GGGCCAGAGT   120
GTTGGCTTTG GATTCAGGAG GGATGGATTC CAGTCCTAGC TTGCCACTTA TTAGGACTCC   180
TGAGAGCAGC CTCCATGAGG CCCTGGACCA GTGCATGACC GCCCTGGACC TCTTCCTCAC   240
CAACCAGTTC TCAGAAGCAC TCAGCTACCT CAAGCCCAGA ACCAAGGAAA GCATGTACCA   300
CTCACTGACA TATGCCACCA TCCTGGAGAT GCAGGCCATG ATGACCTTTG ACCCTCAGGA   360
CATCCTGCTT GCCGGCAACA TGATGAAGGA GGCACAGATG CTGTGTCAGA GGCACCGGAG   420
GAAGTCTTCT GTAACAGATT CCTTCAGCAG CCTGGTGAAC CGCCCCACGC TGGGCCAATT   480
CACTGAAGAG GAAATCCACG CTGAGGTCTG CTATGCAGAG TGCCTGCTGC AGCGAGCAGC   540
CCTGACCTTC CTGCAGGGTT CCTCACACGG AGGGGCAGTC AGGCCCAGAG CCTTGCATGA   600
TCCCTCTCAC GCCTGCAGCT GCCCACCTGG GCCAGGCCGT CAGCATCTTT TCCTCCTGCA   660
GGACGAGAAC ATGGTGAGCT TCATCAAAGG CGGCATCAAA GTTCGAAACA GCTACCAGAC   720
CTACAAGGAG CTGGACAGCC TTGTTCAGTC CTCACAATAC TGCAAGGGTG AGAACCACCC   780
GCACTTTGAA GGAGGAGTGA AGCTTGGTGT AGGGGCCTTC AACCTGACAC TGTCCATGCT   840
TCCTACTAGG ATCCTGAGGC TGTTGGAGTT TGTGGGGTTT TCAGGAAACA AGGACTATGG   900
GCTGCTGCAG CTGGAGGAGG GAGCGTCAGG GCACAGCTTC CGCTCTGTGC TCTGTGTCAT   960
GCTCCTGCTG TGCTACCACA CCTTCCTCAC CTTCGTGCTC GGTACTGGGA ACGTCAACAT  1020
CGAGGAGGCC GAGAAGCTCT TGAAGCCCTA CCTGAACCGG TACCCTAAGG GTGCCATCTT  1080
CCTGTTCTTT GCAGGGAGGA TTGAAGTCAT TAAAGGCAAC ATTGATGCAG TGAGTGATGG  1140
GGGTCCGGGC CGGGGCTGGG GATCCCTCGG GGTCTCCCAG ACCAGCAGGA AGTCAGGCAC  1200
ATGTGACATA CTCAGGGACA GGATAGACTG GGGGCGGGGG GGGGGCCAAG AGAGAACCAA  1260
CCAGAGAGCA GGGGCAGGAG AGGCCCTTCT GGCAGAGCAG CCTGGGAAGA CAAGGGAGGA  1320
GGAGGCATTT GTGGTGCCTG GGATTTTGAC TGGGAGATAT AGGACTGCAG CATTGCAGTG  1380
GAGGGAGGTG GAGGGAGGTG CTTGAGGGAG GCAGAGGTTA GGAAAGCCCA TCTGTTTAGG  1440
GCATGACGAT TAGGCTGGAG TCTGGTACCT CCCCTCCATT ATAGCTCTCT CCTGCTCTTT  1500
CATTTTGTTA CTAAAAACCA GAGTCCTAGG CGGGGGCTGT ATTTGAGCCC AACGTCATGT  1560
AAGACTTAGG AGGTAAAACC AGGACTGGAG GCCAGATCTC CTGGCTCCTG GGGCCCCACC  1620
TGAGCCTAGC ACAGGGCTGG ACCACTATGC CCTGGAGGAG TCCCGGTCTG CTGTGGTGTT  1680
GGGAGGTTCG GAGGATGCAG AGGGGTTGGG GCTGGGTGGG CACCCGTCAG GCTGACCAGA  1740
AGGTGCCTGC AGGCCATCCG GCGTTTCGAG GAGTGCTGTG AGGCCCAGCA GCACTGGAAG  1800
CAGTTCCACC ACATGTGCTA CTGGGAGCTG ATGTGGTGCT TCACCTACAA GGGCCAGTGG  1860
AAGATGTCCT ACTTCTACGC CGACCTGCTC AGCAAGGAGA ACTGCTGGTC CAAGGTGGGC  1920
TGATGCCACG TGTTAGGGGC ATTGGGTGAC CAGGGCTGAC TGTGTGCCTC CAGACCACGG  1980
GCCAAATCCC TAACTGAACA CAGATGTCTC AGCTGGAATC TAAACATAAC CTTAAATTCT  2040
AATAGGACTC AGGCTTGGAA GGAACTAAAG ACCACAAGAG AAACTTCTGA ACCACAATGT  2100
GTCACAAAGA GATTTCTAGT CACAAAGGAC AGAAACATGG CTCCCTCTGT CCAGTAGAAC  2160
TGTTTCTGTG GTAGAAATGT TCTACTTATG CACTGCCCAA ATATGGTAGT CACCAGCCAC  2220
ATGTGCACAA TGAGCACATG AAATGTGCCT AGTGCAACTG GGAAACTGAT TGTTTTCAGT  2280
TTTATTTAAT TTTAATTAAC TAAATGTTAA ATTTAAATAG CCATGTAGGG CTTGTGGCCA  2340
CTATATTGGA CTATGCAGGT CCAAAACACA AAAGGCTCAT ATAACTGAAC ATTCTTGGCA  2400
CATCCGACTT CAGGTAGGGC TGGATCCAGG AATTCAAATG ATGTCGTCTG GCTTGGTCTT  2460
TCCATTTGTG GCTGTGCTCT CTCCTATGAC ATCTTTGTTT CTGCTGCATC TTTGCAGGAA  2520
GGTTCTCTCC ATGTGACAGG CAAGGTGGCC ACGGGCTGCT TCTACTCATA TCCTCCCCTT  2580
GGTTTCAACC AGAGTCCCAC AGTTTGAGCC TCACTGGTCT GACTTGTCAC CTGCCAATGC  2640
CTGGAACAGA GGGGTGGGAA GATTCCTCAT GGGCTGAGAG TAGGAGAGGG GTGGTTCCAC  2700
AGAAGAAAAT GATGCACCCA GAAATAGTGG AGGGATTAAC AAGATGCCAT ACAGGCAAAA  2760
CAAAGCCAAA CAGATGCCCG CCTACCAAAG ATGAAATTTA TCATGGTAAG TATTGAAATA  2820
AGTGTTAGCT TGTACCATCA TAGTAATGAT AGTGCAGAAA TTGGAACCAA GAGTCTTACA  2880
ACCACCTAGC TCAGCAAACG TCTAATCTGT TATTTGTAAA TACACAGGAC ATGTGTCTTC  2940
ATGGCTTCAT CCCCTGCCCA TAGCAGACAT TGCTAATCAA TCCTCTGCCA TGAGCCTAGC  3000
TGTGACCTTA GATACCTTCC CTGCAAAGCT CCAGGCAGCC GTTAGAACTG ACCCACATTG  3060
GCACCTGTTA GGAGACCTGT CATCTGCATC TGGTCCCTCC CCCTCCTCTG CATGGAGGTC  3120
TCTTCCGTAG CCCTGCCTGG GGACCAAGCT GAAGGGGAAT TCTCTGGGTC TGGGGCAGGT  3180
GGGGCTGGGG AAGGGAGCAG GCTTCTACTG AGCTCTCAAC ATGTCTGGCA CCTGTCATGT  3240
CCTCCACACC ACACCCAGTG AGGAGAAGTT ATTATCTCCA TTGGGCACAT GAGGGCCACT  3300
GATGCTAAGC GAGGACTGTG ACTTTCCCAC CCACATGGCT GTTGGTGACA GACACCGGAT  3360
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TGAGGAGTCG GGGCTTGCCC TGAGCCCACC CTGCTGTTGA AGGTGCTTCC TCAGGCCCAG  3480
CTCCCATGGC CCCCACACCC CCTCCTCATC ACCTCCTACT CCCAAAAAGG ACAAAGCCTC  3540
AGGGAACCTT TTTTCTTTTT TTAGAGACAG GGTCTTGCTA TGTTGGTCAG GCTAGTCTTG  3600
AACTCCTGGG CCCAAGCAAT CTTCCCACCT CTGCCTCCTA AAGTGCTGGG ATTCTGGGCC  3660
TTAGGGAACC TTTTTGAACT GAAAGTGACT CTCGAAGCCT TCCTGTAGAG TGAGGTGGGT  3720
GGCTGGGGCT AACCATATGG GGAAGGAGAG ACCTGGTGGG GGCACACAGC TGCTATATAG  3780
AGGAACAGAA GGTGGGCCAG GCCTCCCAGC TGTCAGGAAA TCTGGCTCAG TCCCCAGACC  3840
GCTGTGTGGC TTTGGGGTGG CCAGTCCCTC TCTCTCTGCA ACACTCTCCT CATGAGGACT  3900
TCTGTGAAAA ATGGGGGTTG TAACCCTCTG AGTTCTGGGG CCCCACCCAT TTCTAATCTC  3960
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CAGAACTTGG CCACCACAGA CTCCACCAAC TTCTAGTCCT GGGGCCTGGG CCTCTGGCCA  4020
TTGCCATAGG CACCACCTGC TCTGTGCAGG CAGCGCCCCC CTCTGCCAGG ATCCTCCGAG  4080
GTCAGCTGCT GGGTCTGACC CGCAGACCCT GGCTGAGCGA CGGATGAACG GAGTATGCAG  4140
ACACAGGCTT GCCTGTCAGC AGATGGGGGA CCCCTGCCAG AGTCAGCAGC GGCCCCCATA  4200
AGCCTGCCAC GCTTGCATTT ATTTAGTACA GATGTAATGA CAAAGGCCTA AAGCAAACTC  4260
CATTTGTGGG TAATTAACAT TGTCGCCCCC CCAGAAAGAG CAGTCCTCCG CATGATGATT  4320
AAAGGCCAGG TTCCGAGGCC TAAGTAAACC AACTTATCTA GATCAATTCC CTTACTTCTT  4380
GTTATCTACT CTGAGAGAAT TCAGCTGCCT TCAGCCAAAT CCTTTCCCGA AGCTTTTGCA  4440
AAACCTCCGA GCCTTCCAAG GTTTGCTTCT TTCTGTAATT TTTCTCACCA CCCTGACCTA  4500
TCTCCTGCAG TCAGCCCTGT GGAGGCCTTT GTGTTTCCCC CAGTGCTGGC AGCCTAGAGG  4560
CTGAGATGGC CAGAAACAAG GTGGTGACAG TGGCGTGCTC AGGGCTTGGG AAACCCAAGG  4620
AGCTAAAGGC ATGCCCAGGC AACCAAAGAG GACAGGAAGG CTTCTGAGGA GAGACCTCTG  4680
AGGTGGGTCT TGGAGAGGAA GGACTTAGGG AGGCAGAGTG GAGGAAGTGA GAGGACACCC  4740
CAAGCCAAGA GGGCGGCAGG ACCAAAGGCT CAGAAGCCAG GGCGCTGCAG AGGGGCTGTG  4800
TGCCACAGGG TGAAGAGTTT GTGTGGCAGA AGGGCAGGGG GCTTGCATCA GGGGTGACAG  4860
CTGCTCTTTT GTCCCAGCAT AGCCCCTGTA CATCCCTGGA GAGCTGGGCC GTCCACAACT  4920
CTAAGTCACA GCCCCCATCC TAACCCTGGT GGTGCAGTGA GGGTGAGCTG TCTGTGGGCA  4980
GGAGGGAAGA CTCTTGGAGA TGAGCCTGGT GAAGGGATAA TGGCATCCCG GGCCGAGGAG  5040
CAGCACAGGC AGAGGCCTGG GGAGAGTTTA AGGAGTGTAG GGGAGGAAAT GGCAGAAGAT  5100
GAGCCAGAAA AAGAAAGGTT AGGGCAGGTC CTGGAGGACA TGAGTGGCTG TTTGGGCTTT  5160
ATCCAGCAGT GGGGGAGCCT TGGCAGGCTT GTGGCTTAGA TAGGTGCTTT AGAAAGCCCA  5220
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Seq ID NO: 86 Protein sequence
Protein Accession #: XP_027172.1

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EVCYAECLLQ RAALTFLQGS SHGGAVRPRA LHDPSHACSC PPGPGRQHLF LLQDENMVSF   180
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Nucleic Acid Accession #: AB007921
Coding sequence: 143..1363

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Seq ID NO: 88 Protein sequence
Protein Accession #: BAA32297.1

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          ILLAGNMMKE AQMLCQRHRR KSSVTDSFSS LVNRPTLGQF TEEEIHAEVC YAECLLQRAA   180
          LTFLQGSSHG GAVRPRALHD PSHACSCPPG PGRQHLFLLQ DENMVSFIKG GIKVRNSYQT   240
          YKELDSLVQS SQYCKGENHP HFEGGVKLGV GAFNLTLSML PTRILRLLEF VGFSGNKDYG   300
          LLQLEEGASG HSFRSVLCVM LLLCYHTFLT FVLGTGNVNI EEAEKLLKPY LNRYPKGAIF   360
          LFFAGRIEVI KGNIDAVSDG GPGRGWGSLG VSQTSRKSGT CDILRDRIDW GRGGGPRENQ   420
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          EVCYAECLLQ RAALTFLQDE NMVSFIKGGI KVRNSYQTYK ELDSLVQSSQ YCKGENHPHF   180
          EGGVKLGVGA FNLTLSMLPT RILRLLEFVG FSGNKDYGLL QLEEGASGHS FRSVLCVMLL   240
          LCVHTFLTFV LGTGNVNIEE AEKLLKPYLN RYPKGAIFLF FAGRIEVIKG NIDAAIRRFE   300
          ECCEAQQHWK QFHHMCYWEL MWCFTYKGQW KMSYFYADLL SKENCWSKAT YIYMKAAYLS   360
          MFGKEDHKPF GDDEVELFRA VPGLKLKIAG KSLPTEKFAI RKSRRYFSSN PISLPVPALE   420
          MMYIWNGYAV IGKQPKLTDG ILEIITKAEE MLEKGPENEY SVDDECLVKL LKGLCLKYLG   480
          RVQEAEENFR SISANEKKIK YDHYLIPNAL LELALLLMEQ DRNEEAIKLL ESAKQNYKNY   540
          SMESRTHFRI QAATLQAKSS LENSSRSMVS SVSL

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TCCCGCCAGC CAATCTACAT GAGTCTAGCA GGCTGGACCT GTCGGGACGA CTGTAAGTAT   240
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TTTGGGGAGG AGGAAGGGGC GATTTGAGGG AGAAGGGGAG AAAGCTTATG GCTGGGTCTG  2220
GTTTCTTCCC TTCCCAGAGG GTCTTACTGT TCCAGGGTGG CCCCAGGGCA GGCAGGGGCC  2280
ACACTATGCC TGCGCCCTGG TAAAGGTGAC CCCTGCCATT TACCAGCAGC CCTGGCATGT  2340
TCCTGCCCCA CAGGAATAGA ATGGACGGAC CTCCAGAAAC TTTCCATCCC AAAGGCAGTC  2400
TCCGTGGTTG AAGCAGACTG GATTTTTGCT CTGCCCCTGA CCCCTTGTCC CTCTTTGAGG  2460
GAGGGGAGCT ATGCTAGGAC TCCAACCTCA GGGACTCGGG TGGCCTGCGC TAGCTTCTTT  2520
TGATACTGAA AACTTTTAAG GTGGGAGGGT GGCAAGGGAT GTGCTTAATA AATCAATTCC  2580
AAGCCTCAAA AAAAAAAAAA AAAAAAAAAA AAAAAA
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Seq ID NO: 92 Protein sequence
Protein Accession #: Eos sequence

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|          |          |          |          |          |
MAGLAARLVL LAGAAALASG SQGDREPVYR DCVLQCEEQN CSGGALNHFR SRQPIYMSLA    60
GWTCRDDCKY ECMWVTVGLY LQEGHKVPQF HGKWPFSRFL FFQEPASAVA SFLNGLASLV   120
MLCRYRTFVP ASSPMYHTCV AFAWVSLNAW FWSTVFHTRD TDLTEKMDYF CASTVILHSI   180
YLCCVRTVGL QHPAVVSAFR ALLLLMLTVH VSYLSLIRFD YGYNLVANVA IGLVNVVWWL   240
AWCLWNQRRL PHVRKCVVVV LLLQGLSLLE LLDFPPLFWV LDAHAIWHIS TIPVHVLFFS   300
FLEDDSLYLL KESEDKFKLD
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Seq ID NO: 93 DNA sequence
Nucleic Acid Accession #: NM_033419.1
Coding sequence: 18..980

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CGGCGCTGGC GAGCGGCTCC CAGGGCGACC GTGAGCCGGT GTACCGCGAC TGCGTACTGC   120
AGTGCGAAGA GCAGAACTGC TCTGGGGGCG CTCTGAATCA CTTCCGCTCC CGCCAGCCAA   180
TCTACATGAG TCTAGCAGGC TGGACCTGTC GGGACGACTG TAAGTATGAG TGTATGTGGG   240
TCACCGTTGG GCTCTACCTC CAGGAAGGTC ACAAAGTGCC TCAGTTCCAT GGCAAGTGGC   300
CCTTCTCCCG GTTCCTGTTC TTTCAAGAGC CGGCATCGGC CGTGGCCTCG TTTCTCAATG   360
GCCTGGCCAG CCTGGTGATG CTCTGCCGCT ACCGCACCTT CGTGCCAGCC TCCTCCCCCA   420
TGTACCACAC CTGTGTGGCC TTCGCCTGGG TGTCCCTCAA TGCATGGTTC TGGTCCACAG   480
TTTTCCACAC CAGGGACACT GACCTCACAG AGAAAATGGA CTACTTCTGT GCCTCCACTG   540
TCATCCTACA CTCAATCTAC CTGTGCTGCG TCAGGACCGT GGGGCTGCAG CACCCAGCTG   600
TGGTCAGTGC CTTCCGGGCT CTCCTGCTGC TCATGCTGAC CGTGCACGTC TCCTACCTGA   660
GCCTCATCCG CTTCGACTAT GGCTACAACC TGGTGGCCAA CGTGGCTATT GGCCTGGTCA   720
ACGTGGTGTG GTGGCTGGCC TGGTGCCTGT GGAACCAGCG GCGGCTGCCT CACGTGCGCA   780
AGTGCGTGGT GGTGGTCTTG CTGCTGCAGG GGCTGTCCCT GCTCGAGCTG CTTGACTTCC   840
CACCGCTCTT CTGGGTCCTG GATGCCCATG CCATCTGGCA CATCAGCACC ATCCCTGTCC   900
ACGTCCTCTT TTTCAGCTTT CTGGAAGATG ACAGCCTGTA CCTGCTGAAG GAATCAGAGG   960
ACAAGTTCAA GCTGGACTGA AGACCTTGGA GCGAGTCTGC CCCAGTGGGG ATCCTGCCCC  1020
CGCCCTGCTG GCCTCCCTTC TCCCCTCAAC CCTTGAGATG ATTTTCTCTT TTCAACTTCT  1080
TGAACTTGGA CATGAAGGAT GTGGGCCCAG AATCATGTGG CCAGCCCACC CCCTGTTGGC  1140
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CCTCACCAGC CTTGGAGTCT GTTCTAGGGA AGGCCTCCCA GCATCTGGGA CTCGAGAGTG  1200
GGCAGCCCCT CTACCTCCTG GAGCTGAACT GGGGTGGAAC TGAGTGTGCT CTTAGCTCTA  1260
CCGGGAGGAC AGCTGCCTGT TTCCTCCCCA TCAGCCTCCT CCCCACATCC CCAGCTGCCT  1320
GGCTGGGTCC TGAAGCCCTC TGTCTACCTG GGAGACCAGG GACCACAGGC CTTAGGGATA  1380
CAGGGGGTCC CCTTCTGTTA CCACCCCCCA CCCTCCTCCA GGACACCACT AGGTGGTGCT  1440
GGATGCTTGT TCTTTGGCCA GCCAAGGTTC ACGGCGATTC TCCCCATGGG ATCTTGAGGG  1500
ACCAAGCTGC TGGGATTGGG AAGGAGTTTC ACCCTGACCA TTGCCCTAGC CAGGTTCCCA  1560
GGAGGCCTCA CCATACTCCC TTTCAGGGCC AGGGCTCCAG CAAGCCCAGG GCAAGGATCC  1620
TGTGCTGCTG TCTGGTTGAG AGCCTGCCAC CGTGTGTCGG GAGTGTGGGC CAGGCTGAGT  1680
GCATAGGTGA CAGGGCCGTG AGCATGGGCC TGGGTGTGTG TGAGCTCAGG CCTAGGTGCC  1740
CAGTGTGGAG ACGGGTGTTG TCGGGGAAGA GGTGTGGCTT CAAAGTGTGT GTGTGCAGGG  1800
GGTGGGTGTG TTAGCGTGGC TTAGGGGAAC GTGTGTGCGC GTGCTGGTGG GCATGTGAGA  1860
TGAGTGACTG CCGGTGAATG TGTCCACAGT TGAGAGGTTG GAGCAGGATG AGGGAATCCT  1920
GTCACCATCA ATAATCACTT GTGGAGCGCC AGCTCTGCCC AAGGCGCCAC CTGGGCGGAC  1980
AGCCAGGAGC TCTCCATGGC CAGGCTGCCT GTGTGCATGT TCCCTGTCTG GTGCCCCTTT  2040
GCCCGCCTCC TGCAAACCTC ACAGGGTCCC CACACAACAG TGCCCTCCAG AAGCAGCCCC  2100
TCGGAGGCAG AGGAAGGAAA ATGGGGATGG CTGGGGCTCT CTCCATCCTC CTTTTCTCCT  2160
TGCCTTCGCA TGGCTGGCCT TCCCCTCCAA AACCTCCATT CCCCTGCTGC CAGCCCCTTT  2220
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GCAGGCAGGG GCCACACTAT GCCTGCGCCC TGGTAAAGGT GACCCCTGCC ATTTACCAGC  2400
AGCCCTGGCA TGTTCCTGCC CCACAGGAAT AGAATGGAGG GAGCTCCAGA AACTTTCCAT  2460
CCCAAAGGCA GTCTCCGTGG TTGAAGCAGA CTGGATTTTT GCTCTGCCCC TGACCCCTTG  2520
TCCCTCTTTG AGGGAGGGGA GCTATGCTAG GACTCCAACC TCAGGGACTC GGGTGGCCTG  2580
CGCTAGCTTC TTTTGATACT CAAAACTTTT AAGGTGGGAG GGTGGCAAGG GATGTGCTTA  2640
ATAAATCAAT TCCAAGCCTC AAAAAAAAAA AAAAAAAAAA AA
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Seq ID NO: 94 Protein sequence
Protein Accession #: NP_219487.1

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1          11         21         31         41         51
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MKDVGPESCG QPTPCWPSPA LESVLGKASQ HLGLESGQPL YLLELNWGGT ECALSSTGRT    60
AACFLPISLL PTSPAAWLGP EALCLPGRPG TTGLRDTGGP LLLPPPTLLQ DTTRWCWMLV   120
LWPAKVHGDS PHGILRDQAA GIGKEFHPDH CPSQVPRRPH HTPFQGQGSS KPRARILCCC   180
LVESLPPCVG SVGQAECIGD RAVSMGLGVC ELRPRCAVWR RVLSGKRCGF KVCVCRGWVC
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Seq ID NO: 95 DNA sequence
Nucleic Acid Accession #: XM_090469
Coding sequence:

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TGCCGCGTGC TGGACAGGAC GCAGGTGAAC AAGCCCTGCC TGCTGGAGGC TGCCAAGCAC   120
AGCCCACACC CCTTGCATGG ACAGTCGGTC AACAGCCACC CATCAGGTGC TCATCAGAAA   180
CCACCTGAAG TGAAAATGTT TGGAGCCAGT CAAGGTTTGC TGACAATGGA AACAAACCAG   240
TCCCTGGCAC AAGGCACAGG CTGCTCAGTG TGCTGGGAGG TGAACGGCCC AGGGTTGGAA   300
ATGTCTCTTC CTGGAGTGCT CAGTGCTGAT GCTGGCCAGG TGGAGCACAG AAGACAAATG   360
AACTCCGCAG ATACTGACTG GGGAACTGAG GAGGGACCAG GAAGTCTAGA TTTCGCCGTG   420
GCTGCCCACC AGGAAGACAC TTTCTTTTTG AAAGACATCA AGCACACAAG TACGTTCAGG   480
CAATCAGTTC AGCAGCAGAA TTGCATTTAC AGCCCCAGAG AAAAACCCTG TGGGAATGTC   540
AGGGCACCTT GCGCGCCACC AAGGCGAGAG GCCCCGCTTG CCCTCAGCAG GCCCTGGCGG   600
CTCAGCCGCA GCCCGGCGCC GTCCCCACGT ACACCCATGG CGCCCTTCCC GACCTCTGAC   660
CGCGAGCTAG ACGCGCCAGG CCCGCCCCCC GGGCTGCGGA GCTCGGCAGC AGCCCCTCAC   720
TGCCTGCCCG CGGCTCCAGA AGCCCAGAAA CTCTTCTTCC TGCTGCCCCT TTATCCAGAT   780
GGCAGCCCAC CACCTAAGGA CATCTTGCAG ACGCTCCAGC ACAAGGCACC TGGGAAGAGA   840
CTGCATCAAG AATCACCAGG TTCATTTCCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA   900
TGTATCAAAG GGGCTCTGGG TGTGGCTGCT GAAGCAGCAT TTCACTTACA GTTTTCCAGT   960
GAATGA
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Seq ID NO: 96 Protein sequence
Protein Accession #: XP_090469

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1          11         21         31         41         51
|          |          |          |          |          |
MGFGDQGTVE GSLGTSKDSS CRVLDRTQVN KPCLLEAAKH SPHPLHGQSV NSHPSGAHQK    60
PPEVKMFGAS QGLLTMETNQ SLAQGTGCSV CWEVNGPGLE MSLPGVLSAD AGQVEHRRQM   120
NSADTDWGTE EGPGSLDFAV AAHQEDTFFL KDIKHTSTFR QSVQQQNCIY SPREKPCGNV   180
RAPCAPPRRE APLALSRPWR LSRSPAPSPR TPMAPFPTSD RELDAPGPPP GLRSSAAAPH   240
CLPAAPEAQK LPFLLPLYPD GSPPPKDILQ TLQHKAPGKR LHQESPGSFP IGLCNRTAEP   300
CIKGALGVAA EAAFHLQFSS E
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Seq ID NO: 97 DNA sequence
Nucleic Acid Accession #: NM_003474.2
Coding sequence: 37..3036

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1          11         21         31         41         51
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TCAAGGCTGG CTTGTGCCAG AACGGCGCGC GCGCGACGCA CGCACACACA CGGGGGGAAA   120
CTTTTTTAAA AATGAAAGGC TAGAAGAGCT CAGCGGCGGC GCGGGCCGTG CGCGAGGGCT   180
CCGGAGCTGA CTCGCCGAGG CAGGAAATCC CTCCGGTCGC GACGCCCGGC CCCGCTCGGC   240
GCCCGCGTGG GATGGTGCAG CGCTCGCCGC CGGGCCCGAG AGCTGCTGCA CTGAAGGCCG   300
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GCGACGATGG CAGCGCGCCC GCTGCCCGTG TCCCCCGCCC GCGCCCTCCT GCTCGCCCTG   360
GCCGGTGCTC TGCTCGCGCC CTGCGAGGCC CGAGGGGTGA GCTTATGGAA CGAAGGAAGA   420
GCTGATGAAG TTGTCAGTGC CTCTGTTCGG AGTGGGGACC TCTGGATCCC AGTGAAGAGC   480
TTCGACTCCA AGAATCATCC AGAAGTGCTG AATATTCGAC TACAACGGGA AAGCAAAGAA   540
CTGATCATAA ATCTGGAAAG AAATGAAGGT CTCATTGCCA GCAGTTTCAC GGAAACCCAC   600
TATCTGCAAG ACGGTACTGA TGTCTCCCTC GCTCGAAATT ACACGGTAAT TCTGGGTCAC   660
TGTTACTACC ATGGACATGT ACGGGGATAT TCTGATTCAG CAGTCAGTCT CAGCACGTGT   720
TCTGGTCTCA GGGGACTTAT TGTGTTTGAA AATGAAAGCT ATGTCTTAGA ACCAATGAAA   780
AGTGCAACCA ACAGATACAA ACTCTTCCCA GCGAAGAAGC TGAAAAGCGT CCGGGGATCA   840
TGTGGATCAC ATCACAACAC ACCAAACCTC GCTGCAAAGA ATGTGTTTCC ACCACCCTCT   900
CAGACATGGG CAAGAAGGCA TAAAAGAGAG ACCCTCAAGG CAACTAAGTA TGTGGAGCTG   960
GTGATCGTGG CAGACAACCG AGAGTTTCAG AGGCAAGGAA AAGATCTGGA AAAAGTTAAG  1020
CAGCGATTAA TAGAGATTGC TAATCACGTT GACAAGTTTT ACAGACCACT GAACATTCGG  1080
ATCGTGTTGG TAGGCGTGGA AGTGTGGAAT GACATGGACA AATGCTCTGT AAGTCAGGAC  1140
CCATTCACCA GCCTCCATGA ATTTCTGGAC TGGAGGAAGA TGAAGCTTCT ACCTCGCAAA  1200
TCCCATGACA ATGCGCAGCT TGTCAGTGGG GTTTATTTCC AAGGGACCAC CATCGGCATG  1260
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GACTTGGAGA CCAGCCTGGA GAAAGGAATG GGGGTGTGCC TGTTTAACCT GCCGGAAGTC  1560
AGGGAGTCTT TCGGGGGCCA GAAGTGTGGG AACAGATTTG TGGAAGAAGG AGAGGAGTGT  1620
GACTGTGGGG AGCCAGAGGA ATGTATGAAT CGCTGCTGCA ATGCCACCAC CTGTACCCTG  1680
AAGCCGGACG CTGTGTGCGC ACATGGGCTG TGCTGTGAAG ACTGCCAGCT GAAGCCTGCA  1740
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GGCTACTGCT ACAATGGCAT CTGCCAGACT CACGAGCAGC AGTGTGTCAC ACTCTGGGGA  1920
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CACGTGTACT TGGGCGATGA CATGCCCGAC CCAGGGCTTG TGCTTGCAGG CACAAAGTGT  2220
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GAGTGTGCAA TGCAGTGCCA CGGCAGAGGG GTGTGCAACA ACAGGAAGAA CTGCCACTGC  2340
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TGTCTTCTTG CTGCCGGATT TGTGGTTTAT CTCAAAAGGA AGACCTTGAT ACGACTGCTG  2520
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CGTGGCTTCC AACCCTGTCA GGCTCACCTC GGCCACCTTG GAAAAGGCCT GATGAGGAAG  2640
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ATGGGATTCT GGACAGGATG TGTTTGCTTT CTGATCAAGG CCTTATTGGA AAGCAGTCCC  3420
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CTCAGTTGAT TTTCTGGATT CCCCATCTCA GGCCAGAGCC AAGGGGCTTC AGGTCCAGGC  3540
TGTGTTTGGC TTTCAGGGAG GCCCTGTGCC CCTTGACAAC TGGCAGGCAG GCTCCCAGGG  3600
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CCAGTAGGTT ATTTAGCTTG GGAAAGGTGG TGTTTCTGTA AGAAACCTAC TGCCCAGGCA  3900
CTGCAAACCG CCACCTCCCT ATACTGCTTG GAGCTGAGCA AATCACCACA AACTGTAATA  3960
CAATGATCCT GTATTCAGAC AGATGAGGAC TTTCCATGGG ACCACAACTA TTTTCAGATG  4020
TGAACCATTA ACCAGATCTA GTCAATCAAG TCTGTTTACT GCAAGGTTCA ACTTATTAAC  4080
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TCCCCACTGT ATCTAGGCAA CATAGTATTC ATGACTATGG ATAAACTAAA CACGTGACAC  4740
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TATATACTAT TAAAAAGGTT TACAGAATTT TATGGTGCAT TACGTGGGCA TTGTCTTTTT  4980
AGATGCCCAA ATCCTTAGAT CTGGCATGTT AGCCCTTCCT CCAATTATAA GAGGATATGA  5040
ACCAAAAAAA AAAAAAAAAA AA
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Seq ID NO: 98 Protein sequence
Protein Accession #: NP_003465

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SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHCY  120
YHGHVRGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPAK KLKSVRGSCG  180
SHHNTPNLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLEKVKQR  240
LIEIANHVDK FYRPLNIRIV LVGVEVWNDM DKCSVSQDPF TSLHEFLDWR KMKLLPRKSH  300
DNAQLVSGVY FQGTTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH  360
DTLDRGCSCQ MAVEKGGCIM NASTGYPFPM VFSSCSRKDL ETSLEKGMGV CLFNLPEVRE  420
SFGGQKCGNR FVEEGEECDC GEPEECMNRC CNATTCTLKP DAVCAHGLCC EDCQLKPAGT  480
ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVDGY CYNGICQTHE QQCVTLWGPG  540
AKPAPGICFE RVNSAGDPYG NCGKVSKSSF AKCEMRDAKC GKIQCQGGAS RPVIGTNAVS  600
IETNIPLQQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRQCQ NISVFGVHEC  660
AMQCHGRGVC NNRKNCHCEA HWAPPFCDKF GFGGSTDSGP IRQADNQGLT IGILVTILCL  720
LAAGFVVYLK RKTLIRLLFT NKKTTIEKLR CVRPSRPPRG FQPCQAHLGH LGKGLMRKPP  780
DSYPPKDNPR RLLQCQNVDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP  840
ALRQAQGTCK PNPPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP  900
RSTHTAYIK
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Seq ID NO: 99 DNA sequence
Nucleic Acid Accession #: NM_003714
Coding sequence: 135..1043

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TAATACCAAG AACCATGTGT GCCGAGCGGC TGGGCCAGTT CATGACCCTG GCTTTGGTGT   180
TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCCAAG   240
ACAGGAGCTC CCAGCAGAAA GGCCGCCTGT CCCTGCAGAA TACAGCGGAG ATCCAGCACT   300
GTTTGGTCAA CGCTGGCGAT GTGGGGTGTG GCGTGTTTGA ATGTTTCGAG AACAACTCTT   360
GTGAGATTCG GGGCTTACAT GGGATTTGCA TGACTTTTCT GCACAACGCT GGAAAATTTG   420
ATGCCCAGGG CAAGTCATTC ATCAAAGACG CCTTGAAATG TAAGGCCCAC GCTCTGCGGC   480
ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGGTG TCCCAGTTGC   540
AGCGGGAATG CTACCTCAAG CACGACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGGTGA   600
TAGTGGAGAT GATCCATTTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA   660
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GCAGGGCCCC CAGAGCTGGG CCACACAGTG GGTGCTGGGC CTCGCCCCGA AGCTTCTGGT  1440
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TCTAAATAAA TGGCTTTCAA ACAAAGCAAC TGGGTCATTA AAACCAGCTC AAAGGGGGTT  1860
TAAAAAAAAA AAAACCAGCC CATCCTTTGA GGCTGATTTT TCTTTTTTTT AAGTTCTATT  1920
TTAAAAGCTA TCAAACAGCG ACATAGCCAT ACATCTGACT GCCTGACATG GACTCCTGCC  1980
CACTTGGGGG AAACCTTATA CCCAGAGGAA AATACACACC TGGGGAGTAC ATTTGACAAA  2040
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CTGGCGATTC CAGGAGACCC AGCTGGAAAC CTGGCTTCTC CATGTGAGGG GATGGGAAAG  2160
GAAAGAAGAG AATGAAGACT ACTTAGTAAT TCCCATCAGG AAATGCTGAC CTTTTACATA  2220
AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAA  2280
TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA  2340
GGGAGAGGAA GAAAAGAGAG AGAGAAAAGA GCCTCGTGCC
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Seq ID NO: 100 Protein sequence
Protein Accession #: NP_003705

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GDVGCGVFEC FENNSCEIRG LHGICMTFLH NAGKFDAQGK SFIKDALKCK AHALRHRFGC   120
ISRKCPAIRE MVSQLQRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT   180
CGEEVKEAIT HSVQVQCEQN WGSLCSILSF CTSAIQKPPT APPERQPQVD RTKLSRAHHG   240
EAGHHLPEPS SRETGRGAKG ERGSKSHPNA HARGRVGGLG AQGPSGSSEW EDEQSEYSDI   300
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Seq ID NO: 101 DNA sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23..1489

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AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACGCAG GAAGCCCCCC GGCCTGCCAG   240
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CCGACAGAAG AGGTTCGTGC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG   360
GATCCTTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC   420
CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCACG AGGGCCCTGC   480
TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCGT TTGATGGGCC   540
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT   600
CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAGGGC ACAGACCTGC TGCAGGTGGC   660
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CATTTGGTTC TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCCTGGG  1140
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Seq ID NO: 102 Protein sequence
Protein Accession #: NP_005931

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LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DGPGGILAHA   180
FFPKTHREGD VHFDYDETWT IGDDQGTDLL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR   240
YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA   300
VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA   360
QYWVYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS   420
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Seq ID NO: 103 DNA sequence
Nucleic Acid Accession #: NM_033151.2
Coding sequence: 351..4499

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TAAGGAGAGG AAAGAGCAGG CACCCAAACC TCTGCATGGC CCCAATATGC TCCCTGCAGG   240
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GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCCACCG TGGGGGAAGT   540
ATGATGCTGC CTTGAGAACC ATGATTCCCT TCCGTCCCAA GCCGAGGTTT CCTGCCCCCC   600
AGCCCCTGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC ACCCCGCTCA   660
TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCCTCCACTG TCAGTCCATG   720
ATGCCTCAGA CAAAAATGTC CAAAGGCTTC ACCGCCTTTG GGAAGAAGAA GTCTCAAGGC   780
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TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG CCAATATTGA   900
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PILIIPKILE YSEEQLGNVV HGVGLCFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS   240
FAFEKLIQFK SVIHITSGEA ISFFTGDVNY LFEGVCYGPL VLITCASLVI CSISSYFIIG   300
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ARYLQVLHCC SLNRDLELLP FGDMTEIGER GLNLSGGQKQ RISLARAVYS DRQIYLLDDP   660
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VNIVLQLASS FQATARIGLE TEAQFTAVER ILQYMKMCVS EAPLHMEGTS CPQGWPQHGE  1140
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Seq ID NO: 105 DNA sequence
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ATCCAGCGCA CAATCCGTGA AGCCTTCCAG GGCTGCACCG TGCTCGTCAT TGCCCACCGT  3900
GTCACCACTG TGCTGAACTG TGACCACATC CTGGTTATGG GCAATGGGAA GGTGGTAGAA  3960
TTTGATCGGC CGGAGGTACT GCGGAAGAAG CCTGGGTCAT TGTTCGCAGC CCTCATGGCC  4020
ACAGCCACTT CTTCACTGAG ATAA
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Seq ID NO: 106 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MTRKRTYWVP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQERNP EAPGRAAVPP    60
WGKYDAALRT MIPFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLDENTIPPL'  120
SVHDASDKNV QRLHRLWEEE VSRRGIEKAS VLLVMLRFQR TRLIPDALLG ICFCIASVLG  180
PILIIPKILE YSEEQLGNVV HGVGLCFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS  240
FAFEKLIQFK SVIHITSGEA ISFFTGDVNY LFEGVCYGPL VLITCASLVI CSISSYFIIG  300
YTAFIAILCY LLVFPLAVFM TRMAVKAQHH TSEVSDQRIR VTSEVLTCIK LIKMYTWEKP  360
FAKIIEGMES LTFCSKPGDG MAFSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRPKKFF  420
LQESPVFYVQ TLQDPSKALV FEEATLSWQQ TCPGIVNGAL ELERNGHASE GMTRPRDALG  480
PEEEGNSLGP ELHKINLVVS KGMMLGVCGN TGSGKSSLLS AILEEMHLLE GSVGVQGSLA  540
YVPQQAWIVS GNIRENILMG GAYDKARYLQ VLHCCSLNRD LELLPFGDMT EIGERGLNLS  600
GGQKQRISLA RAVYSDRQIY LLDDPLSAVD AHVGKHIFEE CIKKTLRGKT VVLVTHQLQY  660
LEFCGQIILL ENGKICENGT HSELMQKKGK YAQLIQKMHK EATSDMLQDT AKIAEKPKVE  720
SQALATSLEE SLNGNAVPEH QLIQEEEMEE GSLSWRVYHH YIQAAGGYMV SCIIFFFVVL  780
IVFLTIFSFW WLSYWLEQGS GTNSSRESNG TMADLGNIAD NPQLSFYQLV YGLNALLLIC  840
VGVCSSGIFT KVTRKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLLP  900
IFSEQFLVLS LMVIAVLLIV SVLSPYILLM GAIIMVICFI YYMMFKKAIG VFKRLENYSR  960
SPLFSHILNS LQGLSSIHVY GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALRLEIMTN 1020
LVTLAVALFV AFGISSTPYS FKVMAVNIVL QLASSFQATA RIGLETEAQF TAVERILQYM 1080
KMCVSEAPLH MEGTSCPQGW PQHGEIIFQD YHMKYRDNTP TVLHGINLTI RGHEVVGIVG 1140
RTGSGKSSLG MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRFN 1200
LDPFDRHTDQ QIWDALERTF LTKAISKFPK KLHTDVVENG GNFSVGERQL LCIARAVLRN 1260
SKIILIDEAT ASIDMETDTL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNGKVVE 1320
FDRPEVLRKK PGSLFAALMA TATSSLR
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Seq ID NO: 107 DNA sequence
Nucleic Acid Accession #: NM_024022
Coding sequence: 202..1563

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1          11         21         31         41         51
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ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTCATGCCC GTGTGAGCCA    60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG   120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC   180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC   240
TCATTCCGAT CGCTTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA   300
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC   360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC   420
TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC   480
GGAGTCTCGG ATTGCAAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG   540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCATGTGCTC CGATGACTGG   600
AAGGGTCACT ACGCAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA   660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT   720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA   780
TGTGCCTCTG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC   840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC   900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCT GTGGATCATC   960
ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT  1020
CTAGTTTCCC TGTTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC  1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA  1140
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC  1200
GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGG TGACGCCTCC  1260
CCTGTCCTGA ACCACGCGGC CGTCCCTTTG ATTTCCAACA AGATCTGCAA CCACAGGGAC  1320
GTGTACGGTG GCATCATCTC CCCCTCCATG CTCTGCGCGG GCTACCTGAC GGGTGGCGTG  1380
GACAGCTGCC AGGGGGACAG CGGGGGGCCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG  1440
TTAGTGGGAG CGACCAGCTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGGTGTAC  1500
ACCCGTGTCA CCTCCTTCCT GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC  1560
TGAAGAGGAA GGGGACAAGT AGCCACCTGA GTTCCTGAGG TGATGAAGAC AGCCCGATCC  1620
TCCCCTGGAC TCCCGTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTC  1680
CGGCACCAGT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA  1740
GCTGCTTTTT GTTTTTTGTT TTTTGAGGT GGAGTCTCGC TCTGTTGCCC AGGCTGGAGT  1800
GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG  1860
CCTCAGCTTC CCCAGTAGCT GGGACCACAG GTGCCCGCCA CCACACCCAA CTAATTTTTG  1920
TATTTTTAGT AGAGACAGGG TTTCACCATG TTGGCCAGGC TGCTCTCAAA CCCCTGACCT  1980
CAAATGATGT GCCTGCTTCA GCCTCCCACA GTGCTGGGAT TACAGGCATG GGCCACCACG  2040
CCTAGCCTCA CGCTCCTTTC TGATCTTCAC TAAGAACAAA AGAAGCAGCA ACTTGCAAGG  2100
GCGGCCTTTC CCACTGGTCC ATCTGGTTTT CTCTCCAGGG GTCTTGCAAA ATTCCTGACG  2160
AGATAAGCAG TTATGTGACC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA  2220
CCAGCCCAGA AGTGCAGAAC TGCAGTCACT GCACGTTTTC ATCTCTAGGG ACCAGAACCA  2280
AACCCACCCT TTCTACTTCC AAGACTTATT TTCACATGTG GGGAGGTTAA TCTAGGAATG  2340
ACTCGTTTAA GGCCTATTTT CATGATTTCT TTGTAGCATT TGGTGCTTGA CGTATTATTG  2400
TCCTTTGATT CCAAATAATA TGTTTCCTTC CCTCAAAAAA AAAAAAAAAA AAAAAAAAAA  2460
AAAAA
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Seq ID NO: 108 Protein sequence
Protein Accession #: NP_076927

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1          11         21         31         41         51
|          |          |          |          |          |
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI    60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF   120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK   180
VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH   240
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LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR   300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLNHAA   360
VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF   420
GIGCAEVNKP GVYTRVTSFL DWIHEQMERD LKT
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Seq ID NO: 109 DNA sequence
Nucleic Acid Accession #: NM_000493.2
Coding sequence: 97..2139

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1          11         21         31         41         51
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CCAGGAACTC CCAGCACGCA GAATCCATCT GAGAATATGC TGCCACAAAT ACCCTTTTTG   120
CTGCTAGTAT CCTTGAACTT GGTTCATGGA GTGTTTTACG CTGAACGATA CCAAATGCCC   180
ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA   240
AAGAGTAAAG GTATAGCAGT AAGAGGAGAG CAAGGTACTC CTGGTCCACC AGGCCCTGCT   300
GGACCTCGAG GGCACCCAGG TCCTTCTGGA CCACCAGGAA AACCAGGCTA CGGAAGTCCT   360
GGACTCCAAG GAGAGCCAGG GTTGCCAGGA CCACCGGGAC CATCAGCTGT AGGGAAACCA   420
GGTGTGCCAG GACTCCCAGG AAAACCAGGA GAGAGAGGAC CATATGGACC AAAAGGAGAT   480
GTTGGACCAG CTGGCCTACC AGGACCCCGG GGCCCACCAG GACCACCTGG AATCCCTGGA   540
CCGGCTGGAA TTTCTGTGCC AGGAAAACCT GGACAACAGG GACCCACAGG AGCCCCAGGA   600
CCCAGGGGCT TTCCTGGAGA AAAGGGTGCA CCAGGAGTCC CTGGTATGAA TGGACAGAAA   660
GGGGAAATGG GATATGGTGC TCCTGGTCGT CCAGGTGAGA GGGGTCTTCC AGGCCCTCAG   720
GGTCCCACAG GACCATCTGG CCCTCCTGGA GTGGGAAAAA GAGGTGAAAA TGGGGTTCCA   780
GGACAGCCAG GCATCAAAGG TGATAGAGGT TTTCCGGGAG AAATGGGACC AATTGGCCCA   840
CCAGGTCCCC AAGGCCCTCC TGGGGAACGA GGGCCAGAAG GCATTGGAAA GCCAGGAGCT   900
GCTGGAGCCC CAGGCCAGCC AGGGATTCCA GGAACAAAAG GTCTCCCTGG GGCTCCAGGA   960
ATAGCTGGGC CCCCAGGGCC TCCTGGCTTT GGGAAACCAG GCTTGCCAGG CCTGAAGGGA  1020
GAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGGCCAGCA  1080
GGTCTTCCTG GGAAGCCAGG TCTGACTGGA CCCCCTGGGA ATATGGGACC CCAAGGACCA  1140
AAAGGCATCC CGGGTAGCCA TGGTCTCCCA GGCCCTAAAG GTGAGACAGG GCCAGCTGGG  1200
CCTGCAGGAT ACCCTGGGGC TAAGGGTGAA AGGGGTTCCC CTGGGTCAGA TGGAAAACCA  1260
GGGTACCCAG GAAAACCAGG TCTCGATGGT CCTAAGGGTA ACCCAGGGTT ACCAGGTCCA  1320
AAAGGTGATC CTGGAGTTGG AGGACCTCCT GGTCTCCCAG GCCCTGTGGG CCCAGCAGGA  1380
GCAAAGGGAA TGCCCGGACA CAATGGAGAG GCTGGCCCAA GAGGTGCCCC TGGAATACCA  1440
GGTACTAGAG GCCCTATTGG GCCACCAGGC ATTCCAGGAT TCCCTGGGTC TAAAGGGGAT  1500
CCAGGAAGTC CCGGTCCTCC TGGCCCAGCT GGCATAGCAA CTAAGGGCCT CAATGGACCC  1560
ACCGGGCCAC CAGGGCCTCC AGGTCCAAGA GGCCACTCTG GAGAGCCTGG TCTTCCAGGG  1620
CCCCCTGGGC CTCCAGGCCC ACCAGGTCAA GCAGTCATGC CTGAGGGTTT TATAAAGGCA  1680
GGCCAAAGGC CCAGTCTTTC TGGGACCCCT CTTGTTAGTG CCAACCAGGG GGTAACAGGA  1740
ATGCCTGTGT CTGCTTTTAC TGTTATTCTC TCCAAAGCTT ACCCAGCAAT AGGAACTCCC  1800
ATACCATTTG ATAAAATTTT GTATAACAGG CAACAGCATT ATGACCCAAG GACTGGAATC  1860
TTTACTTGTC AGATACCAGG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT  1920
CATGTTTGGG TAGGCCTGTA TAAGAATGGC ACCCCTGTAA TGTACACCTA TGATGAATAC  1980
ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAAATGAC  2040
CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAAATGGCC TATACTCCTC TGAGTATGTC  2100
CACTCCTCTT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCCAC AGAGCTAATC  2160
TAAATCTTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG  2220
AGGTAGGCTG AAAAGAATGT AATTTTTATT TTCTGAAATA CAGATTTGAG CTATCAGACC  2280
AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG  2340
AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTTCT CCAATATTAA AAAATATCAC  2400
CAAAGAAGTC CTGCTATGTT AAAAACAAAC AACAAAAAAC AAAGCAACAA AAAAAAAAAT  2460
TAAAAAAAAA AACAGAAATA GAGCTCTAAG TTATGTGAAA TTTGATTTGA GAAACTCGGC  2520
ATTTCCTTTT TAAAAAAGCC TGTTTCTAAC TATGAATATG AGAACTTCTA GGAAACATCC  2580
AGGAGGTATC ATATAACTTT GTAGAACTTA AATACTTGAA TATTCAAATT TAAAAGACAC  2640
TGTATCCCCT AAAATATTTC TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTTCAT  2700
CAATATCTAT TCAAATATAC AGGTGCATAT ATACTTGTTA AAGCTCTTAT ATAAAAAAGC  2760
CCCAAAATAT TGAAGTTCAT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTTCAAAA  2820
CTTTTCTATG ATTGCAGAGA AGCTTTTTAT ATACCCAGCA TAACTTGGAA ACAGGTATCT  2880
GACCTATTCT TATTTAGTTA ACACAAGTGT GATTAATTTG ATTTCTTTAA TTCCTTATTG  2940
AATCTTATGT GATATGATTT TCTGGATTTA CAGAACATTA GCACATGTAC CTTGTGCCTC  3000
CCATTCAAGT GAAGTTATAA TTTACACTGA GGGTTTCAAA ATTCGACTAG AAGTGGAGAT  3060
ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTAAAAC TTTTAAGCTG  3120
TGCCTCACTT ATTAAAGCAC AAAATGTTTT ACCTACTCCT TATTTACGAC ACAATAAAAT  3180
AACATCAATA GATTTTTAGG CTGAATTAAT TTGAAAGCAG CAATTTGCTG TTCTCAACCA  3240
TTCTTTCAAG GCTTTTCATT CGACACAATA AAATAACATC AATAG
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Seq ID NO: 110 Protein sequence
Protein Accession #: NP_000484.2

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1          11         21         31         41         51
|          |          |          |          |          |
MLPQIPFLLL VSLNLVHGVF YAERYQMPTG IKGPLPNTKT QFFIPYTIKS KGIAVRGEQG    60
TPGPPGPAGP RGHPGPSGPP GKPGYGSPGL QGEPGLPGPP GPSAVGKPGV PGLPGKPGER   120
GPYGPKGDVG PAGLPGPRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GFPGEKGAPG   180
VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG KRGENGVPGQ PGIKGDRGFP   240
GEMGPIGPPG PQGPPGERGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK   300
PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPGLTGPP GNMGPQGPKG IPGSHGLPGP   360
KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPGLDGPK GNPGLPGPKG DPGVGGPPGL   420
PGPVGPAGAK GMPGHNGEAG PRGAPGIPGT RGPIGPPGIP GFPGSKGDPG SPGPPGPAGI   480
ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV   540
SANQGVTGMP VSAFTVILSK AYPAIGTPIP FDKILYNRQQ HYDPRTGIFT CQIPGIYYFS   600
YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN   660
GLYSSEYVHS SFSGFLVAPM
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Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_000949
Coding sequence: 285..2153

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1          11         21         31         41         51
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GGAGGCTGAA ATCCCCAGAC GCCGGTTTTC TGGGCTGGGC TTTCTGCTTA CTCACTCCTT    60
CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTTCCACACA ATGGAGCTTC   120
ATGTCCTCGT GCAGGAAGTA CTCATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC   180
TAAAGAACTC TCCTATTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCCTGAA   240
GTGAACTTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG   300
CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT   360
TACCTCCTGG AAAACCTGAG ATCTTTAAAT GTCGTTCTCC CAATAAGGAA ACATTCACCT   420
GCTGGTGGAG GCCTGGGACA GATGGAGGAC TTCCTACCAA TTATTCACTG ACTTACCACA   480
GGGAAGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCAACTCCT   540
GCCACTTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA   600
CTAACCAGAT GGGAAGCAGT TTCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC   660
AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAAACA GCCAGAAGAC AGAAAACCCT   720
ACCTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAACTGGT TGGTTCACGC   780
TCCTGTATGA AATTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG   840
GGCAGCAAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG   900
TTCGCTGCAA ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTCAGA   960
TACCTAGTGA CTTCACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCTTTCTG  1020
CTGTCATCTG TTTGATTATT GTCTGGGCAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT  1080
GCATCTTTCC GCCAGTTCCT GGGCCAAAAA TAAAAGGATT TGATGCTCAT CTGTTGGAGA  1140
AGGGCAAGTC TGAAGAACTA CTGAGTGCCT TGGGATGCCA AGACTTTCCT CCCACTTCTG  1200
ACTATGAGGA CTTGCTGGTG GAGTATTTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA  1260
TGTCAGTCCA TTCAAAAGAA CACCCAAGTC AAGGTATGAA ACCCACATAC CTGGATCCTG  1320
ACACTGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCCT TTTGTCTGAA AAGTGTGAGG  1380
AACCCCAGGC CAATCCCTCC ACATTCTATG ATCCTGAGGT CATTGAGAAG CCAGAGAATC  1440
CTGAAACAAC CCACACCTGG GACCCCCAGT GCATAAGCAT GGAAGGCAAA ATCCCCTATT  1500
TTCATGCTGG TGGATCCAAA TGTTCAACAT GGCCCTTACC ACAGCCCAGC CAGCACAACC  1560
CCAGATCCTC TTACCACAAT ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG  1620
CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA  1680
AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTCTGAGA  1740
CTGACCAGGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC  1800
CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAAGATGG TGCATTATCA TTGCTACCAA  1860
AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT  1920
ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGGTGCCA GATCCACATG  1980
CTAAAAACGT GGCTTGCTTT GAAGAATCAG CCAAAGAGGC CCCACCATCA CTTGAACAGA  2040
ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC  2100
TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCCTTTCAC TGATAGCTTG  2160
ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTACGTGA  2220
AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGCTCCA  2280
TTTTTAACCA CTTGCCTCTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCCT  2340
AACTGTGATT TGTAGATTTA CTTTTTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT  2400
AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAG  2460
GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATTGT TTACCATAGA  2520
AAGATGACAA AAGAAAATTT TCCACATAGG AAAATGCCAT GAAAATTGCT TTTGAAAAAC  2580
AACTGCATAA CCTTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT  2640
AAAGAAAGAA TGCATTCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA  2700
TTGCTGATAT GCAAGTAAGA AAT
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Seq ID NO: 112 Protein sequence
Protein Accession #: NP_000940

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1          11         21         31         41         51
|          |          |          |          |          |
MKENVASATV FTLLLFLNTC LLNGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGGLPTNY     60
SLTYHREGET LMHECPDYIT GGPNSCHFGK QYTSMWRTYI MMVNAINQMG SSFSDELYVD    120
VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW    180
EIHFAGQQTE FKILSLHPGQ KYLVQVRCKP DHGYWSAWSP ATFIQIPSDF TMNDTTVWIS    240
VAVLSAVICL IIVWAVALKG YSMVTCIFPP VPGPKIKGFD AHLLEKGKSE ELLSALGCQD    300
FPPTSDYEDL LVEYLEVDDS EDQHLMSVHS KEHPSQGMKP TYLDPDTDSG RGSCDSPSLL    360
SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ    420
PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQREVE    480
SFHSETDQDT PWLLPQEKTP FGSAKPLDYV EIHKVNKDGA LSLLPKQREN SGKPKKPGTP    540
ENNKEYAKVS GVMDNNILVL VPDPHAKNVA CFEESAKEAP PSLEQNQAEK ALANFTATSS    600
KCRLQLGGLD YLDPACFTHS FH
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Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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1          11         21         31         41         51
|          |          |          |          |          |
ATGTGGGGCG CTCGCCGCTC GTCCGTCTCC TCATCCTGGA ACGCCGCTTC GCTCCTGCAG     60
CTGCTGCTGG CTGCGCTGCT GGCGGCGGGG GCGAGGGCCA GCGGCGAGTA CTGCCACGGC    120
TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC    180
GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG    240
GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC    300
CGGGCGGACA AAGACGGCCC CGACGGCTCG GCAGTGCCCA TCTACGTGCC GTTCCTCATT    360
GTTGGCTCCG TGTTTGTCGC CTTTATCATC TTGGGGTCCC TGGTGGCAGC CTGTTGCTGC    420
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AGATGTCTCC GGCCTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG   480
ATGGAGACCA TCCCCATGAT CCCCAGTGCC AGCACCTCCC GGGGGTCGTC CTCACGCCAG   540
TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAACTCAG GGGCCCGGGC GCCCCCAACA   600
AGGTCACAGA CCAACTGTTG CTTGCCGGAA GGGACCATGA ACAACGTGTA TGTCAACATG   660
CCCACGAATT TCTCTGTGCT GAACTGTCAG CAGGCCACCC AGATTGTGCC ACATCAAGGG   720
CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA   780
GCTGTGCCAC CTTTCATGGA CGGCCTGCAG CCTGGCTACA GGCAGATTCA GTCCCCCTTC   840
CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA
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Seq ID NO: 114 Protein sequence
Protein Accession #: XP_062811

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1          11         21         31         41         51
|          |          |          |          |          |
MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG    60
GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDGPDGS AVPIYVPFLI   120
VGSVFVAPII LGSLVAACCC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ   180
SSTAASSSSS ANSGARAPPT RSQTNCCLPE GTMNNVYVNM PTNFSVLNCQ QATQIVPHQG   240
QYLHPPYVGY TVQHDSVPMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV
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Seq ID NO: 115 DNA sequence
Nucleic Acid Accession #: NM_013257
Coding sequence: 223..1512

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1          11         21         31         41         51
|          |          |          |          |          |
GGTGTGCTCT TGAGGGATTA AATGCAAAGA GATCACACCA TGGACTACAA GGAAAGCTGC    60
CCAAGTGTAA GCATTCCCAG CTCCGATGAA CACAGAGAGA AAAAGAAGAG GTTTACTGTT   120
TATAAAGTTC TGGTTTCAGT GGGAAGAAGT GAATGGTTTG TCTTCAGGAG ATATGCAGAG   180
TTTGATAAAC TTTATAACAC TTTAAAAAAA CAGTTTCCTG CTATGGCCCT GAAGATTCCT   240
GCCAAGAGAA TATTTGGTGA TAATTTTGAT CCAGATTTTA TTAAACAAAG ACGAGCAGGA   300
CTAAACGAAT TCATTCAGAA CCTAGTTAGG TATCCAGAAC TTTATAACCA TCCAGATGTC   360
AGAGCATTCC TTCAAATGGA CAGTCCAAAA CACCAGTCAG ATCCATCTGA AGATGAGGAT   420
GAAAGAAGTT CTCAGAAGCT ACACTCTACC TCACAGAACA TCAACCTGGG ACCGTCTGGA   480
AATCCTCATG CCAAACCAAC TGACTTTGAT TTCTTAAAAG TTATTGGAAA AGGCAGCTTT   540
GGCAAGGTTC TTCTTGCAAA ACGGAAACTG GATGGAAAAT TTTATGCTGT CAAAGTGTTA   600
CAGAAAAAAA TAGTTCTCAA CAGAAAAGAG CAAAAACATA TTATGGCTGA ACGTAATGTG   660
CTCTTGAAAA ATGTGAAACA TCCGTTTTTG GTTGGATTGC ATTATTCCTT CCAAACAACT   720
GAAAAGCTTT ATTTTGTTCT GGATTTTGTT AATGGAGGGG AGCTTTTTTT CCACTTACAA   780
AGAGAACGGT CCTTTCCTGA GCACAGAGCT AGGTTTTACG CTGCTGAAAT TGCTAGTGCA   840
TTGGGTTACT TACATTCCAT CAAAATAGTA TACAGAGACT TGAAACCAGA AAATATTCTT   900
TTGGATTCAG TAGGACATGT TGTCTTAACA GATTTTGGGC TTTGTAAAGA AGGAATTGCT   960
ATTTCTGACA CCACTACCAC ATTTTGTGGG ACACCAGAGT ATCTTGCACC TGAAGTAATT  1020
AGAAAACAGC CCTATGACAA TACTGTAGAT TGGTGGTGCC TTGGGGCTGT TCTGTATGAA  1080
ATGCTGTATG GATTGCCTCC TTTTTATTGC CGAGATGTTG CTGAAATGTA TGACAATATC  1140
CTTCACAAAC CCCTAAGTTT GAGGCCAGGA GTGAGTCTTA CAGCCTGGTC CATTCTGGAA  1200
GAACTCCTAG AAAAAGACAG GCAAAATCGA CTTGGTGCCA AGGAAGACTT TCTTGAAATT  1260
CAGAATCATC CTTTTTTTGA ATCACTCAGC TGGGCTGACC TTGTACAAAA GAAGATTCCA  1320
CCACCATTTA ATCCTAATGT GGCTGGACCA GATGATATCA GAAACTTTGA CACAGCATTT  1380
ACAGAAGAAA CAGTTCCATA TTCTGTGTGT GTATCTTCTG ACTATTCTAT AGTGAATGCC  1440
AGTGTATTGG AGGCAGATGA TGCATTCGTT GGTTTCTCTT ATGCACCTCC TTCAGAAGAC  1500
TTATTTTTGT GAGCAGTTTG CCATTCAGAA ACCATTGAGC AAAATAAGTC TATAGATGGG  1560
ACTGAAACTT CTATTTGTGT GAATATATTC AAATATGTAT AACTAGTGCC TCATTTTTAT  1620
ATGTAATGAT GAAAACTATG AAAAAATGTA TTTTCTTCTA TGTGCAAGAA AAATAGGGCA  1680
TTTCAAAGAG CTGTTTTGAT TAAAATTTAT ATTCTTGTTT AATAAGCTTA TTTTTAAACA  1740
ATTTAAAAGC TATTATTCTT AGCATTAACC TATTTTTAAA GAAACCTTTT TTGCTATTGA  1800
CTGTTTTTTC CCTCTAAGTT TACACTAACA TCTACCCAAG ATAGACTGTT TTTTAACAGT  1860
CAATTTCAGT TCAGCTAACA TATATTAATA CCTTTGTAAC TCTTTGCTAT GGCTTTTGTT  1920
ATCACACCAA AACTATGCAA TTGGTACATG GTTGTTTAAG AAGAAACCGT ATTTTTCCAT  1980
GATAAATCAC TGTTTGAAAT ATTTGGTTCA TGGTATGATC GAAATGTAAA AGCATAATTA  2040
ACACATTGGC TGCTAGTTAA CAATTGGAAT AACTTTATTC TGCAGATCAT TTAAGAAGTA  2100
ACAGGCCGGG CGCGGTGGCT CACGCCTGTA ATCCCAGCAC TTTGGGAGGC TGAGGCGGGC  2160
AGATCACCTG AGGTCAGGAG TTGGAGACCA GCCTGACCAA CATGGACAAA CCCCGTCTCT  2220
ACTAAAAATA CAAAATTGGC AGGGTGTGGT GGCACATGCC TATAATCCCA GCTACTTGGG  2280
AGGCTAAGGC AGGAGAATCG CTTGAACCCG GGAGGCGGAG GTTGCAGTGA GCCGAGATCG  2340
CACCATTGCA CTCCTGCCTG GGCAACAAGA GTGAAACTCC ATCTCCAAAA A
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Seq ID NO: 116 Protein sequence
Protein Accession #: NP_037389

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1          11         21         31         41         51
|          |          |          |          |          |
MALKIPAKRI PGDNFDPDFI KQRRAGLNEF IQNLVRYPEL YNHPDVRAFL QMDSPKHQSD    60
PSEDEDERSS QKLHSTSQNI NLGPSGNPHA KPTDFDFLKV IGKGSFGKVL LAKRKLDGKF   120
YAVKVLQKKI VLNRKEQKHI MAERNVLLKN VKHPFLVGLH YSFQTTEKLY FVLDFVNGGE   180
LFFHLQRERS FPEHRARFYA AEIASALGYL HSIKIVYRDL KPENILLDSV GHVVLTDFGL   240
CKEGIAISDT TTTFCGTPEY LAPEVIRKQP YDNTVDWWCL GAVLYEMLYG LPPFYCRDVA   300
EMYDNILHKP LSLRPGVSLT AWSILEELLE KDRQNRLGAK EDFLEIQNHP FFESLSWADL   360
VQKKIPPPFN PNVAGPDDIR NFDTAFTEET VPYSVCVSSD YSIVNASVLE ADDAFVGFSY   420
APPSEDLFL
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Seq ID NO: 117 DNA sequence
Nucleic Acid Accession #: NM_004004.1

Coding sequence: 1..681

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACACTC CACCAGCATT    60
GGAAAGATCT GGCTCACCGT CCTCTTCATT TTTCGCATTA TGATCCTCGT TGTGGCTGCA   120
AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCCTGCA GCCAGGCTGC   180
AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCCACA TCCGGCTATG GGCCCTGCAG   240
CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT   300
GAGAAGAAGA GGAAGTTCAT CAAGGGGGAG ATAAAGAGTG AATTTAAGGA CATCGAGGAG   360
ATCAAAACCC AGAAGGTCCG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC   420
TTCTTCCGGG TCATCTTCGA AGCCGCCTTC ATGTACGTCT TCTATGTCAT GTACGACGGC   480
TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC   540
TTTGTGTCCC GGCCCACGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA   600
ATTTGCATCC TGCTGAATGT CACTGAATTG TGTTATTTGC TAATTAGATA TTGTTCTGGG   660
AAGTCAAAAA AGCCAGTTTA A
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Seq ID NO: 118 Protein sequence
Protein Accession #: NP_003995.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDWGTLQTIL GGVNKHSTSI GKIWLTVLFI FRIMILVVAA KEVWGDEQAD FVCNTLQPGC    60
KNVCYDHYFP ISHIRLWALQ LIFVSSPALL VAMHVAYRRH EKKRKFIKGE IKSEFKDIEE   120
IKTQKVRIEG SLWWTYTSSI FFRVIFEAAF MYVFYVMYDG FSMQRLVKCN AWPCPNTVDC   180
FVSRPTEKTV FTVFMIAVSG ICILLNVTEL CYLLIRYCSG KSKKPV
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Seq ID NO: 119 DNA sequence
Nucleic Acid Accession #: XM_061091.1
Coding sequence: 1..2481

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCAAATA CTTCAGGAAC AACCAGGATT GAAATTTGGC TTCTCCAAGA GCCGCCCGGG    60
CACCGAGCGC TGGTCGCCGC TCTCCTTCCG GTGAGTCCCA GCCCCGAGTT GGCTCTGGCG   120
CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT   180
CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTTA   240
GTTGGGAAGC CTCCTTTTGA GGCAAACGAA GTCCATGTAA GCAAAGAAAC CATCGGGAAG   300
ATTTCAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCTGTTA   360
GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA   420
GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT   480
TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA   540
AGAATCAAGA GGATGGTTTT CAAAGGAGGG CGCACGGAGA CGGAACTTGC TCTGAAATAC   600
CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC   660
GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG   720
GGTGTCACTG TGTTTGCTGT GGGGGTCAGG TTTCCCAGGT GGGAGGAGCT GCATGCACTG   780
GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC   840
GGCCTCTTCA GCACCCTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC   900
CCCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG   960
CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCTC  1020
TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG  1080
GTCGACCTCC TCTTCCTGCT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTTCCTGCGG  1140
GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCCGTGCTGA GCGAGGACTC TCGGGCCCGA  1200
GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCCTGTGGG GGAGTACCAG  1260
GATGTGCCTG ACCTGGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCCACCCTG  1320
ACGGGCAGTG CCTTGCGGCA GGCGGCAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC  1380
CAGGACCGGC CACGTAGAGT GGTGGTTTTG CTCACTGAGT CACACTCCGA GGATGAGGTT  1440
GCGGGCCCAG CGCGTCACGC AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG  1500
GCCGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG  1560
GATCCTCAGG ATCTGTTCAA CCAAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG  1620
CGGCCAGGGT GCCGGACACA AGCCCTGGAC CTCGTCTTCA TGTTGGACAC CTCTGCCTCA  1680
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT  1740
GAGGTGAACC CTGACGTGAC ACAGGTCGGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT  1800
GCCTTCGGGC TGGACACCAA ACCCACCCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC  1860
CCCTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGCACATCTA TGACAAAGTG  1920
ATGACCGTCC AGAGGGGTGC CCGGCCTGGT GTCCCCAAAG CTGTGGTGGT GCTCACAGGC  1980
GGGAGAGGCG CAGAGGATGC AGCCGTTCCT GCCCAGAAGC TGAGGAACAA TGGCATCTCT  2040
GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC  2100
CGGGATTCCC TGATCCACGT GGCAGCTTAC GCCGACCTGC GGTACCACCA GGACGTGCTC  2160
ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAACC CAGCCCGTGC  2220
ATGAATGAGG GCAGCTGCGT CCTGCAGAAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC  2280
TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG  2340
GGATGGATTC TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT  2400
ACCCCTCCCA GCAACTACAG AGAAGGCCTG GGCACTGAAA TGGTGCCTAC CTTCTGGAAT  2460
GTCTGTGCCC CAGGTCCTTA G
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Seq ID NO: 120 Protein sequence
Protein Accession #: XP_061091.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPNTSGTTRI EIWLLQEPPG HRALVAALLP VSPSPELALA PGYPPVPAAD DRFTLPMIGG    60
QMHGEKVDLW SLGVLCYEFL VGKPPFEANE VHVSKETIGK ISAASKMMWC SAAVDIMFLL   120
```

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DGSNSVGKGS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQQEVKA   180
RIKRMVFKGG RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER   240
GVTVFAVGVR FPRWEELHAL ASEPRGQHVL LAEQVEDATN GLFSTLSSSA ICSSATPAGS   300
PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR   360
VDLLFLLDSS AGTTLDGFLR AKVFVKRFVR AVLSEDSRAR VGVATYSREL LVAVPVGEYQ   420
DVPDLVWSLD GIPFRGGPTL TGSALRQAAE RGFGSATRTG QDRPRRVVVL LTESHSEDEV   480
AGPARHARAR ELLLLGVGSE AVRAELEEIT GSPKHVMVYS DPQDLFNQIP ELQGKLCSRQ   540
RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSCALQF EVNPDVTQVG LVVYGSQVQT   600
AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG   660
GRGAEDAAVP AQKLRNNGIS VLVVGVGPVL SEGLRRLAGP RDSLIHVAAY ADLRYHQDVL   720
IEWLCGEAKQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ   780
GWILETPLRH MAPVQEGSSR TPPSNYREGL GTEMVPTFWN VCAPGP
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Seq ID NO: 121 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCCCCTT TCCTGTTGCT GGAGGCCGTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA    60
TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC   120
AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC   180
AGCGTCGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT   240
CTGGACATCA GCCCCGAGAG GGTCAGAGTG GGAGCATTCC AGTTCAGTTC CACTCCTCAT   300
CTGGAATTCC CCTTGGATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG   360
ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAAATACCT TCTGCACAGA   420
GGGTTGCCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG   480
AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG   540
TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT   600
AGAGGGCAGC ACGTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC   660
ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC   720
CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTCG CTGGCAATGC CCCATGCTGG   780
AGAGGATCGC GGCGGACCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG   840
AGAGTGTTCC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC   900
TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAGTGC   960
CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC  1020
AGGGTCGACC TCCTCTTCCT GCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCCTG  1080
CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC  1140
CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCCTGT GGGGGAGTAC  1200
CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCCGTGG TGGCCCCACC  1260
CTGACGGGCA GTGCCTTGCG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA  1320
GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG  1380
GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT  1440
GAGGCCGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC  1500
TCGGATCCTC AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG  1560
CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC  1620
TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG  1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG  1740
ACTGCCTTCG GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG  1800
GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA  1860
GTGATGACCG TCCAGAGGGG TGCCCGGCCT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA  1920
GGCGGGAGAG GCGCAGAGGA TGCAGCCGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC  1980
TCTGTCTTGG TCGTGGGCGT GGGGCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT  2040
CCCCGGGATT CCCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG  2100
CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG  2160
TGCATGAATG AGGGCAGCTG CGTCCTGCAG AATGGGAGCT ACCGCTGCAA GTGTCGGGAT  2220
GGCTGGGAGG GCCCCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC  2280
CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC  2340
CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG  2400
AATGTCTGTG CCCCAGGTCC TTAG
```

Seq ID NO: 122 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN    60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS   780
RTPPSNYREG LGTEMVPTFW NVCAPGP
```

Seq ID NO: 123 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 89..2356

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1          11         21         31         41         51
|          |          |          |          |          |
GCCCCCTGGC CCGAGCCGCG CCCGGGTCTG TGAGTAGAGC CGCCCGGGCA CCGAGCGCTG    60
GTCGCCGCTC TCCTTCCGTT ATATCAACAT GCCCCCTTTC CTGTTGCTGG AAGCCGTCTG   120
TGTTTTCCTG TTTTCCAGAG TGCCCCCATC TCTCCCTCTC CAGGAAGTCC ATGTAAGCAA   180
AGAAACCATC GGGAAGATTT CAGCTGCCAG CAAAATGATG TGGTGCTCGG CTGCAGTGGA   240
CATCATGTTT CTGTTAGATG GGTCTAACAG CGTCGGGAAA GGGAGCTTTG AAAGGTCCAA   300
GCACTTTGCC ATCACAGTCT GTGACGGTCT GGACATCAGC CCCGAGAGGG TCAGAGTGGG   360
AGCATTCCAG TTCAGTTCCA CTCCTCATCT GGAATTCCCC TTGGATTCAT TTTCAACCCA   420
ACAGGAAGTG AAGGCAAGAA TCAAGAGGAT GGTTTTCAAA GGAGGGCGCA CGGAGACGGA   480
ACTTGCTCTG AAATACCTTC TGCACAGAGG GTTGCCTGGA GGCAGAAATG CTTCTGTGCC   540
CCAGATCCTC ATCATCGTCA CTGATGGGAA GTCCCAGGGG GATGTGGCAC TGCCATCCAA   600
GCAGCTGAAG GAAAGGGGTG TCACTGTGTT TGCTGTGGGG GTCAGGTTTC CCAGGTGGGA   660
GGAGCTGCAT GCACTGGCCA GCGAGCCTAG AGGGCAGCAC GTGCTGTTGG CTGAGCAGGT   720
GGAGGATGCC ACCAACGGCC TCTTCAGCAC CCTCAGCAGC TCGGCCATCT GCTCCAGCGC   780
CACGCCAGAC TGCAGGGTCG AGGCTCACCC CTGTGAGCAC AGGACGCTGG AGATGGTCCG   840
GGAGTTCGCT GGCAATGCCC CATGCTGGAG AGGATCGCGG CGGACCCTTG CGGTGCTGGC   900
TGCACACTGT CCCTTCTACA GCTGGAAGAG AGTGTTCCTA ACCCACCCTG CCACCTGCTA   960
CAGGACCACC TGCCCAGGCC CCTGTGACTC GCAGCCCTGC CAGAATGGAG GCACATGTGT  1020
TCCAGAAGGA CTGGACGGCT ACCAGTGCCT CTGCCCGCTG GCCTTTGGAG GGGAGGCTAA  1080
CTGTGCCCTG AAGCTGAGCC TGGAATGCAG GGTCGACCTC CTCTTCCTGC TGGACAGCTC  1140
TGCGGGCACC ACTCTGGACG GCTTCCTGCG GGCCAAAGTC TTCGTGAAGC GGTTTGTGCG  1200
GGCCGTGCTG AGCGAGGACT CTCGGGCCCG AGTGGGTGTG GCCACATACA GCAGGGAGCT  1260
GCTGGTGGCG GTGCCTGTGG GGGAGTACCA GGATGTGCCT GACCTGGTCT GGAGCCTCGA  1320
TGGCATTCCC TTCCGTGGTG GCCCCACCCT GACGGGCAGT GCCTTGCGGC AGGCGGCAGA  1380
GCGTGGCTTC GGGAGCGCCA CCAGGACAGG CCAGGACCGG CCACGTAGAG TGGTGGTTTT  1440
GCTCACTGAG TCACACTCCG AGGATGAGGT TGCGGGCCCA GCGCGTCACG CAAGGGCGCG  1500
AGAGCTGCTC CTGCTGGGTG TAGGCAGTGA GGCCGTGCGG GCAGAGCTGG AGGAGATCAC  1560
AGGCAGCCCA AAGCATGTGA TGGTCTACTC GGATCCTCAG GATCTGTTCA ACCAAATCCC  1620
TGAGCTGCAG GGGAAGCTGT GCAGCCGGCA GCGGCCAGGG TGCCGGACAC AAGCCCTGGA  1680
CCTCGTCTTC ATGTTGGACA CCTCTGCCTC AGTAGGGCCC GAGAATTTTG CTCAGATGCA  1740
GAGCTTTGTG AGAAGCTGTG CCCTCCAGTT TGAGGTGAAC CCTGACGTGA CACAGGTCGG  1800
CCTGGTGGTG TATGGCAGCC AGGTGCAGAC TGCCTTCGGG CTGGACACCA AACCCACCCG  1860
GGCTGCGATG CTGCGGGCCA TTAGCCAGGC CCCCTACCTA GGTGGGGTGG GCTCAGCCGG  1920
CACCGCCCTG CTGCACATCT ATGACAAAGT GATGACCGTC CAGAGGGGTG CCCGGCCTGG  1980
TGTCCCCAAA GCTGTGGTGG TGCTCACAGG CGGGAGAGGC GCAGAGGATG CAGCCGTTCC  2040
TGCCCAGAAG CTGAGGAACA ATGGCATCTC TGTCTTGGTC GTGGGCGTGG GGCCTGTCCT  2100
AAGTGAGGGT CTGCGGAGGC TTGCAGGTCC CCGGGATTCC CTGATCCACG TGGCAGCTTA  2160
CGCCGACCTG CGGTACCACC AGGACGTGCT CATTGAGTGG CTGTGTGGAG AAGCCAAGCA  2220
GCCAGTCAAC CTCTGCAAAC CCAGCCCGTG CATGAATGAG GGCAGCTGCG TCCTGCAGAA  2280
TGGGAGCTAC CGCTGCAAGT GTCGGGATGG CTGGGAGGGC CCCCACTGCG AGAACCGATT  2340
CTTGAGACGC CCCTGAGGCA CATGGCTCCC GTGCAGGAGG GCAGCAGCCG TACCCCTCCC  2400
AGCAACTACA GAGAAGGCCT GGGCACTGAA ATGGTGCCTA CCTTCTGGAA TGTCTGTGCC  2460
CCAGGTCCTT AGAATGTCTG CTTCCCGCCG TGGCCAGGAC CACTATTCTC ACTGAGGGAG  2520
GAGGATGTCC CAACTGCAGC CATGCTGCTT AGAGACAAGA AAGCAGCTGA TGTCACCCAC  2580
AAACGATGTT GTTGAAAAGT TTTGATGTGT AAGTAAATAC CCACTTTCTG TACCTGCTGT  2640
GCCTTGTTGA GGCTATGTCA TCTGCCACCT TTCCCTTGAG GATAAACAAG GGGTCCTGAA  2700
GACTTAAATT TAGCGGCCTG ACGTTCCTTT GCACACAATC AATGCTCGCC AGAATGTTGT  2760
TGACACAGTA ATGCCCAGCA GAGGCCTTTA CTAGAGCATC CTTTGGACGG
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Seq ID NO: 124 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN    60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP
```

Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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1          11         21         31         41         51
|          |          |          |          |          |
CCCGAGCCCC GCCCCTCCGG GCCCGGGTCG GCGCGCCCAG CCTGCCAGCC GCGCTGCTGC    60
TGCTCCTCCT GCTGTGGGAC CGCTGACCGC GCGGCTGCTC CGCTCTCCCC GCTCCAAGCG   120
CCGATCTGGG CACCCGCCAC CAGCATGGAC GCTCGCCGCG TGCCGCAGAA AGATCTCAGA   180
GTAAAGAAGA ACTTAAAGAA ATTCAGATAT GTGAAGTTGA TTTCCATGGA AACCTCGTCA   240
TCCTCTGATG ACAGTTGTGA CAGCTTTGCT TCTGATAATT TTGCAAACAC GAGGCTGCAG   300
TCAGTTCGGG AAGGCTGTAG GACCCGCAGC CAGTGCAGGC ACTCTGGACC TCTCAGGGTG   360
GCGATGAAGT TTCCAGCGCG GAGTACCAGG GGAGCAACCA ACAAAAAAGC AGAGTCCCGC   420
CAGCCCTCAG AGAATTCTGT GACTGATTCC AACTCCGATT CAGAAGATGA AAGTGGAATG   480
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AATTTTTTGG AGAAAAGGGC TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC   540
ATGTCTGAAT TAGAAAGCTT CCCTGGCTCG TTCCGTGGAA GACATCCCCT CCCAGGCTCC   600
GACTCACAAT CAAGGAGACC GCGAAGGCGT ACATTCCCGG GTGTTGCTTC CAGGAGAAAC   660
CCTGAACGGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCCTCGG GTCCCTTGAC   720
GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTTGGTGAG AAAGAGGAAG   780
ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCCAGAA GCCGTCGCTC CAGATCATCC   840
GTGACCCTTC CGCATATAAT TCGCCCAGTG GAAGAAATTA CAGAGGAGGA GTTGGAGAAC   900
GTCTGCAGCA ATTCTCGAGA GAAGATATAT AACCGTTCAC TGGGCTCTAC TTGTCATCAA   960
TGCCGTCAGA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGGCGTT  1020
CGAGGCCAGT TCTGTGGCCC CTGCCTTCGA AACCGTTATG GTGAAGAGGT CAGGGATGCT  1080
CTGCTGGATC CGAACTGGCA TTGCCCGCCT TGTCGAGGAA TCTGCAACTG CAGTTTCTGC  1140
CGGCAGCGAG ATGGACGGTG TGCGACTGGG GTCCTTGTGT ATTTAGCCAA ATATCATGGC  1200
TTTGGGAATG TGCATGCCTA CTTGAAAAGC CTGAAACAGG AATTTGAAAT GCAAGCATAA  1260
TATCTGGAAA ATTTGCTGCC TGCCTTCTAC TTCTCAAATC TTTCTTGTAA AAGTTTCCAA  1320
TTTTTTCACT GAAACCTGAG TTAAAAATCT TGATGATCAG CCTGTTTCAT AAGAAACTCC  1380
AATCAAGTTA ATCTTAGCAG ACATGTGTTT CTGGAGCATC ACAGAAGGTA TATTGCTAGT  1440
TACACTTTGC CCTCCTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCCC  1500
TCTATTTCCA ATGCTCCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT  1560
TATGAAAGCA TATTTTATTT ACTTGGTGTT GAAATAGCCC TCATAAAACC TAAGCACTTG  1620
GAAACACAAT AATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA  1680
CTTGTTTACA CAAAAACGAG TATGATTTAG CACTCATACT AGTTGAAATT TTTAATAGAA  1740
TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT  1800
CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT  1860
CTCCTAATTT CTTCTGCCCG AAGGGTAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA  1920
AAGGTTGGTG GGCAATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT  1980
ATGAGTAAGC TGATTTGAAT TTTCAGTATA AAACTTTAGT ATAATTGTAG TTTGCAAAGT  2040
TTATTTCAGT TCACATGTAA GGTATTGCAA ATAAATTCTT GGACAATTTT GTATGGAAAC  2100
TTGATATTAA AAACTAGTCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAGGCA  2160
CAAGGTTCAA GTTTAGATTT TAAGCACTTT TATAACAATG ATAAGTGCCT TTTTGGAGAT  2220
GTAACTTTTA GCAGTTTGTT AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC  2280
CTGTGTCAGT ATTCCCCCTC CTCTTTGCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT  2340
AAGTGTTTGT ATGTCCAATT TACTTGCATA TGTAAACCAT TGCTGTGCCA TTCAATGTTT  2400
GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTTGATCT GTAATGCTTT  2460
TATACAAAAG TTTATTTTAA TAATAAAATG TTTGTTCTAA AAAAAAAAAA
```

Seq ID NO: 126 Protein sequence
Protein Accession #: NP_114148.1

```
1           11          21          31          41          51
|           |           |           |           |           |
MDARRVPQKD LRVKKNLKKF RYVKLISMET SSSSDDSCDS FASDNFANTR LQSVREGCRT    60
RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSENSVT DSNSDSEDES GMNFLEKRAL   120
NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL   180
TRSRSRILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR   240
PVEEITEEEL ENVCSNSREK IYNRSLGSTC HQCRQKTIDT KTNCRNPDCW GVRGQFCGPC   300
LRNRYGEEVR DALLDPNWHC PPCRGICNCS FCRQRDGRCA TGVLVYLAKY HGFGNVHAYL   360
KSLKQEFEMQ A
```

Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: AF305616.1
Coding sequence: 1..863

```
1           11          21          31          41          51
|           |           |           |           |           |
ATGCACCGCT TGATGGGGGT CAACAGCACC GCCGCCGCCG CCGCCGGGCA GCCCAATGTC    60
TCCTGCACGT GCAACTGCAA ACGCTCTTTG TTCCAGAGCA TGGAGATCAC GGAGCTGGAG   120
TTTGTTCAGA TCATCATCAT CGTGGTGGTG ATGATGGTGA TGGTGGTGGT GATCACGTGC   180
CTGCTGAGCC ACTACAAGCT GTCTGCACGG TCCTTCATCA GCCGGCACAG CCAGGGGCGG   240
AGGAGAGAAG ATGCCCTGTC CTCAGAAGGA TGCCTGTGGC CCTCGGAGAG CACAGTGTCA   300
GGCAACGGAA TCCCAGAGCC GCAGGTCTAC GCCCCGCCTC GGCCCACCGA CCGCCTGGCC   360
GTGCCGCCCT TCGCCCAGCG GGAGCGCTTC CACCGCTTCC AGCCCACCTA TCCGTACCTG   420
CAGCACGAGA TCGACCTGCC ACCCACCATC TCGCTGTCAG ACGGGGAGGA GCCCCCACCC   480
TACCAGGGCC CCTGCACCCT CCAGCTTCGG GACCCCGAGC AGCAGCTGGA ACTGAACCGG   540
GAGTCGGTGC GCGCACCCCC AAACAGAACC ATCTTCGACA GTGACCTGAT GGATAGTGCC   600
AGGCTGGGCG GCCCCTGCCC CCCCAGCAGT AACTCGGGCA TCAGCGCCAC GTGCTACGGC   660
AGCGGCGGGC GCATGGAGGG GCCGCCGCCC ACCTACAGCG AGGTCATCGG CCACTACCCG   720
GGGTCCTCCT TCCAGCACCA GCAGAGCAGT GGGCCGCCCT CCTTGCTGGA GGGGACCCGG   780
CTCCACCACA CACACATCGC GCCCCTAGAG AGCGCAGCCA TCTGGAGCAA AGAGAAGGAT   840
AAACAGAAAG GACACCCTCT CTAG
```

Seq ID NO: 128 Protein sequence
Protein Accession #: AAL09357.1

```
1           11          21          31          41          51
|           |           |           |           |           |
MHRLMGVNST AAAAAGQPNV SCTCNCKRSL FQSMEITELE FVQIIIIVVV MMVMVVVITC    60
LLSHYKLSAR SFISRHSQGR RREDALSSEG CLWPSESTVS GNGIPEPQVY APPRPTDRLA   120
VPPFAQRERF HRFQPTYPYL QHEIDLPPTI SLSDGEEPPP YQGPCTLQLR DPEQQLELNR   180
ESVRAPPNRT IFDSDLMDSA RLGGPCPPSS NSGISATCYG SGGRMEGPPP TYSEVIGHYP   240
GSSFQHQQSS GPPSLLEGTR LHHTHIAPLE SAAIWSKEKD KQKGHPL
```

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_004952.1

Coding sequence: 1..718

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGCGGCGG CTCCGCTGCT GCTGCTGCTG CTGCTCGTGC CCGTGCCGCT GCTGCCGCTG    60
CTGGCCCAAG GGCCCGGAGG GGCGCTGGGA AACCGGCATG CGGTGTACTG GAACAGCTCC   120
AACCAGCACC TGCGGCGAGA GGGCTACACC GTGCAGGTGA ACGTGAACGA CTATCTGGAT   180
ATTTACTGCC CGCACTACAA CAGCTCGGGG GTGGGCCCCG GGGCGGGACC GGGGCCCGGA   240
GGCGGGGCAG AGCAGTACGT GCTGTACATG GTGAGCCGCA ACGGCTACCG CACCTGCAAC   300
GCCAGCCAGG GCTTCAAGCG CTGGGAGTGC AACCGGCCGC ACGCCCCGCA CAGCCCCATC   360
AAGTTCTCGG AGAAGTTCCA GCGCTACAGC GCCTTCTCTC TGGGCTACGA GTTCCACGCC   420
GGCCACGAGT ACTACTACAT CTCCACGCCC ACTCACAACC TGCACTGGAA GTGTCTGAGG   480
ATGAAGGTGT TCGTCTGCTG CGCCTCCACA TCGCACTCCG GGGAGAAGCC GGTCCCCACT   540
CTCCCCCAGT TCACCATGGG CCCCAATGTG AAGATCAACG TGCTGGAAGA CTTTGAGGGA   600
GAGAACCCTC AGGTGCCCAA GCTTGAGAAG AGCATCAGCG GGACCAGCCC CAAACGGGAA   660
CACCTGCCCC TGGCCGTGGG CATCGCCTTC TTCCTCATGA CGTTCTTGGC CTCCTAG
```

Seq ID NO: 130 Protein sequence
Protein Accession #: NP_004943.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAAAPLLLLL LLVPVPLLPL LAQGPGGALG NRHAVYWNSS NQHLRREGYT VQVNVNDYLD    60
IYCPHYNSSG VGPGAGPGPG GGAEQYVLYM VSRNGYRTCN ASQGFKRWEC NRPHAPHSPI   120
KFSEKFQRYS AFSLGYEFHA GHEYYYISTP THNLHWKCLR MKVFVCCAST SHSGEKPVPT   180
LPQFTMGPNV KINVLEDFEG ENPQVPKLEK SISGTSPKRE HLPLAVGIAF FLMTFLAS
```

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: NM_012445.1
Coding sequence: 276..1271

```
1          11         21         31         41         51
|          |          |          |          |          |
GCACGAGGGA AGAGGGTGAT CCGACCCGGG GAAGGTCGCT GGGCAGGGCG AGTTGGGAAA    60
GCGGCAGCCC CCGCCGCCCC CGCAGCCCCT TCTCCTCCTT TCTCCCACGT CCTATCTGCC   120
TCTCGCTGGA GGCCAGGCCG TGCAGCATCG AAGACAGGAG GAACTGGAGC CTCATTGGCC   180
GGCCCGGGGC GCCGGCCTCG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GGACCCGACC   240
GCTGCCGGCC GCGCTCCCGC TGCTCCTGCC GGGTGATGGA AAACCCCAGC CCGGCCGCCG   300
CCCTGGGCAA GGCCCTCTGC GCTCTCCTCC TGGCCACTCT CGGCGCCGCC GGCCAGCCTC   360
TTGGGGGAGA GTCCATCTGT TCCGCCAGAG CCCCGGCCAA ATACAGCATC ACCTTCACGG   420
GCAAGTGGAG CCAGACGGCC TTCCCCAAGC AGTACCCCCT GTTCCGCCCC CCTGCGCAGT   480
GGTCTTCGCT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCAGT   540
ACGTCAGTAA CGGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCCTGGGCG CTGATGAAGG   600
AGATCGAGGC GGCGGGGGAG GCGCTGCAGA GCGTGCACGC GGTGTTTTCG GCGCCCGCCG   660
TCCCCAGCGG CACCGGGCAG ACGTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG   720
TCTCGTTTGT GGTGCGCATC GTGCCCAGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG   780
ACCTGTGCGA CGGGGACCGT TGGCGGGAAC AGGCGGCGCT GGACCTGTAC CCCTACGACG   840
CCGGGACGGA CAGCGGCTTC ACCTTCTCCT CCCCCAACTT CGCCACCATC CCGCAGGACA   900
CGGTGACCGA GATAACGTCC TCCTCTCCCA GCCACCCGGC CAACTCCTTC TACTACCCGC   960
GGCTGAAGGC CCTGCCTCCC ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA  1020
GGGCCTTCAT CCCTCCCGCC CCAGTCCTGC CCAGCAGGGA CAATGAGATT GTAGACAGCG  1080
CCTCAGTTCC AGAAACGCCG CTGGACTGCG AGGTCTCCCT GTGGTCGTCC TGGGGACTGT  1140
GCGGAGGCCA CTGTGGGAGG CTCGGGACCA AGAGCAGGAC TCGCTACGTC CGGGTCCAGC  1200
CCGCCAACAA CGGGAGCCCC TGCCCCGAGC TCGAAGAAGA GGCTGAGTGC GTCCCTGATA  1260
ACTGCGTCTA AGACCAGAGC CCCGCAGCCC CTGGGGCCCC CGGAGCCATG GGGTGTCGGG  1320
GGCTCCTGTG CAGGCTCATG CTGCAGGCGG CCGAGGCACA GGGGGTTTCG CGCTGCTCCT  1380
GACCGCGGTG AGGCCGCGCC GACCATCTCT GCACTGAAGG GCCCTCTGGT GGCCGGCACG  1440
GGCATTGGGA AACAGCCTCC TCCTTTCCCA ACCTTGCTTC TTAGGGGCCC CCGTGTCCCG  1500
TCTGCTCTCA GCCTCCTCCT CCTGCAGGAT AAAGTCATCC CCAAGGCTCC AGCTACTCTA  1560
AATTATGGTC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGTCCTTCAT CGTCCAGGGG  1620
CCTGGCTCCC ACGTGGTTGC AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA  1680
CTCTCCCGAG GGCGCATCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC  1740
GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT  1800
TGCTCAC
```

Seq ID NO: 132 Protein sequence
Protein Accession #: NP_036577.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MENPSPAAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY    60
PLFRPPAQWS SLLGAAHSSD YSMWRKNQYV SNGLRDFAER GEAWALMKEI EAAGEALQSV   120
HAVFSAPAVP SGTGQTSAEL EVQRRHSLVS FVVRIVPSPD WFVGVDSLDL CDGDRWREQA   180
ALDLYPYDAG TDSGFTFSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT   240
LVRLRQSPRA FIPPAPVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTKS   300
RTRYVRVQPA NNGSPCPELE EEAECVPDNC V
```

Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC    60
```

```
AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA   120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC   180
TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG   240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT   300
GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA   360
GGGAACTGGT TCTCTGCCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT   420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG   480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT   540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG   600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC   660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC   720
CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA   780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA   840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC   900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA   960
GCCACCCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT  1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT  1080
GCGTACCAGG GGGAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG  1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG  1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCCAGG AGTATACACC  1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
```

Seq ID NO: 134 Protein sequence
Protein Accession #: NP_063947.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLQDPDSDQP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY    60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT   120
GNWFSACFDN FTEALAETAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELRMRNSS   180
GPCLSGSLVS LHCLACGKSL KTPRVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV   240
LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIIE FNPMYPKDND IALMKLQFPL   300
TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD   360
AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT   420
```

Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_003045
Coding sequence: 148..2037

```
1          11         21         31         41         51
|          |          |          |          |          |
CGATCCTGCC GGAGCCCCGC CGCCGCCGGC TTGGATTCTG AAACCTTCCT TGTATCCCTC    60
CTGAGACATC TTTGCTGCAA GATCGAGGCT GTCCTCTGGT GAGAAGGTGG TGAGGCTTCC   120
CGTCATATTC CAGCTCTGAA CAGCAACATG GGGTGCAAAG TCCTGCTCAA CATTGGGCAG   180
CAGATGCTGC GGCGGAAGGT GGTGGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC   240
CTGAACACTT TTGATCTGGT GGCCCTCGGG GTGGGCAGCA CACTGGGTGC TGGTGTCTAC   300
GTCCTGGCTG GAGCTGTGGC CCGTGAGAAT GCAGGCCCTG CCATTGTCAT CTCCTTCCTG   360
ATCGCTGCGC TGGCCTCAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC   420
CCCAAGACGG GCTCAGCTTA CCTCTACAGC TATGTCACCG TTGGAGAGCT CTGGGCCTTC   480
ATCACCGGCT GGAACTTAAT CCTCTCCTAC ATCATCGGTA CTTCAAGCGT AGCGAGGGCC   540
TGGAGCGCCA CCTTCGACGA GCTGATAGGC AGACCCATCG GGGAGTTCTC ACGGACACAC   600
ATGACTCTGA ACGCCCCCGG CGTGCTGGCT GAAAACCCCG ACATATTCGC AGTGATCATA   660
ATTCTCATCT TGACAGGACT TTTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA   720
ATATTCACTT GTATTAACGT CCTGGTCCTG GGCTTCATAA TGGTGTCAGG ATTTGTGAAA   780
GGATCGGTTA AAAACTGGCA GCTCACGGAG GAGGATTTTG GGAACACATC AGGCCGTCTC   840
TGTTTGAACA ATGACACAAA AGAAGGGAAG CCCGGTGTTG GTGGATTCAT GCCCTTCGGG   900
TTCTCTGGTG TCCTGTCGGG GGCAGCGACT TGCTTCTATG CCTTCGTGGG CTTTGACTGC   960
ATCGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCCGT GGGGATCGTG  1020
GCGTCCCTCT TGATCTGCTT CATCGCCTAC TTTGGGGTGT CGGCTGCCCT CACGCTCATG  1080
ATGCCCTACT TCTGCCTGGA CAATAACAGC CCCCTGCCCG ACGCCTTTAA GCACGTGGGC  1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC CGCCAGTCTT  1200
CTAGGTTCCA TGTTTCCCAT GCCTCGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA  1260
TTTAAATTCT TAGCCAACGT CAATGATAGG ACCAAAACAC CAATAATCGC CACATTAGCC  1320
TCGGGTGCCG TTGCTGCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC  1380
ATGTCCATTG GCACTCTCCT GGCTTACTCG TTGGTGGCTG CCTGTGTGTT GGTCTTACGG  1440
TACCAGCCAG AGCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT  1500
CCAGCAGACC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG  1560
GCAGAGATGT TCTCTTTGAA AACCATACTC TCACCCAAAA ACATGGAGCC TTCCAAAATC  1620
TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC  1680
ATTGTGACCG TGCTTGGAAG GGAGGCTCTC ACCAAAGGGG CGCTGTGGGC AGTCTTTCTG  1740
CTCGCAGGGT CTGCCCTCCT CTGTGCCGTG GTCACGGGCG TCATCTGGAG GCAGCCCGAG  1800
AGCAAGACCA AGCTCTCATT TAAGGTTCCC TTCCTGCCAG TGCTCCCCAT CCTGAGCATC  1860
TTCGTGAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCCG GTTTGCTGTG  1920
TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG  1980
TCCCTGGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAGTG CAAGTGACGC  2040
ACAGCCCCGC CCCCCGGAGG TGGCAGCAGC CCCGAGGGAC GCCCCCAGAG GACCGGGAGG  2100
CACCCCACCC TCCCCACCAG TGCAACAGAA ACCACCTGCG TCCACACCCT CACTGCA
```

Seq ID NO: 136 Protein sequence
Protein Accession #: NM_003045

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1          11         21         31         41         51
|          |          |          |          |          |
```

```
MGCKVLLNIG QQMLRRKVVD CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLAGAVARE    60
NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNLILS   120
YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT   180
LGVKESAMVN KIFTCINVLV LGFIMVSGFV KGSVKNWQLT EEDFGNTSGR LCLNNDTKEG   240
KPGVGGFMPF GFSGVLSGAA TCFYAFVGFD CIATTGEEVK NPQKAIPVGI VASLLICFIA   300
YFGVSAALTL MMPYFCLDNN SPLPDAFKHV GWEGAKYAVA VGSLCALSAS LLGSMFPMPR   360
VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLVD LMSIGTLLAY   420
SLVAACVLVL RYQPEQPNLV YQMASTSDEL DPADQNELAS TNDSQLGFLP EAEMFSLKTI   480
LSPKNMEPSK ISGLIVNIST SLIAVLIITF CIVTVLGREA LTKGALWAVF LLAGSALLCA   540
VVTGVIWRQP ESKTKLSFKV PFLPVLPILS IFVNVYLMMQ LDQGTWVRFA VWMLIGFIIY   600
FGYGLWHSEE ASLDADQART PDGNLDQCK
```

Seq ID NO: 137 DNA sequence
Nucleic Acid Accession #: NM_032044.1
Coding sequence: 182..658

```
1          11         21         31         41         51
|          |          |          |          |          |
AAGATATAAA AGCTCCAGAA ACGTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG    60
GCCCTTAGAG TCTTGGTTGC CAAACAGATT TGCAGATCAA GGAGAACCCA GGAGTTTCAA   120
AGAAGCGCTA GTAAGGTCTC TGAGATCCTT GCACTAGCTA CATCCTCAGG GTAGGAGGAA   180
GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCTGGCCA AAACAGGAGT   240
CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTTACC ACAAGTCCAA   300
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CAAGAATCAA GATTCTGCTA ACTCCTGCAC AGCCCCGTCC TCTTCCTTTC TGCTAGCCTG   720
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GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT   960
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CACTCAACTC CTGCTTGTTT TTCCTTTGGC CATAGGAAGG TTTACCAGTA GAATCCTTGC  1140
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Seq ID NO: 138 Protein sequence
Protein Accession #: NP_114433.1

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YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG   120
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Seq ID NO: 139 DNA sequence
Nucleic Acid Accession #: XM_051860.2
Coding sequence: 52..3042

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Seq ID NO: 140 Protein sequence
Protein Accession #: XP_051860.2

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NSILQGIPWQ LFNYVATIPD NSIVLMASKG RYVSRGPWTR VLEKLGADRG LKLKEQMAFV   960
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Seq ID NO: 141 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 261..2861

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Seq ID NO: 142 Protein sequence
Protein Accession #: Eos sequence

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Seq ID NO: 143 NM DNA sequence
Nucleic Acid Accession #: NM_006017
Coding sequence: 38..2635

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GATTATTCTA TGCTGTGTCC TGGGGCTGCT GTTTATTATT CTGATGCCTC TGGTGGGGTA   420
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CAGCAGTCTG ACCAGCGTGA AAACTAGCCT GCGGTCATCT CTCAATGACC CTCTGTGCTT   960
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CAACCCTGAA CTGAGGCAGC TTCCACCCGT GGATGCAGAA CTTGACAACG TTAATAACGT  1080
TCTTAGGACA GATTTGGATG GCCTGGTCCA ACAGGGCTAT CAATCCCTTA ATGATATACC  1140
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Protein Accession #: NP_006008.1

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HQVRTRIKRS RKLADSNFKD LRTLLNETPE QIKYILAQYN TTKDKAFTDL NSINSVLGGG   240
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VFLMVGVGLS FLFCWILMII VVLTFVFGAN VEKLICEPYT SKELFRVLDT PYLLNEDWEY   540
YLSGKLFNKS KMKLTFEQVY SDCKKNRGTY GTLHLQNSFN ISEHLNINEH TGSISSELES   600
LKVNLNIFLL GAAGRKNLQD FAACGIDRMN YDSYLAQTGK SPAGVNLLSF AYDLEAKANS   660
LPPGNLRNSL KRDAQTIKTI HQQRVLPIEQ SLSTLYQSVK ILQRTGNGLL ERVTRILASL   720
DFAQNFITNN TSSVIIEETK KYGRTIIGYF EHYLQWIEFS ISEKVASCKP VATALDTAVD   780
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Coding sequence: 38..2605

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AGCTGGACCC ATTGGCATTC TCTTTGAACT AGTGCATATC TTTCTCTATG TGGTACAGCC   240
GCGTGATTTC CCAGAAGATA CTTTGAGAAA ATTCTTACAG AAGGCATATG AATCCAAAAT   300
TGATTATGAC ATTGTCTACT ATGAAGCAGG GATTATTCTA TGCTGTGTCC TGGGGCTGCT   360
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GGCAAATCAC CAGGTAAGAA CCCGGATCAA AAGGAGTCGG AAACTGGCAG ATAGCAATTT   600
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GTTCTCTATC AGTGAGAAAG TGGCATCGTG CAAACCTGTG GCCACCGCTC TAGATACTGC  2340
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Seq ID NO: 146 Protein sequence
Protein Accession #:

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RKLADSNFKD LRTLLNETPE QIKYILAQYN TTKDKAFTDL NSINSVLGGG ILDRLRPNII   240
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VQRQTTTVVA GIKRVLNSIG SDIDNVTQRL PIQDILSAFS VYVNNTESYI HRNLPTLEEY   420
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FLFCWILMII VVLTFVFGAN VEKLICEPYT SKELPRVLDT PYLLNEDWEY YLSGKLFNKS   540
KMKLTFEQVY SDCKKNRGTY GTLHLQNSFN ISEHLNINEH TGSISSELES LKVNLNIFLL   600
GAAGRKNLQD FAACGIDRMN YDSYLAQTGK SPAGVNLLSF AYDLEAKANS LPPGNLRNSL   660
KRDAQTIKTI HQQRVLPIEQ SLSTLYQSVK ILQRTGNGLL ERVTRILASL DFAQNFITNN   720
TSSVIIEETK KYGRTIIGYF EHVLQWIEFS ISEKVASCKP VATALDTAVD VFLCSYIIDP   780
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Seq ID NO: 148 Protein sequence
Protein Accession #: AAH12089.1

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FCMCRCCNKC GGEMHQRQKE NGPPLRKCFA ISLLVICIII SIGIFYGFVA NHQVRTRIKR   180
SRKLADSNFK DLRTLLNETP EQIKYILAQY NTTKDKAFTD LNSINSVLGG GILDRLRPNI   240
IPVLDEIKSM ATAIKETKEA LENMNSTLKS LHQQSTQLSS SLTSVKTSLR SSLNDPLCLV   300
HPSSETCNSI RLSLSQLNSN PELRQLPPVD AELDNVNNVL RTDLDGLVQQ GYQSLNDIPD   360
RVQRQTTIVV AGIKRVLNSI GSDIDNVTQR LPIQDILSAF SVYVNNTESY IHRNLPTLEE   420
YDSYWWLGGL VICSLLTLIV IFYYLGLLCG VCGYDRHATP TTRGCVSNTG GVFLMVGVGL   480
SFLFCWILMI IVVLTFVFGA NVEKLICEPY TSKELPRVLD TPYLLNEDWE YYLSGKLFNK   540
SKMKLTFEQV YSDCKKNRGT YGTLHLQNSF NISEHLNINE HTGSISSELE SLKVNLNIFL   600
LGAAGRKNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLLS FAYDLEAKAN SLPPGNLRNS   660
LKRDAQTIKT IHQQRVLPIE QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFAQNFITN   720
NTSSVIIEET KKYGRTIIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYIID   780
PLNLFWFGIG KATVFLLPAL IFAVKLAKYY RRMDSEDVYD DVETIPMKNM ENGNNGYHKD   840
HVYGIHNPVM TSPSQH
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Seq ID NO: 149 DNA sequence
Nucleic Acid Accession #: NM_033049.1
Coding sequence: 28..1566

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CTCCTTTCTG TAAACACAGC CACCAACCAA GGCAACTCAG CTGATGCTGT AACAACCACA   120
GAAACTGCGA CTAGTGGTCC TACAGTAGCT GCAGCTGATA CCACTGAAAC TAATTTCCCT   180
GAAACTGCTA GCACCACAGC AAATACACCT TCTTTCCCAA CAGCTACTTC ACCTGCTCCC   240
CCCATAATTA GTACACATAG TTCCTCCACA ATTCCTACAC CTGCTCCCCC CATAATTAGT   300
ACACATAGTT CCTCCACAAT TCCTATACCT ACTGCTGCAG ACAGTGAGTC AACCACAAAT   360
GTAAATTCAT TAGCTACCTC TGACATAATC ACCGCTTCAT CTCCAAATGA TGGATTAATC   420
ACAATGGTTC CTTCTGAAAC ACAAAGTAAC AATGAAATGT CCCCCACCAC AGAAGACAAT   480
CAATCATCAG GGCCTCCCAC TGGCACCGCT TTATTGGAGA CCAGCACCCT AAACAGCACA   540
GGTCCCAGCA ATCCTTGCCA AGATGATCCC TGTGCAGATA ATTCGTTATG TGTTAAGCTG   600
CATAATACAA GTTTTTGCCT GTGTTTAGAA GGGTATTACT ACAACTCTTC TACATGTAAG   660
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CCAAGATCTG AAATGCGTGC TGATGACAAG TTTGTTAATG TAACAATAGT AACAATTTTG   900
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AGGCCTAACC CACAGAGCCC TTTCTGCGTT GCTTCCAGTC TCAAGTGTCC TGATGCCTGC  1140
AACGCACAGC ACAAGCAATG CTTAATAAAG AAGAGTGGTG GGGCCCCTGA GTGTGCGTGC  1200
GTGCCCGGCT ACCAGGAAGA TGCTAATGGG AACTGCCAAA AGTGTGCATT TGGCTACAGT  1260
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Seq ID NO: 150 Protein sequence
Protein Accession #: NP_149038.1

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ITASSPNDGL ITMVPSETQS NNEMSPTTED NQSSGPPTGT ALLETSTLNS TGPSNPCQDD   180
PCADNSLCVK LHNTSPCLCL EGYYYNSSTC KKGKVFPGKI SVTVSETFDP EEKHSMAYQD   240
LHSEITSLFK DVFGTSVYGQ TVILTVSTSL SPRSEMRADD KFVNVTIVTI LAETTSDNEK   300
TVTEKINKAI RSSSSNFLNY DLTLRCDYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC   360
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LILTIVGTIA GIVILSMIIA LIVTARSNNK TKHIEEENLI DEDFQNLKLR STGFTNLGAE   480
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Seq ID NO: 151 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 87..914

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AGTTCTACAA CACGATCAGC AATGTCTTAT TTTTCATTTT ACCGCCCATC TGCATGTGCT   240
TGTTTCGTCA GTATGCAACA TGCTTCAACA GTGGCATCTA CTTAATCTGG ACTCTTTTGG   300
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GCATGTGGCA CATCCTCATC TGCCTTGCTG CCTACCTGGG CTGTGTATGC TTTGCCTACT   780
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Seq ID NO: 152 Protein sequence
Protein Accession #: Eos sequence

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DRGRFKVVVS VLSAVTTCLA FVKPAINNIS LMTLGVPCTA LLIAELKRCD NMRVFKLGLF   180
SGLWWTLALF CWISDRAFCE LLSSFNFPYL HCMWHILICL AAYLGCVCFA YFDAASEIPE   240
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Seq ID NO: 153 DNA sequence
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Coding sequence: 167..676

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GAGGATGGAG ATGCTCTGTG CCGGCAGGGT CCCTGCGCTG CTGCTCTGCC TGGGTTTCCA   240
TCTTCTACAG GCAGTCCTCA GTACAACTGT GATTCCATCA TGTATCCCAG GAGAGTCCAG   300
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AACAAAGTGT AGCTCTGACA TGAATGGCTA TTGTTTGCAT GGACAGTGCA TCTATCTGGT   420
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Seq ID NO: 154 Protein sequence
Protein Accession #: NP_001423.1

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Seq ID NO: 155 DNA sequence
Nucleic Acid Accession #: NM_013282.2
Coding sequence: 85..2466

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1          11         21         31         41         51
|          |          |          |          |          |
CGACTCCTTA GAGCATGGCA TGGCTCAGAG GTGCTGGTAA AACTGATGGG GGTTTTTGCT    60
GTCCCTCCCC TCAGCGCCGA CACCATGTGG ATCCAGGTTC GGACCATGGA CGGGAGGCAG   120
ACCCACACGG TGGACTCGCT GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG GCGGAAGATC   180
CAGGAGCTGT TCCACGTGGA GCCAGGCCTG CAGAGGCTGT TCTACAGGGG CAAACAGATG   240
GAGGACGGCC ATACCCTCTT CGACTACGAG GTCCGCCTGA ATGACACCAT CCAGCTCCTG   300
GTCCGCCAGA GCCTCGTGCT CCCCCACAGC ACCAAGGAGC GGGACTCCGA GCTCTCCGAC   360
ACCGACTCCG GCTGCTGCCT GGGCCAGAGT GAGTCAGACA AGTCCTCCAC CCACGGCGAG   420
GCGGCCGCCG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG   480
GGGCTGTACA AGGTCAATGA GTACGTCGAT GCTCGGGACA CGAACATGGG GGCGTGGTTT   540
GAGGCGCAGG TGGTCAGGGT GACGCGGAAG GCCCCCTCCC GGGACGAGCC CTGCAGCTCC   600
ACGTCCAGGC CGGCGCTGGA GGAGGACGTC ATTTACCACG TGAAATACGA CGACTACCCG   660
GAGAACGGCG TGGTCCAGAT GAACTCCAGG GACGTCCGAG CGCGCGCCCG CACCATCATC   720
AAGTGGCAGG ACCTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC   780
AAGGAGCGGG GCTTCTGGTA CGACGCGGAG ATCTCCAGGA AGCGCGAGAC CAGGACGGCG   840
CGGGAACTCT ACGCCAACGT GGTGCTGGGG GATGATTCTC TGAACGACTG TCGGATCATC   900
TTCGTGGACG AAGTCTTCAA GATTGAGCGG CCGGGTGAAG GGAGCCCCAT GGTTGACAAC   960
CCCATGAGAC GGAAGAGCGG GCCGTCCTGC AAGCACTGCA AGGACGACGT GAACAGACTC  1020
TGCCGGGTCT GCGCCTGCCA CCTGTGCGGG GGCCGGCAGG ACCCCGACAA GCAGCTCATG  1080
TGCGATGAGT GCGACATGGC CTTCCACATC TACTGCCTGG ACCCGCCCCT CAGCAGTGTT  1140
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CCCAGCGAGG ACGAGTGGTA CTGCCCTGAG TGCCGGAATG ATGCCAGCGA GGTGGTACTG  1200
GCGGGAGAGC GGCTGAGAGA GAGCAAGAAG AAGGCGAAGA TGGCCTCGGC CACATCGTCC  1260
TCACAGCGGG ACTGGGGCAA GGGCATGGCC TGTGTGGGCC GCACCAAGGA ATGTACCATC  1320
GTCCCGTCCA ACCACTACGG ACCCATCCCG GGGATCCCCG TGGGCACCAT GTGGCGGTTC  1380
CGAGTCCAGG TCAGCGAGTC GGGTGTCCAT CGGCCCCACG TGGCTGGCAT ACACGGCCGG  1440
AGCAACGACG GAGCGTACTC CCTAGTCCTG GCGGGGGGCT ATGAGGATGA CGTGGACCAT  1500
GGGAATTTTT TCACATACAC GGGTAGTGGT GGTCGAGATC TTTCCGGCAA CAAGAGGACC  1560
GCGGAACAGT CTTGTGATCA GAAACTCACC AACACCAACA GGGCCCTGGC TCTCAACTGC  1620
TTTGCTCCCA TCAATGACCA AGAAGGGGCC GAGGCCAAGG ACTGGCGGTC GGGGAAGCCG  1680
GTCAGGGTGG TGCGCAATGT CAAGGGTGGC AAGAATAGCA AGTACGCCCC CGCTGAGGGC  1740
AACCGCTACG ATGGCATCTA CAAGGTTGTG AAATACTGGC CCGAGAAGGG GAAGTCCGGG  1800
TTTCTCGTGT GGCGCTACCT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG  1860
GAGGGGAAGG ACCGGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG  1920
GAAGCCCTGG CCAACCGAGA GCGAGAGAAG GAGAACAGCA AGAGGGAGGA GGAGGAGCAG  1980
CAGGAGGGGG GCTTCGCGTC CCCCAGGACG GGCAAGGGCA AGTGGAAGCG GAAGTCGGCA  2040
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CGGCCCATCA CGACCGTGTG CCAGCACAAC GTGTGCAAGG ACTGCCTGGA CAGATCCTTT  2340
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CCTAAAAAGG TTTGTCTTCC TTTTTTTTTA TTTTTATTTT TCAAATCTAT ACATTTTCAG  2640
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CAACTCTTTA AGAAGGCGAC AGGATCAGTC CTTCTCTAGG GTTCTGGCCC CCAAGGTCAG  2880
AGCAAGCATC TTCCTGACAG CATTTTGTCA TCTAAAGTCC AGTGACATGG TTCCCCGTGG  2940
TGGCCCGTGG CAGCCCGTGC CATGGCGTGG CTCAGCTGTC TGTTGAAGTT GTTGCAAGGA  3000
AAAGAGGAAA CATCTCGGGC CTAGTTCAAA CCTTTGCCTC AAAGCCATCC CCCACCAGAC  3060
TGCTTAGCGT CTGAGATCCG CGTGAAAAGT CCTCTGCCCA CGAGAGCAGG GAGTTGGGGC  3120
CACGCAGAAA TGGCCTCAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGACTGACGC  3180
TGTCCGACGA AGGCGGCCAC GGACGGACGC CAGCACACGA AGTCACGTGC AAGTGCCTTT  3240
GATTCGTTCC TTCTTTCTAA AGACGACAGT CTTTGTTGTT AGCACTGAAT TATTGAAAAT  3300
GTCAACCAGA TTCTAGAAAC TGCGGTCATC CAGTTCTTCC TGACACCGGA TGGGTGCTTG  3360
GGAACCGTTT GAGCCTTATA GATCATTTAC ATTCAATTTT TTTAACTCAG CAAGTGAGAA  3420
CTTACAAGAG GGTTTTTTTT TAATTTTTTT TTCTCTTAAT GAACACATTT TCTAAATGAA  3480
TTTTTTTTGT AGTTACTGTA TATGTACCAA GAAAGATATA ACGTTAGGGT TTGGTTGTTT  3540
TTGTTTTTGT ATTTTTTTTC TTTTGAAAGG GTTTGTTAAT TTTTCTAATT TTACCAAAGT  3600
TTGCAGCCTA TACCTCAATA AAACAGGGAT ATTTTAAATC ACATACCTGC AGACAAACTG  3660
GAGCAATGTT ATTTTTAAAG GGTTTTTTTC ACCTCCTTAT TCTTAGATTA TTAATGTATT  3720
AGGGAAGAAT GAGACAATTT TGTGTAGGCT TTTTCTAAAG TCCAGTACTT TGTCCAGATT  3780
TTAGATTCTC AGAATAAATG TTTTTCACAG ATTGAAAAAA AAAAAAAA
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Seq ID NO: 156 Protein sequence
Protein Accession #: NP_037414.2

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1          11         21         31         41         51
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YEVRLNDTIQ LLVRQSLVLP HSTKERDSEL SDTDSGCCLG QSESDKSSTH GEAAAETDSR   120
PADEDMWDET ELGLYKVNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE   180
DVIYHVKYDD YPENGVVQMN SRDVRARART IIKWQDLEVG QVVMLNYNPD NPKERGFWYD   240
AEISRKRETR TARELYANVV LGDDSLNDCR IIFVDEVFKI ERPGEGSPMV DNPMRRKSGP   300
SCKHCKDDVN RLCRVCACHL CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSEDEWYC   360
PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWGKG MACVGRTKEC TIVPSNHYGP   420
IPGIPVGTMW RFRVQVSESG VHRPHVAGIH GRSNDGAYSL VLAGGYEDDV DHGNFFTYTG   480
SGGRDLSGNK RTAEQSCDQK LTNTNRALAL NCFAPINDQE GAEAKDWRSG KPVRVVRNVK   540
GGKNSKYAPA EGNRYDGIYK VVKYWPEKGK SGFLVWRYLL RRDDDEPGPW TKEGKDRIKK   600
LGLTMQYPEG YLEALANRER EKENSKREEE EQQEGGFASP RTGKGKWKRK SAGGGPSRAG   660
SPRRTSKKTK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE   720
TFQCICCQEL VFRPITTVCQ HNVCKDCLDR SFRAQVFSCP ACRYDLGRSY AMQVNQPLQT
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Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence: 186..776

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CTAACATGCG GCTGCCGCTG CTTGTGTCCG CGGGAGTCCT GCTGGTGGCT CTCCTGCCCT   240
GCCCGCCATG CAGGGCGCTC CTGAGCCGCG GGCCGGTCCC GGGAGCTCGG CAGGCGCCGC   300
AGCACCCTCA GCCCTTGGAT TTCTTCCAGC CGCCGCCGCA GTCCGAGCAG CCCCAGCAGC   360
CGCAGGCTCG GCCGGTCCTG CTCCGCATGG GAGAGGAGTA CTTCCTCCGC CTGGGGAACC   420
TCAACAAGAG CCCGGCCGCT CCCCTTTCGC CCGCCTCCTC GCTCCTCGCC GGAGGCAGCG   480
GCAGCCGCCC TTCGCCGGAA CAGGCGACCG CCAACTTTTT CCGCGTGTTG CTGCAGCAGC   540
TGCTGCTGCC TCGGCGCTCG CTCGACAGCC CCGCGGCTCT CGCGGAGCGC GGCGCTAGGA   600
ATGCCCTCGG CGGCCACCAG GAGGCACCGG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA   660
TCTCCCTGGA TCTCACCTTC CACCTCCTCC GGGAAGTCTT GGAAATGGCC AGGGCCGAGC   720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGCA GATTATTGGG AAATAAAACG   780
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GTGCGTTTGG CCAAAAAGAA TCTGCATTTA GCACAAAAAA AATTTAAAAA AATACAGTAT 840
TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA 900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAAGTGTA TTCACGTGCA 960
GCAGCAACAC AATGTTATTC GTTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020
TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAAACGTTT TGTTTGAAAA AGCAGACAGA 1080
AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTTGGGTGGG 1140
TAACACTAAA TCTGTAAGCT CTTTGAAACA ACTTTCTCTT GTAAACGTTT CAGTAATAAA 1200
ACATCTTTCC AGTCCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAAGT TGCAAAGGT

Seq ID NO: 158 Protein sequence
Protein Accession #: NP_000747.1

1 11 21 31 41 51
MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ 60
ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SSLLAGGSGS RPSPEQATAN FFRVLLQQLL 120
LPRRSLDSPA ALAERGARNA LGGHQEAPER ERRSEEPPIS LDLTFHLLRE VLEMARAEQL 180
AQQAHSNRKL MEIIGK

Seq ID NO: 159 DNA sequence
Nucleic Acid Accession #: NM_001200.1
Coding sequence: 325..1514

1 11 21 31 41 51
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TGCCCCAGCG GAGCCTGCTT CGCCATCTCC GAGCCCCACC GCCCCTCCAC TCCTCGGCCT 120
TGCCCGACAC TGAGACGCTG TTCCCAGCGT GAAAAGAGAG ACTGCGCGGC CGGCACCCGG 180
GAGAAGGAGG AGGCAAAGAA AAGGAACGGA CATTCGGTCC TTGCGCCAGG TCCTTTGACC 240
AGAGTTTTTC CATGTGGACG CTCTTTCAAT GGACGTGTCC CCCCGTGCTT CTTAGACGGA 300
CTGCGGTCTC CTAAAGGTCG ACCATGGTGG CCGGGACCCG CTGTCTTCTA GCGTTGCTGC 360
TTCCCCAGGT CCTCCTGGGC GGCGCGGCTG GCCTCGTTCC GGAGCTGGGC CGCAGGAAGT 420
TCGCGGCGGC GTCGTCGGGC CGCCCCTCAT CCCAGCCCTC TGACGAGGTC CTGAGCGAGT 480
TCGAGTTGCG GCTGCTCAGC ATGTTCGGCC TGAAACAGAG ACCCACCCCC AGCAGGGACG 540
CCGTGGTGCC CCCCTACATG CTAGACCTGT ATCGCAGGCA CTCAGGTCAG CCGGGCTCAC 600
CCGCCCCAGA CCACCGGTTG GAGAGGGCAG CCAGCCGAGC CAACACTGTG CGCAGCTTCC 660
ACCATGAAGA ATCTTTGGAA GAACTACCAG AAACGAGTGG GAAAACAACC CGGAGATTCT 720
TCTTTAATTT AAGTTCTATC CCCACGGAGG AGTTTATCAC CTCAGCAGAG CTTCAGGTTT 780
TCCGAGAACA GATGCAAGAT GCTTTAGGAA ACAATAGCAG TTTCCATCAC CGAATTAATA 840
TTTATGAAAT CATAAAACCT GCAACAGCCA ACTCGAAATT CCCCGTGACC AGACTTTTGG 900
ACACCAGGTT GGTGAATCAG AATGCAAGCA GGTGGGAAAG TTTTGATGTC ACCCCCGCTG 960
TGATGCGGTG GACTGCACAG GGACACGCCA ACCATGGATT CGTGGTGGAA GTGGCCCACT 1020
TGGAGGAGAA ACAAGGTGTC TCCAAGAGAC ATGTTAGGAT AAGCAGGTCT TTGCACCAAG 1080
ATGAACACAG CTGGTCACAG ATAAGGCCAT TGCTAGTAAC TTTTGGCCAT GATGGAAAAG 1140
GGCATCCTCT CCACAAAAGA GAAAAACGTC AAGCCAAACA CAAACAGCGG AAACGCCTTA 1200
AGTCCAGCTG TAAGAGACAC CCTTTGTACG TGGACTTCAG TGACCTGGGG TGGAATGACT 1260
GGATTGTGGC TCCCCCGGGG TATCACGCCT TTTACTGCCA CGGAGAATGC CCTTTTCCTC 1320
TGGCTGATCA TCTGAACTCC ACTAATCATG CCATTGTTCA GACGTTGGTC AACTCTGTTA 1380
ACTCTAAGAT TCCTAAGGCA TGCTGTGTCC CGACAGAACT CAGTGCTATC TCGATGCTGT 1440
ACCTTGACGA GAATGAAAAG GTTGTATTAA AGAACTATCA GGACATGGTT GTGGAGGGTT 1500
GTGGGTGTCG CTAGTACAGC AAAATTAAAT ACATAAATAT ATATATA

Seq ID NO: 160 Protein sequence
Protein Accession #: NP_001191.1

1 11 21 31 41 51
MVAGTRCLLA LLLPQVLLGG AAGLVPELGR RKFAAASSGR PSSQPSDEVL SEFELRLLSM 60
FGLKQRPTPS RDAVVPPYML DLYRRHSGQP GSPAPDHRLE RAASRANTVR SFHHEESLEE 120
LPETSGKTTR RFFFNLSSIP TEEFITSAEL QVFREQMQDA LGNNSSFHHR INIYEIIKPA 180
TANSKFPVTR LLDT

Seq ID NO: 161 DNA sequence
Nucleic Acid Accession #: NM_001999.2
Coding sequence: 1..8736

1 11 21 31 41 51
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CAGCCGCCCC CGCAACAGGT TCGGTCCGCT ACAGCAGGCT CTGAAGGCGG GTTTCTAGCG 180
CCCGAGTATC GCGAGGAGGG TGCCGCAGTG GCCAGCCGCG TCCGCCGGCG AGGACAGCAG 240
GACGTGCTCC GAGGGCCCAA CGTGTGCGGC TCCAGATTCC ACTCCTACTG CTGCCCTGGA 300
TGGAAGACGC TCCCTGGAGG AAACCAGTGC ATTGTCCCGA TTTGTAGAAA TAGTTGTGGA 360
GATGGATTTT GTTCCCGTCC TAACATGTGT ACTTGTTCCA GTGGGCAAAT ATCATCAACC 420
TGTGGATCAA AATCAATTCA GCAGTGCAGT GTGAGATGCA TGAATGGTGG GACCTGTGCA 480
GATGACCACT GCCAGTGCCA GAAAGGATAT ATTGGAACTT ATTGTGGACA ACCTGTCTGT 540
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TACCTCAGCG AGGATACCCG CATCTGTGAG GATATTGATG AGTGTTTTGC ACATCCTGGT  5100
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CGAAGCTATA ATGGAACCAC TTGTGAGAAT GAGTTGCCTT TCAATGTGAC AAAAAGGATG  5280
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CAGCGGAATG CAGACTGCAT CAATAGTCCT GGTAGTTACC GCTGTGAATG TGCCGCGGGT  5640
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GTTTGCAGTC ATGGCTTGTG TGTTGATCTG CAAGGAAGTT ACCAGTGCAT CTGCCACAAT  5760
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Seq ID NO: 162 Protein sequence
Protein Accession #: NP_001990.1

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ENGCQNGGRC IAQPCACVYG FTGPQCERDY RTGPCFTQVN NQMCQGQLTG IVCTKTLCCA   240
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Seq ID NO: 163 DNA sequence
Nucleic Acid Accession #: NM_013372.1
Coding sequence: 63..617

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Seq ID NO: 165 DNA sequence
Nucleic Acid Accession #: CAT cluster

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Seq ID NO: 166 DNA sequence
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Seq ID NO: 167 Protein sequence
Protein Accession #: FGENESH predicted

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MPPLPSRMSR GPSLVTGRML PITDRLLHLL GLEKTAFRIY AVSTLLLFLL FFLFRLLLRF    60
LRLCRSFYIT CRRLRCFPQP PRRNWLLGHL GMYLPNEAGL QDEKKVLDNM HHVLLVWMGP   120
VLPLLVLVHP DYIKPLLGAS AAIAPKDDLF YGFLKPWLGD GLLLSKGDKW SRHRRLLTPA   180
FHFDILKPYM KIFNQSADIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC   240
QEKMSDYISA IIELSALSVR RQVRLHHYLD FIYYRSADGR RFRQACDMVH HFTTEVIQER   300
RRALRQQGAE AWLKAKQGKT LDFIDVLLLA RDEDGKELSD EDIRAEADTF MFEGHDTTSS   360
GISWMLFNLA KYPEYQEKCR EEIQEVMKGR ELEELEWDDL TQLPFTTMCI KESLRQYPPV   420
TLVSRQCTED IKLPDGRIIP KGIICLVSIY GTHHNPTVWP DSKVYNPYRF DPDNPQQRSP   480
LAYVPFSAGP RNCIGQSFAM AELRVVVALT LLRFRLSVDR TRKVRRKPEL ILRTENGLWL   540
KVEPLPPRA
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Seq ID NO: 168 DNA sequence
Nucleic Acid Accession #: AK058088.1
Coding sequence: 252..1772

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1          11         21         31         41         51
|          |          |          |          |          |
AGGAAACCAA GGCAAGCTCC CCCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA    60
GCCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCCC AGCTCTCCTG   120
TAACTCAGAG GCCAGTGTGA TGGGAGTTCC TCCACTCAGC ACACTTCCCC TGTAAACACG   180
CCTGTGGTGG GCAAAAGGGC TTTGGAACGG TTGCTTGTCT TTTCTCTCCT GCGTAATTTC   240
CACTTTCATT CATGATAATG TCGAACACGC ACAAAGCTCG GCTGGAACGC CGGGTCACTG   300
GCTCAACCAA CCGGTGGCGT TTGCCCAAAC AGCCTTTCTC TGGGGACCTG CTCTCACTTT   360
CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT   420
TATGCATTTC ACAAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAG GACATCCAAA   480
GTGGGGAAGC AGATGTGATT CTCGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC   540
GGCTTTTTCA GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA   600
CACACCCCCT GAGGGAGCTG GAGGAGCTTC TGCCAGCTCA ATCACCTAAG AAGACCAAAG   660
AAAAATCCCC TGCAAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA   720
AAGTCGCCTT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACTTGG   780
AAGACCTACT GGGAGTGCTG GCTTCCGCCC ACATCCTCCA GTTCAGTGGC CTGTTTCAAA   840
GGTGCGTGGA TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG   900
CCGGCTGCAA GTACAAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAAATGA   960
ACTTGGTTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCCACAG GACCTGCTCC  1020
ACAAAGTGCT GAAGTCCCCC AGGTTATTTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA  1080
TGCTTTTGTG GGTCTTCTTG CAACTGAACT ACAAGATTCA GGCAATTCCG ACTTATGAAA  1140
CCGTGATGAC ATTTTTTAAG AGCTTTCCTG AGAACTGTTG CTTTCTGGAC CGGGACATAG  1200
GACGGAGCTT GAGGCCGCTC TTCCTCTGCT TGCGTCTGCA CGGCATCACC AAAGGCAAGG  1260
ATCTGGAGGT GCTGCGGCAC CTTAACTTCT TCCCAGAGTC ATGGCTCGAC CAGGTTACAG  1320
TCAACCATTA CCACGCACTG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA  1380
CCCAGGCTGT GAGATTTGGG CTGCTCTTTA ACCAGGAGAA TACAACTTAT TCGAAAACGA  1440
TTGCTCTATA TGGATTCTTC TTTAAGATAA AGGGACTCAA ACATGATACT ACCTCTTATA  1500
GTTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCCTCTGCG GTCTACGACC  1560
ACAACCACGT CAGCCTGCGA GCGGCACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCCC  1620
TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACCAGAT CAAGCAGAAG TTTGGGTTGA  1680
CCACGTCATC CTGCAAAAGC CATACCTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG  1740
TAAGTTTTGC ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT  1800
CCCCCCACTG GTCTGCATAA AACAAAATAA AATGACATAA AAGGGAGC
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Seq ID NO: 169 Protein sequence
Protein Accession #: BAB71658.1

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1          11         21         31         41         51
|          |          |          |          |          |
MIMSNTHKAR LERRVTGSTN RWRLPKQPFS GDLLSLSQMC KALSIDFEEA LRNPDRLCIS    60
QIQKFFFENF KNKDIQSGEA DVILECLGFK WELHQPRLFQ SETLAKLYLK ALAQGTTHPL   120
RELEELLRAQ SPKKTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL   180
GVLASAHILQ FSGLFQRCVD VMIARLKPST IKKFYEAGCK YKEEQLTTGC EKWLEMNLVP   240
LGGTQIHLHK IPQDLLHKVL KSPRLFTFSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT   300
FFKSFPENCC FLDRDIGRSL RPLFLCLRLH GITKGKDLEV LRHLNFFPES WLDQVTVNHY   360
HALENGGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFFKIKGLK HDTTSYSFYM   420
QRIKHTDLES PSAVYEHNHV SLRAARLVKY EIRAEALVDG KWQEFRTNQI KQKFGLTTSS   480
CKSHTLKIQT VGIPIYVSFA FIFPAS
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Seq ID NO: 170 DNA sequence
Nucleic Acid Accession #: NM_007000.1
Coding sequence: 1...777

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGCGTCTG CGGCAGCAGC GGAGGCCGAG AAGGGATCTC CAGTTGTGGT GGGCCTGCTA    60
GTTGTGGGCA ATATCATTAT TCTGCTGTCA GGCCTGTCCC TGTTTGCTGA GACCATATGG   120
GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATCACGTC   180
TTCGCTGGTG CCTGGATTGC CATCTTCTGC GGCTTCTCCT TCTTCATGGT AGCCAGTTTT   240
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GGTGTGGGTG CCGCACTCTG CCGCCGCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG   300
CTCATCGTCT ACATCTTCGA GTGCGCCTCC TGCATCACGT CCTACACCCA CCGTGACTAC   360
ATGGTGTCCA ACCCATCCCT GATCACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC   420
GACCAGGGCC AGGAGCTGAC CCGCCTCTGG GACCGCGTCA TGATTGAGCA ACAATGCTGT   480
GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCACGTCAG CCTTCCGGGC GGCCACTCCG   540
GAGGTGGTGT TCCCCTGGCC CCCACTGTGC TGTCGCCGGA CGGGAAACTT CATCCCCCTC   600
AACGAGGAGG GCTGCCGCCT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA   660
CACATCGGCC ACGCCATCGA CAGCTACACG TGGGGTATCT CGTGGTTTGG GTTTGCCATC   720
CTGATGTGGA CGCTCCCCGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGA
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Seq ID NO: 171 Protein sequence
Protein Accession #: NP_008931.1

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1          11         21         31         41         51
|          |          |          |          |          |
MASAAAAEAE KGSPVVVGLL VVGNIIILLS GLSLFAETIW VTADQYRVYP LMGVSGKDDV    60
FAGAWIAIFC GFSFFMVASF GVGAALCRRR SMVLTYLVLM LIVYIFECAS CITSYTHRDY   120
MVSNPSLITK QMLTFYSADT DQGQELTRLW DRVMIEQECC GTSGPMDWVN FTSAFRAATP   180
EVVFPWPPLC CRRTGNFIPL NEEGCRLGHM DYLFTKGCFE HIGHAIDSYT WGISWFGFAI   240
LMWTLPVMLI AMYFYTML
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Seq ID NO: 172 DNA sequence
Nucleic Acid Accession #: NM_006760.1
Coding sequence: 39..593

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1          11         21         31         41         51
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GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCCAGCAT GGCACCCCTG CTGCCCATCC    60
GGACCTTGCC CTTGATCCTG ATTCTGCTGG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA   120
ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCT   180
TGCCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGGAGA GCCAATGACA   240
GCAAAGTGGT GACGTCCAGC TTTGTGGTGC CTCCGTGCCG TGGGCGCAGG GAACTGGTGA   300
GTGTGGTGGA CAGTGGTGCT GGCTTCACAG TCACTCGGCT CAGTGCATAC CAGGTGACAA   360
ACCTCGTGCC AGGAACCAAA TTCTACATTT CCTACCTAGT GAAGAAGGGG ACAGCCACTG   420
AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCCATTGGGC   480
TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCACGGT GCTGCTCTCT GTCGCCATGT   540
TCCTGCTGGT GCTGGGCTTC ATCATTGCCC TGGCACTGGG CTCCCGCAAG TAAGGAGGTC   600
TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACCA TCCAGCTCCC CAGCCCACCT   660
GCTCCCAGGC CCCAGGCCTG TGGCTCCCTT GGTGCCCTCG CCTCCTCCTC CTGCCCTCCT   720
CTCCCCTAGA GCCCTCTCCT CCCTCTGTCC CTCTCCTTGC CCCCAGTGCC TCACCTTCCA   780
ACACTCCATT ATTCCTCTCA CCCCACTCCT GTCAGAGTTG ACTTTCCTCC CATTTTACCA   840
CTTTAAACAC CCCCATAACA ATTCCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG   900
GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA
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Seq ID NO: 173 Protein sequence
Protein Accession #: NP_006751.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAPLLPIRTL PLILILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGGNATL    60
MVRRANDSKV VTSSFVVPPC RGRRELVSVV DSGAGFTVTR LSAYQVTNLV PGTKFYISYL   120
VKKGTATESS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLL VLGFIIALAL   180
GSRK
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Seq ID NO: 174 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2733

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1          11         21         31         41         51
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TTCCTGGGGA AAAATGATGG CATCAAAACA AAAAAAGAAC TCATTGTGAA TAAGAAAAAA   120
CATCTAGGCC CAGTCGAAGA ATATCAGCTG CTGCTTCAGG TGACCTATAG AGATTCCAAG   180
GAGAAAAGAG ATTTGAGAAA TTTTCTGAAG CTCTTGAAGC CTCCATTATT ATGGTCACAT   240
GGGCTAATTA GAATTATCAG AGCAAAGGCT ACCACAGACT GCAACAGCCT GAATGGAGTC   300
CTGCAGTGTA CCTGTGAAGA CAGCTACACC TGGTTTCCTC CCTCATGCCT TGATCCCCAG   360
AACTGCTACC TTCACACGGC TGGAGCACTC CCAAGCTGTG AATGTCATCT CAACAACCTC   420
AGCCAGAGTG TCAATTTCTG TGAGAGAACA AAGATTTGGG GCACTTTCAA AATTAATGAA   480
AGGTTTACAA ATGACCTTTT GAATTCATCT TCTGCTATAT ACTCCAAATA TGCAAATGGA   540
ATTGAAATTC AACTTAAAAA AGCATATGAA AGAATTCAAG GTTTTGAGTC GGTTCAGGTC   600
ACCCAATTTC GAAATGGAAG CATCGTTGCT GGGTATGAAG TTGTTGGCTC CAGCAGTGCA   660
TCTGAACTGC TGTCAGCCAT TGAACATGTT GCCGAGAAGG CTAAGACAGC CCTTCACAAG   720
CTGTTTCCAT TAGAAGACGG CTCTTTCAGA GTGTTCGGAA AAGCCCAGTG TAATGACATT   780
GTCTTTGGAT TTGGGTCCAA GGATGATGAA TATACCCTGC CCTGCAGCAG TGGCTACAGG   840
GGAAACATCA CAGCCAAGTG TGAGTCCTCT GGGTGGCAGG TCATCAGGGA GACTTGTGTG   900
CTCTCTCTGC TTGAAGAACT GAACAAGAAT TTCAGTATGA TTGTAGGCAA TGCCACTGAG   960
GCAGCTGTGT CATCCTTCGT GCAAAATCTT TCTGTCATCA TTCGGCAAAA CCCATCAACC  1020
ACAGTGGGGA ATCTGGCTTC GGTGGTGTCG ATTCTGAGCA ATATTTCATC TCTGTCACTG  1080
GCCAGCCATT TCAGGGTGTC CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAT  1140
ATCCTTAATT CAGCCTCAGT AACCAACTGG ACAGTCTTAC TGCGGGAAGA AAAGTATGCC  1200
AGCTCACGGT TACTAGAGAC ATTAGAAAAC ATCAGCACTC TGGTGCCTCC GACAGCTCTT  1260
CCTCTGAATT TTTCTCGGAA ATTCATTGAC TGGAAAGGGA TTCCAGTGAA CAAAAGCCAA  1320
CTCAAAAGGG GTTACAGCTA TCAGATTAAA ATGTGTCCCC AAAATACATC TATTCCCATC  1380
AGAGGCCGTG TGTTAATTGG GTCAGACCAA TTCCAGAGAT CCCTTCCAGA AACTATTATC  1440
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AGCATGGCCT CGTTGACTCT GGGGAACATT CTACCCGTTT CCAAAAATGG AAATGCTCAG  1500
GTCAATGGAC CTGTGATATC CACGGTTATT CAAAACTATT CCATAAATGA AGTTTCCTA   1560
TTTTTTTCCA AGATAGAGTC AAACCTGAGC CAGCCTCATT GTGTGTTTTG GGATTTCAGT  1620
CATTTGCAGT GGAACGATGC AGGCTGCCAC CTAGTGAATG AAACTCAAGA CATCGTGACG  1680
TGCCAATGTA CTCACTTGAC CTCCTTCTCC ATATTGATGT CACCTTTTGT CCCCTCTACA  1740
ATCTTCCCCG TTGTAAAATG GATCACCTAT GTGGGACTGG GTATCTCCAT TGGAAGTCTC  1800
ATTTTATGCC TGATCATCGA GGCTTTGTTT TGGAAGCAGA TTAAAAAAAG CCAAACCTCT  1860
CACACACGTC GTATTTGCAT GGTGAACATA GCCCTGTCCC TCTTGATTGC TGATGTCTGG  1920
TTTATTGTTG GTGCCACAGT GGACACCACG GTGAACCCTT CTGGAGTCTG CACAGCTGCT  1980
GTGTTCTTTA CACACTTCTT CTACCTCTCT TTGTTCTTCT GGATGCTCAT GCTTGGCATC  2040
CTGCTGGCTT ACCGGATCAT CCTCGTGTTC CATCACATGG CCCAGCATTT GATGATGGCT  2100
GTTGGATTTT GCCTGGGTTA TCGGTGCCCT CTCATTATAT CTGTCATTAC CATTGCTGTC  2160
ACGCAACCTA GCAATACCTA CAAAAGGAAA GATGTGTGTT GGCTTAACTG GTCCAATGGA  2220
AGCAAACCAC TCCTGGCTTT TGTTGTCCCT GCACTGGCTA TTGTGGCTGT GAACTTCGTT  2280
GTGGTGCTGC TAGTTCTCAC AAAGCTCTGG AGGCCGACTG TTGGGGAAAG ACTGAGTCGG  2340
GATGACAAGG CCACCATCAT CCGCGTGGGG AAGAGCCTCC TCATTCTGAC CCCTCTGCTA  2400
GGGCTCACCT GGGGCTTTGG AATAGGAACA ATAGTGGACA GCCAGAATCT GGCTTGGCAT  2460
GTTATTTTTG CTTTACTCAA TGCATTCCAG GGATTTTTTA TCTTATGCTT TGGAATACTC  2520
TTGGACAGTA AGCTGCGACA ACTTCTGTTC AACAAGTTGT CTGCCTTAAG TTCTTGGAAG  2580
CAAACAGAAA AGCAAAACTC ATCAGATTTA TCTGCCAAAC CCAAATTCTC AAAGCCTTTC  2640
AACCCACTGC AAAACAAAGG CCATTATGCA TTTTCTCATA CTGGAGATTC CTCCGACAAC  2700
ATCATGCTAA CTCAGTTTGT CTCAAATGAA TAA
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Seq ID NO: 175 Protein sequence
Protein Accession #: Eos sequence

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1           11          21          31          41          51
|           |           |           |           |           |
MKVGVLWLIS PFTFTDGHGG PLGKNDGIKT KKELIVNKKK HLGPVEEYQL LLQVTYRDSK    60
EKRDLRNFLK LLKPPLLWSH GLIRIIRAKA TTDCNSLNGV LQCTCEDSYT WFPPSCLDPQ   120
NCYLHTAGAL PSCECHLNNL SQSVNFCERT KIWGTFKINE RFTNDLLNSS SAIYSKYANG   180
IEIQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK   240
LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV   300
LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNISSLSL   360
ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLETLEN ISTLVPPTAL   420
PLNFSRKFID WKGIPVNKSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRSLPETII   480
SMASLTLGNI LPVSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDFS   540
HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPST IFPVVKWITY VGLGISIGSL   600
ILCLIIEALF WKQIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPSGVCTAA   660
VFFTHFFYLS LFFWMLMLGI LLAYRIILVF HHMAQHLMMA VGFCLGYGCP LIISVITIAV   720
TQPSNTYKRK DVCWLNWSNG SKPLLAFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR   780
DDKATIIRVG KSLLILTPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL   840
LDSKLRQLLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGHYA FSHTGDSSDN   900
IMLTQFVSNE
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Seq ID NO: 176 DNA sequence
Nucleic Acid Accession #: AB035089.1
Coding sequence: 9845..10219

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1           11          21          31          41          51
|           |           |           |           |           |
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CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAAGAAGG   120
CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTTGGT   180
TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTTGG CAGAGTAGGA   240
AGGAGGAAGG GAGGCAAGAG ATAATATCAT TTTCTCTGTG CTCCAACTGT ACTTACATAT   300
GAGACTATTT CCCTCTCTGC TTTTCAAACC TTACTGGAGT TGTTTTCCCT CATGAAAACC   360
AAGAAAGGAA AGCTAGTTAG TCTTGTTCTG AGGTTGTTCA ATGTATACAT ATCTATATCT   420
GTAGACAGAA TCCTTGGGAA TACAGTAATT GACATATATT CTGTTATTTG ATGCTTGAAA   480
AATCTCCTCC ACTAACCAGT TTCCCTATAG ATTGCCACAA GCACATAATA AGAAACAATA   540
AATAAAATGT TCTCTTGACT TTGTTACTTA ACAATGCTGA GAAAACTTTA CAGCCTTCAT   600
AAGGAAGTGA GGTCCAGGAA AATCTAGGAG ATATTTCTTA ACCAATCTAT AAAGGCATTA   660
GTAATGACAG GATATTTCCT GAAAGTGTAA TTTCCCATTG AGGATTTGTT TTTAATTTCT   720
GGATTCCTGG AGCCAATGAA GTTGGTGTAT GTTTATGAAA TATCAAGAGA CATAAGTTGG   780
CAAGTGTTCA TATGCAAAAA CTTCTTGGAA TTTCTGAGTT CTCTGTGGCA ATATATGACA   840
TCAGGATATG TCCAGTCTCA CACACCAGGA TATGTCCTTT CTAGCCTGTC TATCACATGC   900
TAGGAGAACT ATTTAGGAAC AGAAAAAAAT GCCTGAAATG ATTTCTCATT TGAACTCATC   960
CAAGCTTTCT CTAAATTTAA GCAAACTCCT GGTCATTTTC AGTTAGTACC TTTCCTTAAG  1020
TTCAACCTTC AGGGCAAACC TCCGTGCCTC AGACGTTTAG CCATAGTCTG AAATTCTCTT  1080
CCATAGATTG GTCCCCTGTA ACCCCGGTTT GTCTCAGCTT GTTATCCTGT TTTTTCTTC   1140
CCTCCATTCC CAGGATGAGC TTGTTGCTTC TGTCCTATGA GACATTAGAT TCCTTTTCTT  1200
TGGTACCCGA GTAAATCCAT CCTACTCCAA TAGAGGAAGG TCCATTTTTG TCTTATAGCG  1260
CTGGATGCAG ACTCAGCTGA GAAGACCATT ATTCATTTTT GGAATTCTTT ATCTCAGATA  1320
TTTCCTCTTC TTTCTTTTTC TTCTATCTTT GGATTTTTAG TCCATCAACG CCCCATTAGT  1380
CTATTCCCCG ACTTCAATCA GGGAACTTAT ACCTCTTAAA CTCATTCAGA GACTCAAAAC  1440
ATATATATTG ATACAGGAGA CCTAAGAAGA GCATGTCTTG GGGGTTGAGG AAACAGGCAG  1500
GTGAGAAATT TCCAGATTGG AAACACAGCT TCCTTTCTCC CATCCAGCCC CTACTTTCAG  1560
CCTATGTGTT TCTGGCACCT TGTTGTAGAT AAATCTCCCT TGACTTTGTG ATGTGCTGAG  1620
AAAACAAACT CACGGCTGGT GTTAAAAAGG GCCCATGACA ATACCAAGTG TTGGGGAGAA  1680
TGTGGAGAAA TCAGAACTCT ATTCACGGTC GGTTGGAATG CACACTTGTG CAGAATTCTA  1740
TGGAGAAGAG TCTGGCATTT CCTCAAAATG TTAACCTGGA TTTACCATAT GACCCAGCGA  1800
TTTCATTCAT AGGTTTATAC TCAAAAGAAA TGAAGAAATA TGCCATGCAA AAAAATGTAC  1860
ATGAAAGGTC ACAACATCAT TATTCATAAT AGTAAAAGGA TGGAAACAAC ACAAATGTCC  1920
ATCAACTTAT GATTAAAGAA AATCTGGTCT ATTCATAGAA TGGAATATTA TTCGACCACA  1980
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AAAAGGAATG ATGTACTGAT CCATGCAATG ATGTGGACAA ACCATGAAAA TAACACTAGA 2040
TTAAAGAAGC CAGTCACAAA AGGACTTACT GTATGATTCC ATTTACCTGA AATGTTTGGA 2100
ATAGGCAAAT CCATAGAAAC AGGAGGTAGA TTCCTGGTTT CCAGGGTCTC CAGGAAGGGA 2160
AGAATGAAGT ACAAGATTTC TTTTGGAGGT AGTGAAATTG TTGTGGAATG AGATCATGAT 2220
GATGATAGCA CAACTTTGTG AATATAATAA AATCATTGAA TTGTACAGTT GAATTTATGG 2280
TATATAAATT ATATGTTAAT AAAAAGGGGG TCCACAAAAC AAACAGCCCC CCACTCTGGT 2340
TGTCAGGGAG ATATTGGATT AAATGGCCTT GGACAACAAC CCCTCTCCCT GGCCACAGAC 2400
ATTCTTCAGA TTACAAGATA TTCCAGGGGA AACACTGGAA TGAGTCTGAA GCCAGGTGCT 2460
AAACAGAAGG ACCATTGAGA AATGTTGTGA TCCTGACAGG TCAAGCAATT TATTTTTCGG 2520
CTTCATTTTT AAATGTAAAA TTAGAAAGCT GCCATTTAAA ATGGCCCGTC TGTTTCAATT 2580
GCTCTTCTCA GTGTCAGCCT GTTAACTCAA TGTGTTAGTC TGTTTTCATG CTGCTGATAA 2640
AAACATACCT GAGACTGGCA AGAAAAAGAG GTTTAATTGG GCTTAGAGTT CCACGTGATT 2700
GGGGAGGCCT CAGAATCACA GTAGGAGGCA AAAGTTATTC TTACATGGTG GCTGCAAGAG 2760
AAGATGAGGA AGAAGCAAAA GAAGAAACCC CTGATAAACC CATCGGATCT CCTGAGGCTT 2820
ATTAACTATC ATGAGAATAG CACAAGAAAG ACCGGCCCCC ATGATTCAAT TACCTCTACC 2880
TGGGTCCCTC CAATAACATG TGGAAATTCT GGTAGATACA ATTCAAGTTG AGATTTGGGT 2940
GGGAACACAG CCAAACCATA TCACTCAGCA AGGCAGATAA CTTTCTCACT GAGCCTATGC 3000
AACAGAAAAC CATCTGGGAT GGTTGTAAGG GGCACAGGAA GTGACTGGTA GGATCACTGC 3060
CAAAGCTGAG CACTCAGGAG AAGGCAATAG AATCCTATTC TCCATAGTAT GCTATAAGAT 3120
ACTGAAGTAC ACTTCTTCAC TATCTCTTTG GACTTAGAAT TAGCACTACA TTCCTTGTTA 3180
TACAGAAAAA TTACTAAGGA AATTCATAGG ATGACAAAAA CTTTCAGAAC TGAAAAACAG 3240
GAAATGTAAG CTTTTTAGTT CTTTGGTATT CGAAGTATGC CTAAAAGACA ATGCAAAATC 3300
CAAGAAAAGA ATGGTGGGGT TTTTGTTTGT TTGGTTTTGT TTTTGTTTTA CAGCTGGAGT 3360
AGAATACAAA GGGATGGAGT TGAAACAAAT GAGAGGAAAT TGGAATTCTA AACTTATTCT 3420
CATTGGCATT AGAAAGGCAC CTACATGTAT TTCACATGAG CCGGTGACTG CTGACTTGCA 3480
TTCTTATTTT TTCCCTATAG ATTAAAAAGG AGGTACAATG GTAGAACTGT AATCCTGTCC 3540
TTTGTCATAA ATTTTCATAT TCATAAAGGT GAGTGTTAGC CCGCTTGTGA AATCTGAAGT 3600
TGAGTAACTT CAAATACTAA CCACAGAGGG AAAGGCAGCA AGAGGAGAGG CATAAATTTA 3660
GGATCTCACC CTTCATTCCA CAGACACACA CAGCCTCTCT GCCCACCTCT GCTTCCTCTA 3720
GGAACACAGG TAAGAGCTTC AAGCCTCTCC AGCTTAATAA CATGAATTAT TTTTGAGAAT 3780
AATAATGATA CTGTGTTCTA TATCATGCAT CTCCTGCATT CTGTCTGATT ATATTTTACT 3840
TATTCTGCCA GAGCAAAATT AAAATACCTA TTTCATCTGA TTTGTCCTTT ATCTAAATTG 3900
CTTAGTTCCA AGTAAACCAA GGCACTTTTA GGAACACAGA GGGAGAGTGC CTTGCAGCCA 3960
GAGAGTCTTG AAGGAGATGT CAGGGACGCA TCTTAACAGC TGGTTGGATG TGATCCACAG 4020
AGGTCTCCTG TTAGCATTCA TTGTAAAGCC ATCCTACCTA GCTCTAGTGT AACCAGCAAT 4080
GAAAGAAAGA TAAAGAGGGT CGATTACTTA TTTACAATAG TCTTTAAAAA CGTAGTTTTG 4140
TAAGCCTTCT AATTAGGACA TTAATATATT TAATATATGC ACATTGTAGA AAGATTGAAG 4200
CGTTAAAAAT AAGAGAAAAA CTTTAAATGT CAAAATCTCA CAACCCAGAT ATATCATTTC 4260
TTTAAGAAAA TTGTACTACA AAATACCATT CCATTTATTA AAGTCATTCT GACAGGAATC 4320
TGATGCTTTT CCAGGAGTTC CAGATCACAT CGAGTTCACC ATGAATTCAC TCAGTGAAGC 4380
CAACACCAAG TTCATGTTCG ATCTGTTCCA ACAGTTCAGA AAATCAAAAG AGAACAACAT 4440
CTTCTATTCC CCTATCAGCA TCACATCAGC ATTAGGGATG GTCCTCTTAG GAGCCAAAGA 4500
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Seq ID NO: 177 Protein sequence
Protein Accession #: BAB21525.1

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LSMIVLLPNE IDGLQKLEEK LTAEKLMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR   300
TMGMVNIFNG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAVV VVELSSPSTN   360
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Seq ID NO: 179 Protein sequence
Protein Accession #: NP_001901.1

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FDGILGLGYP SLAVGGVTPV FDNMMAQNLV DLPMFSVYMS SNPEGGAGSE LIFGGYDHSH   240
FSGSLNWVPV TKQAYWQIAL DNIQVGGTVM FCSEGCQAIV DTGTSLITGP SDKIKQLQNA   300
IGAAPVDGEY AVECANLNVM PDVTFTINGV PYTLSPTAYT LLDFVDGMQF CSSGFQGLDI   360
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Coding sequence: 319..1575

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Seq ID NO: 181 Protein sequence
Protein Accession #: NP_060528.1

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Seq ID NO: 182 DNA sequence
Nucleic Acid Accession #: AJ279016
Coding sequence: 1..1962

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GCTCAGCCGC TGTCCGTCTT CCGGGGCAAT CAGGGCTTCA ACAACAACTG GCTGCGAGTG  1320
GTGCCACGCA CCCGGTTTGG GGCCTTTGCC AGGGGAGCTA AGGTCGTGCT CTACACCAAG  1380
AAGAGTGGGG CCCACCTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG  1440
CCCGTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA  1500
GATGGCAAGA TGGTGAGCCG GAACGTGGCC AGCGGGGAGA TGAACTCAGT GCTGGAGATC  1560
CTCTACCCCC GGGATGAGGA CACACTTCAG GACCCAGCCC CACTGGAGTG TGGCCAAGGA  1620
TTCTCCCAGC AGGAAAATGG CCATTGCATG GACACCAATG AATGCATCCA GTTCCCATTC  1680
GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGCTACAG GTGCCGGACC  1740
AACAAGAAGT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCCTG CGTGGGGACT  1800
CTCGGCCAGT CACCGGGCCC CCGCCCCACC ACCCCCACCG CTGCTGCTGC CACTGCCGCT  1860
GCTGCTGCCG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT  1920
CTGGGGTCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA  1980
CCAGCGGATG GAGTCCAGCA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CCTAGACAGT  2040
AGGGATGTAA AGGCCTGGGA GCTAGACCCT CCCCAAGCCC ATCCATGCAC ATTACTTAGC  2100
TAACAATTAG GGAGACTCGT AAGGCCAGGC CCTGTGCTGG GCACATAGCT GTGATCACAG  2160
CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCCAGTG GGTCTAATGA CCATATCTTA  2220
GGACACAGAT GTGCCCAGGG AGGTGGTGTC ACTGCACAGG AAGTATGAGG ACTTTAGTGT  2280
CCTGAGTTCA AATCCTGATT CAGGAACTCA CAAAGCTATG TGACCTTACA CCAGTCACTT  2340
AACTTGTTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAATAG AATCTTGGGG  2400
TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT  2460
AAAGGCTCAA TAAAAACAAG TGCCTCTCAC TGGGCTTTGT CAACACG
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Seq ID NO: 183 Protein sequence
Protein Accession #: CAC08451

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EIYFLNTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS   180
GRYSIYIANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI   240
LSSSASDIFC DNENGPNFLF HNRGDGTFVD AAASAGVDDP HQHGRGVALA DFNRDGKVDI   300
VYGNWNGPHR LYLQMSTHGK VRFRDIASPK FSMPSPVRTV ITADFDNDQE LEIFFNNIAY   360
RSSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTDFDGDGML DLILSHGESM   420
AQPLSVFRGN QGFNNNWLRV VPRTRFGAFA RGAKVVLYTK KSGAHLRIID GGSGYLCEME   480
PVAHFGLGKD EASSVEVTWP DGKMVSRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG   540
FSQQENGHCM DTNECIQFPF VCPRDKPVCV NTYGSYRCRT NKKCSRGYEP NEDGTACVGT   600
LGQSPGPRPT TPTAAAATAA AAAAAGAATA APVLVDGDLN LGSVVKESCE PSC
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Seq ID NO: 184 DNA sequence
Nucleic Acid Accession #: FGENESHH
Coding sequence: 1..4794

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TCACCCTACT ACGCGCTGCG GGACCGGCAG GGGAACGCCA TCGGGGTCAC AGCCTGCGAC   240
ATCGACGGGG ACGGCCGGGA GGAGATCTAC TTCCTCAACA CCAATAATGC CTTCTCGGGC   300
CACAGCAGCT CAGCGCAGGT CCCTTCTGGG CTCCACAGAA ACAGGCCTGT GCTGAAGCCT   360
CCACCTACAA CCCCTGCAGG CCTCCTGGGT CTGCCTCCAC TCAGCGGAAG GGACTTTTCC   420
TCCTCCCTGG GTCAGGCTTC TCCGGACAGC AGGCAGGGAG AGAGGGTGCC GGTTCCCTGC   480
TGTCGGGGTG GACTGAGACC TACCCATGAA CCAGAACCAT TTCTTCTGAG ACCCAAATCA   540
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CTGAGCGATG AGGTCAACGT GGCCCGTGGT GTGGCCAGCC TCTTTGCCGG ACGCTCTGTG   660
GCCTGTGTGG ACAGAAAGGG CTCTGGACGC TACTCTATCT ACATTGCCAA TTACGCCTAC   720
GGTAATGTGG GCCCTGATGC CCTCATTGAA ATGGACCCTG AGGCCAGTGA CCTCTCCCGG   780
GGCATTCTGG CGCTCAGAGA TGTGGCTGCT GAGGCTGGGG TCAGCAAATA TACAGAAGGC   840
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GGAGGAGACC CAGAGGAGGC AGATGAGGAG CACAGTGGGG ATGGAAGCAC CAGCCAACTG   960
TGCCGGCTGG GCTGGAAGGA CGGGCAGTTC AAGGAAGAAG CAGCAGCTTT GGTGGAGGAA  1020
CAGAGGGAGG CTGGGGCAGC TGGCGTGCCC AGAGGACGTG TTCGAACAGC TCTGCAGACT  1080
TCCAAAAGCC ATTTGGCTGA CAAGAACCTA TTTGGCCCAC CATCTTACTA TTCTGTCTGC  1140
GCGCCTTCTC CAGCCCACCC TTTCCCTGCC CGCCAAGCCC CCCAACACTA CCCTGTAGCC  1200
CCCCTTGTCA CTCAGCTAAT GACACATGGA CGTCTGGCTG GAAAACTAGC CCGGAGTGTC  1260
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CTGAGAAGCT GGGAGGAAAG CAGGCAGAAG GGGCAGGCCA TGTCCAGATG TGCACTCAGG  1440
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CTGGCGTGGA ACCAGATGGA AAAGAGGAG GGGAAGATTC ATGGAGACCA TGAGCCCAGA  1860
TTTAGGCTCA GGAAAGCACG GGAAGCAGAA TTCCCCCCAG GCTCCTCTGA GGAGCCTCTG  1920
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TCTGCCACTC ACTGTGGGTC GATGTCTTTT CTAGGGGGCC GAGGCGTCAG CGTGGGCCCC  2040
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GCCTTCATCG TTCACCTCAA ATATCACCTC TGCAGAGATT TTCCTCACTC CCTGTGCCAC  2220
CTAGCAGAAA CTGGTCCTTC CTCCTCCTGC TGCCCGTGGC ATGCACGTCT TCTTCAGGCT  2280
CCACATTGCC ATCATGGTTT GTCTATGAGC TTTACAAGGA CCGGGTCACG GTTCTATTCA  2340
TTCTTGACGC AAGGCTTGGC CTCCAGTGCC CACCGGAGGA CACTCAGCCT CCAGGGTTCT  2400
CAGGGGGCCC CACCCTGCCT TCTGGCAAGA GCTCCCTGTG TCCTGGGGTC TCTGATCCCC  2460
ACTGCCTATT ACATTGTCCT GTGGTCTGCC ATCCCAGAGA GCCTGATGAC CCACAGCTAT  2520
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GCCCTGGCTG ACTTCAACCG TGATGGCAAA GTGGACATCG TCTATGGCAA CTGGAATGGC  2640
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TCACCCAAGT TCTCCATGCC CTCCCCTGTC CGCACGGTCA TCACCGCCGA CTTTGACAAT  2760
GACCAGGAGC TGGAGATCTT CTTCAACAAC ATTGCCTACC GCAGCTCCTC AGCCAACCGC  2820
CTCTTCCGAT GCTCCATCCT GGCTCGTGGC TCTTCATCCT TGACAGCTGG TGGGAGGAAC  2880
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CCACACTACC ACAAAAAGGG GCTACAGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG  3180
GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC ACTACCAGGA AAAGGGGCTA  3240
CGGGGTCCAA TCACTACCAG GAAAAGGGGC TACGGGGTCC AATCACTACC AGGAAAAGGG  3300
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CCAGGAAAAG GGGCTACAGG GTCCAATCAC TACCAGGAAA AGGGGCTACG GGGTCCAATC  3540
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WO03042661 [file:///E:/WO03042661.epc]


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GCTATGGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG CTCCAATCAC TACCAGGAAA  3840
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AACAACAACT GGCTGCGAGT GGTGCCACGC ACCCGGTTTG GGGCCTTTGC CAGGGGAGCT  4140
AAGGTCGTGC TCTACACCAA GAAGAGTGGG GCCCACCTGA GGATCATCGA CGGGGGCTCA  4200
GGCTACCTGT GTGAGATGGA GCCCGTGGCA CACTTTGGCC TGGGGAAGGA TGAAGCCAGC  4260
AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAACGTGGC CAGCGGGGAG  4320
ATGAACTCAG TGCTGGAGAT CCTCTACCCC CGGGATGAGG ACACACTTCA GGACCCAGCC  4380
CCACTGGAGT GTGGCCAAGG ATTCTCCCAG CAGGAAAATG GCCATTGCAT GGACACCAAT  4440
GAATGCATCC AGTTCCCATT CGTGTGCCCT CGAGACAAGC CCGTATGTGT CAACACCTAT  4500
GGAAGCTACA GGTGCCGGAC CAACAAGAAG TGCAGTCGGG GCTACGAGCC CAACGAGGAT  4560
GGCACAGCCT GCGTGGGTAC TGAGCTAGGC TCTAGGCATA CAATGACGTG GAAACCAAGG  4620
CCCAAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCACCC CCGTCTGGTC CTTTTTCCTG  4680
CCGGGTTGCC GGCTGCTCCT CAAAAGAGCT CAGCTCCAGG CTGCTCCCAG CACCCTTCTC  4740
CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA
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Seq ID NO: 185 Protein sequence
Protein Accession #: FGENESHH

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SPYYALRDRQ GNAIGVTACD IDGDGREEIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP   120
PPTTPAGLLG LPPLSGRDFS SSLGQASPDS RQGERVPVPC CRGGLRPTHE PEPFLLRPKS   180
GVATYTDKLF KFRNNRWEDI LSDEVNVARG VASLFAGRSV ACVDRKGSGR YSIYIANYAY   240
GNVGPDALIE MDPEASDLSR GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE   300
GGDPEEADEE HSGDGSTSQL CRLGWKDGQF KEEAAALVEE QREAGAAGVP RGRVRTALQT   360
SKSHLADKNL FGPPCYYSVC APSPAHPFPA RQAPQHYPVA PLVTQLMTHG RLAGKLARSV   420
PHPRAPGMDP KCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCALR   480
ELGGPWSQAT QHLPARELYD LGEPPILQRT DGDPGRRRDS PKVTQECHLV ATMPALGGLE   540
GPGRVAKREI GRETGAVGRP LSHPLVPNFP SCLRPLEAGT VPGAALPGNP GNWVLDMAKA   600
LAWNQMEKEE GKIHGDHEPR FRLRKAREAE FPPGSSEEPL LQFPSGLRGS PVLQVGLGLA   660
SATHCGSMSF LGGRGVSVGP ILSSSASDIF CDNENGPNFL PHNRGDGTFV DAAASAERRL   720
AFIVHLKYHL CRDFPHSLCH LAETGPSSSC CPWHARLLQA PHCHHGLSMS FTRTGSRFYS   780
FLTQGLASSA HRRTLSLQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY   840
LSSERVNVGV DDPHQHGRGV ALADFNRDGK VDIVYGNWNG PHRLYLQMST HGKVRFRDIA   900
SPKFSMPSPV RTVITADFDN DQELEIFFNN IAYRSSSANR LFRCSILARG SSSLTAGGRN   960
GQGEGLRIRR GGFPGPGGQA KVNTGPLMKK QKGRKDEDWA RGCGNAGQSL AKEPASAIAG  1020
KGKGNVAQSV PRTQAPQDTK PHYHKKGLQG PITTRKRGYG VQSLPGKGAT GSNHYQEKGL  1080
RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPITTRK RGYGLQSLPG KGATGSNHYH  1140
RKGLRAPITT RKRGYGVQSL PGKGATGSNH YQEKGLRGPI TTRKRGYGLQ SLPGKGATGS  1200
NHYQEKGLQG PITTRKRGYR VQSLPQKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE  1260
AMGSNHYQEK GLRAPITTRK RGYGVQSLPQ KGATGSNVIR REHGDPLIEE LNPGDALEPE  1320
GRGTGGVVTD FDGDGMLDLI LSHGESMAQP LSVFRGNQGF NNNWLRVVPR TRFGAFARGA  1380
KVVLYTKKSG AHLRIIDGGS GYLCEMEPVA HFGLGKDEAS SVEVTWPDGK MVSRNVASGE  1440
MNSVLEILYP RDEDTLQDPA PLECGQGFSQ QENGHCMDTN ECIQFPFVCP RDKPVCVNTY  1500
GSYRCRTNKK CSRGYEPNED GTACVGTELG SRHTMTWKPR PKKELQLSQG ICTPVWSFFL  1560
PGCRLLLKRA QLQAAPSTLL QKAPGIPEAQ VYEQDQE
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Seq ID NO: 186 DNA sequence
Nucleic Acid Accession #: NM_000584.1
Coding sequence: 75..374

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CACTGTGTGT AAACATGACT TCCAAGCTGG CCGTGGCTCT CTTGGCAGCC TTCCTGATTT   120
CTGCAGCTCT GTGTGAAGGT GCAGTTTTGC CAAGGAGTGC TAAAGAACTT AGATGTCAGT   180
GCATAAAGAC ATACTCCAAA CCTTTCCACC CCAAATTTAT CAAAGAACTG AGAGTGATTG   240
AGAGTGGACC ACACTGCGCC AACACAGAAA TTATTGTAAA GCTTTCTGAT GGAAGAGAGC   300
TCTGTCTGGA CCCCAAGGAA AACTGGGTGC AGAGGGTTGT GGAGAAGTTT TTGAAGAGGG   360
CTGAGAATTC ATAAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT   420
GAAACTTCAA GCAAATCTAC TTCAACACTT CATGTATTGT GTGGGTCTGT TGTAGGGTTG   480
CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTTCA GTAAACAATG AATAGTTTTT   540
CATTGTACCA TGAAATATCC AGAACATACT TATATGTAAA GTATTATTTA TTTGAATCTA   600
CAAAAAACAA CAAATAATTT TTAAATATAA GGATTTTCCT AGATATTGCA CGGGAGAATA   660
TACAAATAGC AAAATTGAGC CAAGGGCCAA GAGAATATCC GAACTTTAAT TTCAGGAATT   720
GAATGGGTTT GCTAGAATGT GATATTTGAA GCATCACATA AAAATGATGG GACAATAAAT   780
TTTGCCATAA AGTCAAATTT AGCTGGAAAT CCTGGATTTT TTTCTGTTAA ATCTGGCAAC   840
CCTAGTCTGC TAGCCAGGAT CCACAAGTCC TTGTTCCACT GTGCCTTGGT TTCTCCTTTA   900
TTTCTAAGTG GAAAAAGTAT TAGCCACCAT CTTACCTCAC AGTGATGTTG TGAGGACATG   960
TGGAAGCACT TTAAGTTTTT TCATCATAAC ATAAATTATT TTCAAGTGTA ACTTATTAAC  1020
CTATTTATTA TTTATGTATT TATTTAAGCA TCAAATATTT GTGCAAGAAT TTGGAAAAAT  1080
AGAAGATGAA TCATTGATTG AATAGTTATA AAGATGTTAT AGTAAATTTA TTTTATTTTA  1140
GATATTAAAT GATGTTTTAT TAGATAAATT TCAATCAGGG TTTTTAGATT AAACAAAGAA  1200
ACAATTGGGT ACCCAGTTAA ATTTTCATTT CAGATAAACA ACAAATAATT TTTTAGTATA  1260
AGTACATTAT TGTTTATCTG AAAGTTTTAA TTGAACTAAC AATCCTAGTT TGATACTCCC  1320
AGTCTTGTCA TTGCCAGCTG TGTTGGTAGT GCTGTGTTGA ATTACGGAAT AATGAGTTAG  1380
AACTATTAAA ACAGCCAAAA CTCCACAGTC AATATTAGTA ATTTCTTGCT GGTTGAAACT  1440
TGTTTATTAT GTACAAATAG ATTCTTATAA TATTATTTAA ATGACTGCAT TTTTAAATAC  1500
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AAGGCTTTAT ATTTTTAACT TTAAGATGTT TTTATGTGCT CTCCAAATTT TTTTTACTGT 1560
TTCTGATTGT ATGGAAATAT AAAAGTAAAT ATGAAACATT TAAAATATAA TTTGTTGTCA 1620
AAGTAAAAAA AAAAAAAAA

Seq ID NO: 187 Protein sequence
Protein Accession #: NP_000575.1

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CANTEIIVKL SDGRELCLDP KENWVQRVVE KFLKRAENS
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Seq ID NO: 188 DNA sequence
Nucleic Acid Accession #: NM_003661.1
Coding sequence: 1..1152

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GCTGCTGGCA CCATGGACCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC   180
AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC   240
GGATTCGTGG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG   300
GACAACCTTG CAAGACAAAT GATCATGAAA GACAAAAACT GGCACGATAA AGGCCAGCAG   360
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ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA   840
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GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAA TGAGCAGAGG AGTCAAGCTC   960
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TCAAAGCACT TACATGAGGG GGCAAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT  1080
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CAAGAACTGT GA
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Seq ID NO: 189 Protein sequence
Protein Accession #: NP_003652.1

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1          11         21         31         41         51
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KEKVSTQNLL LLLTDNEAWN GFVAAAELPR NEADELRKAL DNLARQMIMK DKNWHDKGQQ   120
YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLSIS SGILTLVGMG   180
LAPFTEGGSL VLLEPGMELG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR   240
EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG   300
EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVYE SKHLHEGAKS ETAEELKKVA   360
QELEEKLNIL NNNYKILQAD QEL
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Seq ID NO: 190 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

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GCCACAGCCA CGATGATCGC GGGCTCCCTT CTCCTGCTTG GATTCCTTAG CACCACCACA   120
GCTCAGCCAG AACAGAAGGC CTCGAATCTC ATTGGCACAT ACCGCCATGT TGACCGTGCC   180
ACCGGCCAGG TGCTAACCTG TGACAAGTGT CCAGCAGGAA CCTATGTCTC TGAGCATTGT   240
ACCAACACAA GCCTGCGCGT CTGCAGCAGT TGCCCTGTGG GGACCTTTAC CAGGCATGAG   300
AATGGCATAG AGAAATGCCA TGACTGTAGT CAGCCATGCC CATGGCCAAT GATTGAGAAA   360
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ACAGAGACTG AGGATGTGCG GTGTAAGCAG TGTGCTCGGG GTACCTTCTC AGATGTGCCT   540
TCTAGTGTGA TGAAATGCAA AGCATACACA GACTGTCTGA GTCAGAACCT GGTGGTGATC   600
AAGCCGGGGA CCAAGGAGAC AGACAACGTC TGTGGCACAC TCCCGTCCTT CTCCAGCTCC   660
ACCTCACCTT CCCCTGGCAC AGCCATCTTT CCACGCCCTG AGCACATGGA AACCCATGAA   720
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TCAGCAAGGG GGAAGGAAGA CGTGAACAAG ACCCTCCCAA ACCTTCAGGT AGTCAACCAC   900
CAGCAAGGCC CCCACCACAG ACACATCCTG AAGCTGCTGC CGTCCATGGA GGCCACTGGG   960
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CCCCGGCAGG ATCCCAGTGC CATTGTGGAA AAGGCAGGGC TGAAGAAATC CATGACTCCA  1200
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GCCCTGCGCC AGCACCGGAG AAACGATGTT GTGGAGAAGA TTCGTGGGCT GATGGAAGAC  1500
ACCACCCAGC TGGAAACTGA CAAACTAGCT CTCCCGATGA GCCCCAGCCC GCTTAGCCCG  1560
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AGCCCCATCC CCAGCCCCAA CGCGAAACTT GAGAATTCCG CTCTCCTGAC GGTGGAGCCT  1620
TCCCCACAGG ACAAGAACAA GGGCTTCTTC GTGGATGAGT CGGAGCCCCT TCTCCGCTGT  1680
GACTCTACAT CCAGCGGCTC CTCCGCGCTG AGCAGGAACG GTTCCTTTAT TACCAAAGAA  1740
AAGAAGGACA CAGTGTTGCG GCAGGTACGC CTGGACCCCT GTGACTTGCA GCCTATCTTT  1800
GATGACATGC TCCACTTTCT AAATCCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG  1860
GCTGAGGACA AACTAGACCG GCTATTCGAA ATTATTGGAG TCAAGAGCCA GGAAGCCAGC  1920
CAGACCCTCC TGGACTCTGT TTATAGCCAT CTTCCTGACC TGCTGTAG
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Seq ID NO: 191 Protein sequence
Protein Accession #: NP_055267.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGTSPSSSTA LASCSRIARR ATATMIAGSL LLLGFLSTTT AQPEQKASNL IGTYRHVDRA   60
TGQVLTCDKC PAGTYVSEHC TNTSLRVCSS CPVGTFIRHE NGIEKCHDCS QPCPWPMIEK  120
LPCAALTDRE CTCPPGMFQS NATCAPHTVC PVGWGVRKKG TETEDVRCKQ CARGTFSDVP  180
SSVMKCKAYT DCLSQNLVVI KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPEHMETHE  240
VPSSTYVPKG MNSTESNSSA SVRPKVLSSI QEGTVPDNTS SARGKEDVNK TLPNLQVVNH  300
QQGPHHRHIL KLLPSMEATG GEKSSTPIKG PKRGHPRQNL HKHFDINEHL PWMIVLFLLL  360
VLVVIVVCSI RKSSRTLKKG PRQDPSAIVE KAGLKKSMTP TQNREKWIYY CNGHGIDILK  420
LVAAQVGSQW KDIYQFLCNA SEREVAAFSN GYTADHERAY AALQHWTIRG PEASLAQLIS  480
ALRQHRRNDV VEKIRGLMED TTQLETDKLA LPMSPSPLSP SPIPSPNAKL ENSALLTVEP  540
SPQDKNKGFF VDESEPLLRC DSTSSGSSAL SRNGSFITKE KKDTVLRQVR LDPCDLQPIF  600
DDMLHFLNPE ELRVIEEIPQ AEDKLDRLFE IIGVKSQEAS QTLLDSVYSH LPDLL
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Seq ID NO: 192 DNA sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

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1          11         21         31         41         51
|          |          |          |          |          |
GCTCTGCCCA AGCCGAGGCT GCGGGGCCGG CGCCGGCGGG AGGACTGCGG TGCCCCGCGG   60
AGGGGCTGAG TTTGCCAGGG CCCACTTGAC CCTGTTTCCC ACCTCCCGCC CCCCAGGTCC  120
GGAGGCGGGG GCCCCCGGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCCGCCCGTG  180
AGTCCGGCCG AGCCACCTGA GCCCGAGCCG CGGGACACCG TCGCTCCTGC TCTCCGAATG  240
CTGCGCACCG CGATGGGCCT GAGGAGCTGG CTCGCCGCCC CATGGGGCGC GCTGCCGCCT  300
CGGCCACCGC TGCTGCTGCT CCTGCTGCTG CTGCTCCTGC TGCAGCCGCC GCCTCCGACC  360
TGGGCGCTCA GCCCCCGGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCC ATTCCTCAGA  420
TTCGAAGCTG AACACATCTC CAACTACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC  480
CTGTACGTGG GTGCTCGAGA GGCCCTCTTT GCACTCAGTA GCAACCTCAG CTTCCTGCCA  540
GGCGGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCAG AGAAGAAACA GCAGTGCAGC  600
TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAAACTACA TCAAGATCCT CCTGCCGCTC  660
AGCGGCAGTC ACCTGTTCAC CTGTGGCACA GCAGCCTTCA GCCCCATGTG TACCTACATC  720
AACATGGAGA ACTTCACCCT GGCAAGGGAC GAGAAGGGGA ATGTCCTCCT GGAAGATGGC  780
AAGGGCCGTT GTCCCTTCGA CCCGAATTTC AAGTCCACTG CCCTGGTGGT TGATGGCGAG  840
CTCTACACTG GAACAGTCAG CAGCTTCCAA GGGAATGACC CGGCCATCTC GCGGAGCCAA  900
AGCCTTCGCC CCACCAAGAC CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG  960
GCCTCAGCCT ACATTCCTGA GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC 1020
TTTTTCTTCA GCGAGACTGG CCAGGAATTT GAGTTCTTTG AGAACACCAT TGTGTCCCGC 1080
ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC 1140
TCCTTCCTCA AGGCCCAGCT GCTGTGCTCA CGGCCCGACG ATGGCTTCCC CTTCAACGTG 1200
CTGCAGGATG TCTTCACGCT GAGCCCCAGC CCCCAGGACT GGCGTGACAC CCTTTTCTAT 1260
GGGGTCTTCA CTTCCCAGTG GCACAGGGGA ACTACAGAAG GCTCTGCCGT CTGTGTCTTC 1320
ACAATGAAGG ATGTGCAGAG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CCGTGAGACA 1380
CAGCAGTGGT ACACCGTGAC CCACCCGGTG CCCACACCCC GGCCTGGAGC GTGCATCACC 1440
AACAGTGCCC GGGAAAGGAA GATCAACTCA TCCCTGCAGC TCCCAGACCG CGTGCTGAAC 1500
TTCCTCAAGG ACCACTTCCT GATGGACGGG CAGGTCCGAA GCCGCATGCT GCTGCTGCAG 1560
CCCCAGGCTC GCTACCAGCG CGTGGCTGTA CACCGCGTCC CTGGCCTGCA CCACACCTAC 1620
GATGTCCTCT TCCTGGGCAC TGGTGACGGC CGGCTCCACA AGGCAGTGAG CGTGGGCCCC 1680
CGGGTGCACA TCATTGAGGA GCTGCAGATC TTCTCATCGG GACAGCCCGT GCAGAATCTG 1740
CTCCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCCTCAC ACTCGGGCGT AGTCCAGGTG 1800
CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCCTCGC CCGGGACCCC 1860
TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CACGTCAGCC TCTACCAGCC TCAGCTGGCC 1920
ACCAGGCCGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCGTCT 1980
TCGGTTGTGT CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040
CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC 2100
TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCCTCCT GCCACGTGCT ACCCACTGGG 2160
GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGCTGGTC ACTAGAGGAG 2220
GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC 2280
CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGCACCA 2340
GCTGGTGGCA AGGCCAGCTG GGGTGCAGAC AGGTCCTACT GGAAGGAGTT CCTGGTGATG 2400
TGCACGCTCT TTGTGCTGGC CGTGCTGCTC CCAGTTTTAT TCTTGCTCTA CCGGCACCGG 2460
AACAGCATGA AAGTCTTCCT GAAGCAGGGG GAATGTGCCA GCGTGCACCC CAAGACCTGC 2520
CCTGTGGTGC TGCCCCCTGA GACCCGCCCA CTCAACGGCC TAGGGCCCCC TAGCACCCCG 2580
CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640
GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCCAGTGTGC 2700
CCCCGGCCCC GGGTCCGCCT TGGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT 2760
TCCAGAGGAC GCTGCCCTGG CTTCAGGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820
TCCCCTCCGC TCTGCTCTTC GTGGAACACG ACCGTGGTGC CCGGCCCTTG GGAGCCTTGG 2880
GGCCAGCTGG CCTGCTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACCC AGACACCCAA 2940
ACAGCCGTGG CCCCAGAGGT CCTGGCCAAA TATGGGGGCC TGCCTAGGTT GGTGGAACAG 3000
TGCTCCTTAT GTAAACTGAG CCCTTTGTTT AAAAAACAAT TCCAAATGTG AAACTAGAAT 3060
GAGAGGCAAG AGATAGCATG GCATCCAGCA CACACGGCTG CTCCAGTTCA TGGCCTCCCA 3120
GGGGTGCTGG GGATGCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAAC CCTCACCAAC 3180
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TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT  3240
CAGGACCAGC TTGGGCTGCG TGCGTTCTGC CTTGCCAGTC AGCCGAGGAT GTAGTTGTTG  3300
CTGCCGTCGT CCCACCACCT CAGGGACCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA  3360
GGTCCTGGGC TCGGACCCAA CTCCTGGACC TTTCCAGCCT GTATCAGGCT GTGGCCACAC  3420
GAGAGGACAG CGCGAGCTCA GGAGAGATTT CGTGACAATG TACGCCTTTC CCTCAGAATT  3480
CAGGGAAGAG ACTGTCGCCT GCCTTCCTCC GTTGTTGCGT GAGAACCCGT GTGCCCCTTC  3540
CCACCATATC CACCCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACTAA CTGCACCCTG  3600
GTCCTCTCCC CAGTCCCCAG TTCACCCTCC ATCCCTCACC TTCCTCCACT CTAAGGGATA  3660
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG  3720
ATGCACTTTA TGTCATTTTT TAATAAAGTC TGAAGAATTA CTGTTT
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Seq ID NO: 193 Protein sequence
Protein Accession #: XP_044533.3

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1          11         21         31         41         51
|          |          |          |          |          |
MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL    60
RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC   120
SFKGKDPQRD CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED   180
GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF   240
VASAYIPESL GSLQGDDDKI YFFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW   300
TSFLKAQLLC SRPDDGFPFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV   360
FTMKDVQRVF SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL   420
NFLKDHFLMD GQVRSRMLLL QPQARYQRVA VHRVPGLHHT YDVLFLGTGD GRLHKAVSVG   480
PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD   540
PYCAWSGSSC KHVSLYQPQL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCEQVQ   600
FQPNTVNTLA CPLLSNLATR LWLRNGAPVN ASASCHVLPT GDLLLVGTQQ LGEFQCWSLE   660
EGFQQLVASY CPEVVEDGVA DQTDEGGSVP VIISTSRVSA PAGGKASWGA DRSYWKEFLV   720
MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST   780
PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV
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Seq ID NO: 194 DNA sequence
Nucleic Acid Accession #: NM_022819.1
Coding sequence: 1..635

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGCAGATG GGGCAAAGGC CAACCCCAAA GGGTTCAAAA AGAAGGTGCT GGATAGATGC    60
TTCTCTGGGT GGAGGGGCCC ACGCTTCGGG GCCTCCTGTC CTTCAAGAAC CTCCAGGTCT   120
AGCCTGGGTA TGAAGAAGTT CTTCACCGTG GCCATCCTTG CTGGCAGCGT TCTGTCCACA   180
GCTCACGGCA GCCTGCTCAA CCTGAAGGCC ATGGTGGAGG CCGTCACAGG GAGGAGCGCC   240
ATCCTGTCCT TCGTGGGCTA CGGTTGCTAC TGTGGGCTGG GGGGCCGTGG CCAGCCCAAG   300
GATGAGGTGG ACTGGTGCTG CCACGCCCAC GACTGCTGCT ACCAGGAACT CTTTGACCAA   360
GGCTGTCACC CCTATGTGGA CCACTATGAT CACACCATCG AGAACAACAC TGAGATAGTC   420
TGCAGTGACC TCAACAAGAC AGAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG   480
GTTCTGTGCC TCATGAACCA GACGTACCGA GAGGAGTACC GTGGCTTCCT CAATGTCTAC   540
TGCCAGGGCC CCACGCCCAA CTGCAGCATC TATGAACCGC CCCCTGAGGA GGTCACCTGC   600
AGTCACCAAT CCCCAGCGCC CCCCGCCCCT CCCTAG
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Seq ID NO: 195 Protein sequence
Protein Accession #: NP_073730

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1          11         21         31         41         51
|          |          |          |          |          |
MADGAKANPK GFKKKVLDRC FSGWRGPRFG ASCPSRTSRS SLGMKKFFTV AILAGSVLST    60
AHGSLLNLKA MVEAVTGRSA ILSFVGYGCY CGLGGRGQPK DEVDWCCHAH DCCYQELFDQ   120
GCHPYVDHYD HTIENNTEIV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR EEYRGFLNVY   180
CQGPTPNCSI YEPPPEEVTC SHQSPAPPAP P
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Seq ID NO: 196 DNA sequence
Nucleic Acid Accession #: XM_028196.1
Coding sequence: 1315..1791

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1          11         21         31         41         51
|          |          |          |          |          |
GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT    60
GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCCTTTCTGT CTGTCTCCTT GCTCTGCCCC   120
AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG   180
ATGGCCTGGG CTGGGCCCCT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG   240
CTCTTGTGGG CAAAGCAGGG GAGGCGCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG   300
CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCCTG   360
GGGTCACCGT AGGCCCCATG TAGCACCCTG GTTCCCCTGC CTGTAGGTGA CAGGAGCCAG   420
CCCAGCCAGG TGTGCTCCCT CCCCAGGCCC TAGGCAGGCG GGTACAGGGG CCAGCAGCTG   480
CGCCCGCCCC ACCTTCCTTC CCACCCACAT GCCGAAGGGT GGCCAGGCAG GCAGGTGGAC   540
GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGGAATGTTC TGGCCGCTCC CAGCTGCACC   600
CTGCCCCTAC CTGCCACCAC CTCACCTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCCTGC   660
CAGGAATGCA CCTTTAGCCC AGGCCTGCTC AGTGAGCTCC GCCGACAGCC AGCCCTGCTC   720
CTCCCGCCAT GACCCTGCAG ACCCCTCTGG GCTTCCAAGT TCCTGGGGGC TGCAGTGAAC   780
ATGCTCCACC TGCATGGCTG GCAAACCATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT   840
AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGGATGAGA TGGGACCCCC   900
AGGCAGGGCC CAGGGTCCAG GGCCCAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCCTGG   960
TGGAGGACGC ATCCTACAGT GGGGGCAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT  1020
AGGCTGCCCA GGCCCTGCCT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG  1080
GCTGGGCCTG GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCCTTCAG  1140
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CTTCCTGCTG CACAGAACCC TCGCCCCTGG CCACCCCGTG CTGCCTCCTT GCCCTGGCAG  1200
ACCCAGCACT GGCTGCTGCT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC  1260
TCCCAGCTGA CCCAGCCTCC TGGGCCGCTT CTTCCAAACC AGCAGGGTAG AAAGATGGGG  1320
CACCCACCAG TCTCTCCCAG TGCCCCGGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT  1380
ATTCCAGACC TTGTCGCCGG GACCCCCTGT GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG  1440
GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC  1500
CCAGGGCCCC GCTGGGCTCT CATTGCCGGC GCCCTTGCCG CGGGCGTCCT CCTCGTCTCC  1560
TGCCTCCTCT GTGCTGCCTG CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGGACAAG  1620
GAGTCCGTGG GTCTGGGCAG TGCCCGCGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC  1680
TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA  1740
GGCGAGTTCA GCCCCAGGGA TGGTTTAACC CCCACAGAGG CAGGGCGTTG AGGACCTTCC  1800
TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCCAT  1860
GGGCCCGAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT  1920
TTTGGGTGGG TTTGGCCGGT CTCACAGAGC GAAGCCGACG ATTTGTGCCT GTTGGGTGGC  1980
CTGGCCTGGA GGCGGGGGGT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCCAGGG  2040
CTCTGATGAG GCATGATGTC AGCACCACCT GCCCCTTGTC CCAACTCACT CCAGGTGCAA  2100
CCTGATGTGG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCCTGCAG  2160
CTCTCCCTGG AGTTCGACTT TGGAAGCCAG GAGGTGAAGG GCCCCGCTGC GCAGGACCAG  2220
CGGTTCTGCG AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG  2280
TGGGGAGCTG ACAGGGCAGG GGCCCTTGGC TGAGCCCACC CCGCTGGCTC CCAGATCAGG  2340
GTGGGCCTGA GGCAGGCAGC CGACCTGAGG CCTGGGGGCA CCGTGGACCC CTATGCCCGG  2400
GTCAGCGTCT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGCACCG AGGCACGCTC  2460
TGCCCCGTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGGATGGTC GGCTGGGTGG  2520
GCCTGGACGG CTGGATGGGC CTGGGCTGGG TGGGCCTGGG CAGCTGGGTG GGCCTGGGCA  2580
GCTGGGTGGG CCTGAGCTAG GGCAGCAGGG CCTGGCTCAC GCCGCTGCCT CAGATCCCGC  2640
AGGCGGAGCT GCCAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG  2700
GGCATGAGCC CCTGGGTGAG CTCCGTCTGC CACTGGGCAC CGTGGATCTG CAGCATGTTC  2760
TGGAGCACTG GTACCTGCTG GGCCCGCCGG CTGCCACTCA GGTGAGGTGC TGGTCACCAG  2820
GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC  2880
CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAACTCGG CCAGAATCAC CCTCCCGGGC  2940
TGAAGCCCCT CTTGCTGCCC ACAGCCCGAG CAGGTCGGGG AGCTGTGCTT CTCTCTCCGG  3000
TACGTGCCCA GCTCAGGCCG GCTGACCGTG GTGGTGCTGG AGGCTCGAGG CCTGCGTCCA  3060
GGACTTGCAG AGCCCTACGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG  3120
AGAAAGACAG CCACCAAAAA GGGCACGGCG GCCCCCTACT TCAATGAGGC CTTCACCTTC  3180
CTGGTGCCCT TCAGCCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GGACCGCAGC  3240
CTGCCGCTCC GAACTGAGCC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG  3300
CCCCTGCAGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGCCCATTGC CCAGCGGCAC  3360
CCCCTGCGGC CAGCCAGGGA GGTGGACCCC ATGCTGGCCC TGCAGCCCCG CCTTCGCCTG  3420
CGCCTGCCCT TGCCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCCG CTGAGCCCAG  3480
GCACTTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC
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Seq ID NO: 197 Protein sequence
Protein Accession #: XP_028196.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGHPPVSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA    60
STPGPRWALI AGALAAGVLL VSCLLCAACC CCRRHRKKPR DKESVGLGSA RGTTTTHLVR   120
SGSLLTQSRE GLKSRLQSPG QRGEFSPRDG LTPTEAGR
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Seq ID NO: 198 DNA sequence
Nucleic Acid Accession #: NM_000612.2
Coding sequence: 553..1095

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1          11         21         31         41         51
|          |          |          |          |          |
TTCTCCCGCA ACCTTCCCTT CGCTCCCTCC CGTCCCCCCC AGCTCCTAGC CTCCGACTCC    60
CTCCCCCCCT CACGCCCGCC CTCTCGCCTT CGCCGAACCA AAGTGGATTA ATTACACGCT   120
TTCTGTTTCT CTCCGTGCTG TTCTCTCCCG CTGTGCGCCT GCCCGCCTCT CGCTGTCCTC   180
TCTCCCCCTC GCCCTCTCTT CGGCCCCCCC CTTTCACGTT CACTCTGTCT CTCCCACTAT   240
CTCTGCCCCC CTCTATCCTT GATACAACAG CTGACCTCAT TTCCCGATAC CTTTTCCCCC   300
CCGAAAAGTA CAACATCTGG CCCGCCCCAG CCCGAAGACA GCCCGTCCTC CCTGGACAAT   360
CAGACGAATT CTCCCCCCCC CCCCAAAAAA AAAAGCCATC CCCCCGCTCT GCCCCGTCGC   420
ACATTCGGCC CCCGCGACTC GGCCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG   480
CCAACGCCCG CTGTTCGGTT TGCGACACGC AGCAGGGAGG TGGGCGGCAG CGTCGCCGGC   540
TTCCAGACAC CAATGGGAAT CCCAATGGGG AAGTCGATGC TGGTGCTTCT CACCTTCTTG   600
GCCTTCGCCT CGTGCTGCAT TGCTGCTTAC CGCCCCAGTG AGACCCTGTG CGGCGGGGAG   660
CTGGTGGACA CCCTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCCGCA   720
AGCCGTGTGA GCCGTCGCAG CCGTGGCATC GTTGAGGAGT GCTGTTTCCG CAGCTGTGAC   780
CTGGCCCTCC TGGAGACGTA CTGTGCTACC CCCGCCAAGT CCGAGAGGGA CGTGTCGACC   840
CCTCCGACCG TGCTTCCGGA CAACTTCCCC AGATACCCCG TGGGCAAGTT CTTCCAATAT   900
GACACCTGGA AGCAGTCCAC CCAGCGCCTG CGCAGGGGCC TGCCTGCCCT CCTGCGTGCC   960
CGCCGGGGTC ACGTGCTCGC CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACGTCACCGT  1020
CCCCTGATTG CTCTACCCAC CCAAGACCCC GCCCACGGGG GCGCCCCCCC AGAGATGGCC  1080
AGCAATCGGA AGTGAGCAAA ACTGCCGCAA GTCTGCAGCC CGGCGCCACC ATCCTGCAGC  1140
CTCCTCCTGA CCACGGACGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCCACGT  1200
CCCCCTGGGG CTTCTCCTGA CCCAGTCCCC GTGCCCCGCC TCCCCGAAAC AGGCTACTCT  1260
CCTCGGCCCC CTCCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAAACAT GTACAAAATC  1320
GATTGGCTTT AAACACCCTT CACATACCCT CCCCCC
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Seq ID NO: 199 Protein sequence
Protein Accession #: NP_000603.1

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1          11         21         31         41         51
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|          |          |          |          |          |
MGIPMGKSML VLLTFLAFAS CCIAAYRPSE TLCGGELVDT LQFVCGDRGF YFSRPASRVS    60
RRSRGIVEEC CFRSCDLALL ETYCATPAKS ERDVSTPPTV LPDNFPRYPV GKFFQYDTWK   120
QSTQRLRRGL PALLRARRGH VLAKELEAFR EAKRHRPLIA LPTQDPAHGG APPEMASNRK
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Seq ID NO: 200 DNA sequence
Nucleic Acid Accession #: AK057131.1
Coding sequence: 61..1146

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1          11         21         31         41         51
|          |          |          |          |          |
AGTCTGGGCG TTTAGGTCAG AACTACCCCG GTAGCCTGAC AGCAGGAGCT CGAGAGAAGC    60
ATGGCTCAGC GGTGCGTTTG CGTGCTGGCC CTGGTGGCTA TGCTGCTCCT AGTTTTCCCT   120
ACCGTCTCCA GATCGATGGG CCCGAGGAGC GGGGAGCATC AAAGGGCGTC GCGAATCCCT   180
TCTCAGTTCA GCAAAGAGGA ACGCGTCGCG ATGAAAGAGG CGCTGAAAGG TGCCATCCAG   240
ATTCCAACAG TGACTTTTAG CTCTGAGAAG TCCAATACTA CAGCCCTGGC TGAGTTCGGA   300
AAATACATTC ATAAAGTCTT TCCTACAGTG GTCAGCACCA GCTTTATCCA GCATGAAGTC   360
GTGGAAGAGT ATAGCCACCT GTTCACTATC CAAGGCTCGG ACCCCAGCTT GCAGCCCTAC   420
CTGCTGATGG CTCACTTTGA TGTGGTGCCT GCCCCTGAAG AAGGCTGGGA GGTGCCCCCA   480
TTCTCTGGGT TGGAGCGTGA TGGCGTCATC TATGGTTGGG GCACACTGGA CGACAAGAAC   540
TCTGTGATGG CATTACTGCA GGCCTTGGAG CTCCTGCTGA TCAGGAAGTA CATCCCCCGA   600
AGATCTTTCT TCATTTCTCT GGGCCATGAT GAGGAGTCAT CAGGGACAGG GGCTCAGAGG   660
ATCTCAGCCC TGCTACAGTC AAGGGGCGTC CAGCTAGCCT TCATTGTGGA CGAGGGGGGC   720
TTCATCTTGG ATGATTTCAT TCCTAACTTC AAGAAGCCCA TCGCCTTGAT TGCAGTCTCA   780
GAGAAGGGTT CCATGAACCT CATGCTGCAA GTAAACATGA CTTCAGGCCA CTCTTCAGCT   840
CCTCCAAAGG AGACAAGCAT TGGCATCCTT GCAGCTGCTG TCAGCCGATT GGAGCAGACA   900
CCAATGCCTA TCATATTTGG AAGCGGGACA GTGGTGACTG TATTGCAGCA ACTGGCAAAT   960
GAGGTTTATG GAGAGAAATC CCTTAACCAA TGCAATAATC AGGACCACCA CGGCACTCAC  1020
CATATTCAAA GCAGGGGTCA AGTTCAATGT CATCCCCCCA GTGGCCCAGG CCACAGTCAA  1080
CTTCCGGATT CACCCTGGAC AGACAGTCCA AGAGGTCCTA GAACTCACGA AGAACATTGT  1140
GGCTGATAAC AGAGTCCAGT TCCATGTGTT GAGTGCCTTT GACCCCCTCC CCGTCAGCCC  1200
TTCTGATGAC AAGGCCTTGG GCTACCAGCT GCTCCGCCAG ACCGTACAGT CCGTCTTCCC  1260
GGAAGTCAAT ATTACTGCCC CAGTTACTTC TATTGGCAAC ACAGACAGCC GATTCTTTAC  1320
AAACCTCACC ACTGGCATCT ACAGGTTCTA CCCCATCTAC ATACAGCCTG AAGACTTCAA  1380
ACGCATCCAT GGAGTCAACG AGAAAATCTC AGTCCAAGCC TATGAGACCC AAGTGAAATT  1440
CATCTTTGAG TTGATTCAGA ATGCTGACAC AGACCAGGAG CCAGTTTCTC ACCTGCACAA  1500
ACTGTGAGGT CAAGGGGCCT GCTGGGTTAG GCATGCCCGA CCCCGGGACA GGACTAACCC  1560
AAGGGGGAAA GCTAGTGTTG ATGAAACTTT TGATCAAAAC CACATTGTAA AACATTGCCC  1620
ATCTGTCTTG CTCACTCTTA AACTCTCCCA AGAACAAGGC CGGGGTAAGG TAAAGTCAGC  1680
AGAAATCTGG CTTCTCCCTT CCTCCCGACA TCTGCATCCC TTGATCCACT GGCATTTGCT  1740
GCCCTCTTGT CCCTTATCTG TCTTATGCTG GTTATTTCAC TGCTTCACCT TCCAGGCTTG  1800
ACTTAACAAA TGTAGATTTG AGAAATCTCA ACCAGTTGTT ACCTGATAGG AGTCTTTAAT  1860
TTAGGGCACT CTTGCTGGGA TGCTTTCTCC AGAGCTTATA TATTTCTTCT TACTAGAACT  1920
TTCTTCCCCC TTTTATTCCC CTCTCTTCTT GGACTCATGA GCTGTCTCTT CATCTCTCCT  1980
CTCTCTCCTG CATCTCTCCC CTTACTCTTC AATTTATTCT ACTTCTGGAC CTGGACTTAC  2040
CCAAACTGTG ATACTACCAT AATTGTCACC ATAATCAGTC AAATAAAGTG ATCTGTGCAT  2100
C
```

Seq ID NO: 201 Protein sequence
Protein Accession #: BAB71368.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAQRCVCVLA LVAMLLLVFP TVSRSMGPRS GEHQRASRIP SQFSKEERVA MKEALKGAIQ    60
IPTVTFSSEK SNTTALAEFG KYIHKVFPTV VSTSFIQHEV VEEYSHLFTI QGSDPSLQPY   120
LLMAHFDVVP APEEGWEVPP FSGLERDGVI YGWGTLDDKN SVMALLQALE LLLIRKYIPR   180
RSFFISLGHD EESSGTGAQR ISALLQSRGV QLAFIVDEGG FILDDFIPNF KKPIALIAVS   240
EKGSMNLMLQ VNMTSGHSSA PPKETSIGIL AAAVSRLEQT PMPIIFGSGT VVTVLQQLAN   300
EVYGEKSLNQ CNNQDHHGTH HIQSRGQVQC HPPSGPGHSQ LPDSPWTDSP RGPRTHEEHC   360
G
```

Seq ID NO: 202 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTTCTC TCTAAGGATG    60
GCCCAGAAGG AGAACTCCTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG   120
AGCACCCTGC CCCAGCGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCCTC   180
ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCCTGGCC AGAAGGTGAT GGAGAATAGC   240
AGTGGGACAC CCGACATCTT AACGCGGCAC TTCACAATTG ATGACTTTGA GATTGGGCGT   300
CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC   360
ATCGTGGCGC TCAAGGTCCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG   420
CTGCGCAGAG AGATCGAAAT CCAGGCCCAC CTGCACCATC CCAACATCCT GCGTCTCTAC   480
AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG   540
CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CACGATCATG   600
GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA   660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTCGGCTGG   720
TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCCTGGA CTACCTGCCC   780
CCAGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGGTGG ATCTGTGGTG CATTGGAGTG   840
CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACCAGACC   900
TATCGCCGCA TCGTCAAGGT GGACCTAAAG TTCCCCGCTT CTGTGCCCAC GGGAGCCCAG   960
GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGGAAC GGCTGCCCCT GGCCCAGGTC  1020
```

```
TCAGCCCACC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA  1080
TCTGTCGCCT GATGGTCCCT GTCATTCACT CGGGTGCGTG TGTTTGTATG TCTGTGTATG  1140
TATAGGGGAA AGAAGGGATC CCTAACTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT  1200
TTAATAAAGG CTGAAGCTTT TTGT
```

Seq ID NO: 203 Protein sequence
Protein Accession #: NP_004208

```
1          11         21         31         41         51
|          |          |          |          |          |
MAQKENSYPW PYGRQTAPSG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN    60
SSGTPDILTR HFTIDDFEIG RPLGKGKFGN VYLAREKKSH FIVALKVLFK SQIEKEGVEH   120
QLRREIEIQA HLHHPNILRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI   180
MEELADALMY CHGKKVIHRD IKPENLLLGL KGELKIADFG WSVHAPSLRR KTMCGTLDYL   240
PPEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA   300
QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSVA
```

Seq ID NO: 204 DNA sequence
Nucleic Acid Accession #: AK055663
Coding sequence: 38..1423

```
1          11         21         31         41         51
|          |          |          |          |          |
AGAACGGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTCG     60
AAAACCACAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA   120
CCGAAGGTCC TGGAAGATAC TGCTCTTTGG TGTAATAAAC TTGATATGTA CTGGCTTCCT   180
GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT   240
TTTTGATCTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC   300
TAGCCCTGTC TATTCATTTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCTCCAC   360
AGTCTTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAAAGAA AGTGCAGAAC GCTTTTTGGA   420
ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA   480
CCTGTTCACG ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG   540
TACGAGCTGG CTTCAAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTATTCC   600
GGGACTTAGC AGTATCTTCC TTCCCCGAAT GAATCCATTT GTTTTGATTG ATCTTGCTGG   660
AGCATTTGCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCCGTAGA   720
CACTGCCTCT GCTATAGCTA TTGCCTTGAT GACATTTGGC ACTATGTATC CCATGAGTGT   780
GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA   840
ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTAGAA GTCCGAAATG AACATTTTTG   900
GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTCGAC GAGATGCCAA   960
TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC  1020
TGTTCAAATT TTCAAGGATG ACTGGATTAG GCCTGCCTTA TTGTCTGGGC CTGTTGCAGC  1080
CAATGTCCTA AACTTTTCAG ATCATCACGT AATCCCAATG CCTCTTTTAA AGGGTACTGA  1140
TGATTTGAAC CCAGTTACAT CAACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC  1200
ATTTAACACT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAAACACAC AAACAAGGCC  1260
TTATGGTTTT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT  1320
TGGAGTTCCA GGAATTGGAG CAACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG  1380
TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACTTATTT  1440
TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAACT TTGCATTGAC  1500
TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC  1560
TATGAAACTA TATTTTTGTA AAATGTATTT GTGACAGTGA AATCCTCGTA AATGTTAAAG  1620
GCTTTAAATA GGCTTCCTTT AGAAAATGTG TTTCTTTAAA TTTGGATTTT GGTATCTTTG  1680
GTTTTGTAGT TGACTGCAGT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT  1740
AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTTTTT TCCGAGACGG AGTCTTGCTC  1800
TGCCACTGTG CCCGGCCAAT ACATTATTAT TAACTTAAGG CTGTACTTTA TTAAGGCTTC  1860
CTTAGTTTTT GTTTTGTTTT GTTTTTTGAG ATGGAGTCTC ACTCTGTCGC CCAGGCTGGA  1920
ATGCAGTGGC ATGATCTCAG CTCACTGCAA CCTCTGCCTC CTGAGTTCAA ATGATTCTCC  1980
TGCCTCAGCC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCCC AGCTAATTTT  2040
TGTATTTTTA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAACTCCTG  2100
ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGCTGGG ATTAGGTGTG AGCCACCGCA  2160
CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT  2220
GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACTT  2280
AATTGCTAAA TTTTTCTTTG AGGTTCTCCT GAATTATGTC TTACAAACTA AAAGCAAAAA  2340
TTTTTAGCAG AAATTTTGGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA  2400
GATTTTTGTT AAAGTTTCTC TCCTTTAAAA ATTTTAGTAC ATTTGTAAAT
```

Seq ID NO: 205 Protein sequence
Protein Accession #: BAB70980.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGTIHLFRKP QRSFFGKLLR EFRLVAADRR SWKILLFGVI NLICTGFLLM WCSSTNSIAL    60
TAYTYLTIFD LFSLMTCLIS YWVTLRKPSP VYSFGFERLE VLAVFASTVL AQLGALFILK   120
ESAERFLEQP EIHTGRLLVG TFVALCFNLF TMLSIRNKPF AYVSEAASTS WLQEHVADLS   180
RSLCGIIPGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFAVDTA SAIAIALMTF   240
GTMYPMSVYS GKVLLQTTPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGSLAGSVH   300
VRIRRDANEQ MVLAHVTNRL YTLVSTLTVQ IFKDDWIRPA LLSGPVAANV LNFSDHHVIP   360
MPLLKGTDDL NPVTSTPAKP SSPPPEFSFN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY   420
SSMLNQGLGV PGIGATQGLR TGFTNIPSRY GTNNRIGQPR P
```

Seq ID NO: 206 DNA sequence
Nucleic Acid Accession #: NM_016361.1
Coding sequence: 397..1662

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1          11         21         31         41         51
```

```
GGAACTCAGG GCCGGCTCCT GTTCCTTCAA GAGTGCTGGA GGCCAAACTT GAAATACAAG    60
TTTAATGTTC CTCGTCGGGC AAAAGATAAG GATCCGATCT CCCCCGGCCC GGTGTGCAGC   120
AGGAGCGACC AACCCCGACC CGGGTTAAAA CTCCCAGGGA CTCTTCGCTG CTGCCACCTC   180
TTGTTCTCTC CCCCGTTCCC ACTCGGGGTC TCCCTCAGGG CCGGGAGGCA CAGCGGTCCC   240
TGCTTGCTGA AGGGCTGGAT GTACGCATCC GCAGGTTCCC GCGGACTTGG GGGCGCCCGC   300
TGAGCCCCGG CGCCCGCAGA AGACTTGTGT TTGCCTCCTG CAGCCTCAAC CCGGAGGCAG   360
CGAGGGCCTA CCACCATGAT CACTGGTGTG TTCAGCATGC GCTTGTGGAC CCCAGTGGGC   420
GTCCTGACCT CGCTGGCGTA CTGCCTGCAC CAGCGGCGGG TGGCCCTGGC CGAGCTGCAG   480
GAGGCCGATG GCCAGTGTCC GGTCGACCGC AGCCTGCTGA AGTTGAAAAT GGTGCAGGTC   540
GTGTTTCGAC ACGGGGCTCG GAGTCCTCTC AAGCCGCTCC CGCTGGAGGA GCAGGTAGAG   600
TGGAACCCCC AGCTATTAGA GGTCCCACCC CAAACTCAGT TTGATTACAC AGTCACCAAT   660
CTAGCTGGTG GTCCGAAACC ATATTCTCCT TACGACTCTC AATACCATGA GACCACCCTG   720
AAGGGGGGCA TGTTTGCTGG GCAGCTGACC AAGGTGGGCA TGCAGCAAAT GTTTGCCTTG   780
GGAGAGAGAC TGAGGAAGAA CTATGTGGAA GACATTCCCT TTCTTTCACC AACCTTCAAC   840
CCACAGGAGG TCTTTATTCG TTCCACTAAC ATTTTTCGGA ATCTGGAGTC CACCCGTTGT   900
TTGCTGGCTG GGCTTTTCCA GTGTCAGAAA GAAGGACCCA TCATCATCCA CACTGATGAA   960
GCAGATTCAG AAGTCTTGTA TCCCAACTAC CAAAGCTGCT GGAGCCTGAG GCAGAGAACC  1020
AGAGGCCGGA GGCAGACTGC CTCTTTACAG CCAGGAATCT CAGAGGATTT GAAAAAGGTG  1080
AAGGACAGGA TGGGCATTGA CAGTAGTGAT AAAGTGGACT TCTTCATCCT CCTGGACAAC  1140
GTGGCTGCCG AGCAGGCACA CAACCTCCCA AGCTGCCCCA TGCTGAAGAG ATTTGCACGG  1200
ATGATCGAAC AGAGAGCTGT GGACACATCC TTGTACATAC TGCCCAAGGA AGACAGGGAA  1260
AGTCTTCAGA TGGCAGTAGG CCCATTCCTC CACATCCTAG AGAGCAACCT GCTCAAAGCC  1320
ATGGACTCTG CCACTGCCCC CGACAAGATC AGAAAGCTGT ATCTCTATGC GGCTCATGAT  1380
GTGACCTTCA TACCGCTCTT AATGACCCTG GGGATTTTTG ACCACAAATG GCCACCGTTT  1440
GCTGTTGACC TGACCATGGA ACTTTACCAG CACCTGGAAT CTAAGGAGTG GTTTGTGCAG  1500
CTCTATTACC ACGGGAAGGA GCAGGTGCCG AGAGGTTGCC CTGATGGGCT CTGCCCGCTG  1560
GACATGTTCT TGAATGCCAT GTCAGTTTAT ACCTTAAGCC CAGAAAAATA CCATGCACTC  1620
TGCTCTCAAA CTCAGGTGAT GGAAGTTGGA AATGAAGAGT AACTGATTTA TAAAAGCAGG  1680
ATGTGTTGAT TTTAAAATAA AGTGCCTTTA TACAAAAAAA AAAAAAAAAA A
```

Seq ID NO: 207 Protein sequence
Protein Accession #: NP_057445.1

```
1           11          21          31          41          51
|           |           |           |           |           |
MRLWTPVGVL TSLAYCLHQR RVALAELQEA DGQCPVDRSL LKLKMVQVVF RHGARSPLKP    60
LPLEEQVEWN PQLLEVPPQT QFDYTVTNLA GGPKPYSPYD SQYHETTLKG GMFAGQLTKV   120
GMQQMFALGE RLRKNYVEDI PFLSPTFNPQ EVFIRSTNIF RNLESTRCLL AGLFQCQKEG   180
PIIIHTDEAD SEVLYPNYQS CWSLRQRTRG RRQTASLQPG ISEDLKKVKD RMGIDSSDKV   240
DFFILLDNVA AEQAHNLPSC PMLKRFARMI EQRAVDTSLY ILPKEDRESL QMAVGPFLHI   300
LESNLLKAMD SATAPDKIRK LYLYAAHDVT FIPLLMTLGI FDHKWPPFAV DLTMELYQHL   360
ESKEWFVQLY YHGKEQVPRG CPDGLCPLDM FLNAMSVYTL SPEKYHALCS QTQVMEVGNE   420
E
```

Seq ID NO: 208 DNA sequence
Nucleic Acid Accession #: CAT cluster

```
1           11          21          31          41          51
|           |           |           |           |           |
TTTGAGGGGG TGGTGGGGCG AGTTTAATTC ATAAAGAAGC CTCCTGATCA GAAAGGGGCC    60
TAACAGCCTG CCCTTGGAGA GAAGTCCTTC CTTGAGGATA AGGCCTCCCA GGGGAGGAGG   120
TGCTGGGGGC CAGTGTTAGG CTTCAGGCCA TCCCTGGAGG CCAGTCCTGT GCTCAGCAAG   180
TAGTGGCAGA GCCTGGAGTG ATGAGTGGGA TGGCCTTCTC AGGTACAGGA CTGTGCTGCT   240
TCTGGCTGCT CTTGCATTTG CATTTGCCAC TCAGAACTGC CGCGATCCCA GCAATGGCCA   300
GGAGCCCTCC GCAGATCAGT CCGCTCAGCT GCAGGTTTTT CCAGTCATAG TAGAAGGGAT   360
CGTCTTTATT GGCAAATGGG TCATTGGCTT CCAAGGCAGT CAGGCCAACT GTGTGACTCT   420
GCAGGTTCCT CACTGCTCCT TCACCAGTGT CCTGCGAGGT CACCTTGGCG AGGGCTCACC   480
TGAGCTGGCA GCGCAG
```

Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..564

```
1           11          21          31          41          51
|           |           |           |           |           |
ATGGAGCCCT GGGCGTGGCT GCAGGGTTTA AAGAGCCGAC CCACGTGCCC AGCAGCCTCC    60
TCAGATCCGT TCTCTGCGCT GCCAGCTCAG GACACTGGTG AAGGAGCAGT GAGGAACCTG   120
CAGAGTCACA CAGTTGGCCT GACTGCCTTG GAAGCCAATG ACCCATTTGC CAATAAAGAC   180
GATCCCTTCT ACTATGACTG GAAAAACCTG CAGCTGAGCG GACTGATCTG CGGAGGGCTC   240
CTGGCCATTG CTGGGATCGC GGCAGTTCTG AGTGGCAAAT GCAAATGCAA GAGCAGCCAG   300
AAGCAGCACA GTCCTGTACC TGAGAAGGCC ATCCCACTCA TCACTCCAGG CAGATTTCTC   360
ACCTTGGCCA AATCAAATAA ACCTTTATCT CCAAGCACCT TTGTCTTGGT GTTTGGCATC   420
AGCTACACAT CAGTCTTCCG AGTGCCTCTT TCTGCGTCCC TGTACCCTGC CATTCCTGGT   480
GATGCTGCTG CCCTCACATC AGGCCATCCA AGCATGCAGA ACATAAGCAT GCAGAACACT   540
GGAACGAAGG GCTGTACCTA ATGA
```

Seq ID NO: 210 Protein sequence
Protein Accession #: FGENESH predicted

```
1           11          21          31          41          51
|           |           |           |           |           |
MEPWAWLQGL KSRPTCPAAS SDPFSALPAQ DTGEGAVRNL QSHTVGLTAL EANDPFANKD    60
DPFYYDWKNL QLSGLICGGL LAIAGIAAVL SGKCKCKSSQ KQHSPVPEKA IPLITPGRFL   120
```

TLAKSNKPLS PSTFVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSGHP SMQNISMQNT 180
GTKGCT

Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..318

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCCGGCC ACCCCGTCTG TGAAGTGAGG AGCACCTCTG CCCGGCTGCC CCGTCTGGGA   60
AGTGAGGAGC GCCTCTGCCC GGCTGCCACC CCGTCTGTGA GTGCCTGCTG CGCTGGGCCC  120
AGGCCGCCCG TGCCCTGCCA GGCCCTCCGG CCCCCCACCT TCCACCCCAG GGCCTGCTCC  180
TCACCCCAGG GTTCCATCTC CCTAGTTTCC ACCAGAGACT GGGTCTTCAT TCTCACCCTG  240
CTACACAGCC CCTACCAGAA CCTTCTGAAA TGCAAACCTA ACAACTGTCT CACCCCAGCA  300
GGAAACTCCC CAGGGTCCCG GGCCCCCTGC GGGGTTGCAG GCCTCACTCT TCGCGCCCAT  360
CCCTCCGCCC TGACCGCCCT GAGCTCGCCC CCAGTGCTGG CCCTTCACGT CCAGTTATCC  420
CTCCCAGCCT CCAAGGTCCC CGTTACCGAA GACCGCCACC ATCACGACAT AGCGCAGCAC  480
ATATGGGACA CTGGTGAAGG AGCAGTGAGG AACCTGCAGA GTCACACAGT TGGCCTGACT  540
GCCTTGGAAG CCAATGACCC ATTTGCCAAT AAAGACGATC CCTTCTACTA TGACTGGAAA  600
AACCTGCAGC TGAGCGGACT GATCTGCGGA GGGCTCCTGG CCATTGCTGG GATCGCGGCA  660
GTTCTGAGTG GCAAATGCAA ATGCAAGAGC AGCCAGAAGC AGCACAGTCC TGTACCTGAG  720
AAGGCCATCC CACTCATCAC TCCAGGCAGA TTTCTCACCT TGGCCAAATC AAATAAACCT  780
TTATCTCCAA GCACCTTTGT CTTGGTGTTT GGCATCAGCT ACACATCAGT CTTCCGAGTG  840
CCTCTTTCTG CGTCCCTGTA CCCTGCCATT CCTGGTGATG CTGCTGCCCT CACATCAGGC  900
CATCCAAGCA TGCAGAACAT AAGCATGCAG AACACTGGAA CGAAGGGCTG TACCTAA
```

Seq ID NO: 212 Protein sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGHPVCEVR STSARLPRLG SEERLCPAAT PSVSACCAGP RPPVPCQALR PPTFHPRACS   60
SPQGSISLVS TRDWVFILTL LHSPYQNVLK CKPNNCLTPA GNSPGSRAPC GVAGLTLRAH  120
PSALTALSSP PVLALHVQLS LPASKVPVTE DRHHHDIAQH IWDTGEGAVR NLQSHTVGLT  180
ALEANDPFAN KDDPFYYDWK NLQLSGLICG GLLAIAGIAA VLSGKCKCKS SQKQHSPVPE  240
KAIPLITPGR FLTLAKSNKP LSPSTFVLVF GISYTSVFRV PLSASLYPAI PGDAAALTSG  300
HPSMQNISMQ NTGTKGCT
```

Seq ID NO: 213 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1758

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGATGGGGT CTCATGTTGC CCAGGCTGGT CTTGAACTCC TGGGCTCGAG TGACCCTCCT   60
GCCTTGGCCT CCGAAAGTGC TGGGATTACA GGACTGTTAT TACAGGAATC CATAACACTG  120
GAGGATGTGG CTGTGGACTT CACTTGGGAG GAGTGGCAAC TCCTGGGCGC TGCTCAGAAG  180
GACCTGTACC GGGATGTGAT GTTGGAGAAC TACAGCAACC TGGTGGCAGT GGGGTATCAA  240
GCCAGCAAAC CGGATGCACT CTTCAAGTTG GAACAAGGAG AACAACTGTG GACAATTGAA  300
GATGGAATCC ACAGTGGAGC CTGTTCAGGT TCTCCAAAGG TCCCGTTCTC CATTTTCTCA  360
TCTGTGCCCT TCACTCTTCA AAATTGCCTT CATTCTAACA TATGGAAAGT TGATCATGTG  420
CTGGAGCGCT TGCAGAGTGA AAGCCTGGTG AACAGAAGGA AACCATGTCA TGAACATGAT  480
GCATTTGAAA ATATTGTTCA TTGCAGCAAA AGTCAGTTTC TGTTAGGGCA AAATCATGAT  540
ATATTTGACT TACGTGGAAA AAGTTTGAAA TCCAATTTAA CTTTAGTTAA CCAGAGCAAA  600
GGCTATGAAA TAAAGAACTC TGTTGAGTTT ACTGGAAATG GGGACTCCTT TCTTCATGCT  660
AACCATGAAC GACTTCATAC TGCAATTAAA TTCCCTGCAA GTCAAAAACT CATCAGCACT  720
AAGTCCCAAT TCATCAGTCC CAAGCATCAG AAAACACGAA AATTAGAGAA GCATCATGTG  780
TGCAGTGAAT GTGGGAAAGC CTTCATCAAG AAGTCTTGGC TAACTGATCA CCAGGTAATG  840
CATACAGGAG AGAAACCCCA CAGATGTAGT CTATGTGAGA AAGCCTTCTC CAGAAAGTTC  900
ATGCTTACTG AACATCAGCG AACTCATACA GGAGAAAAAC CTTATGAATG CCCTGAATGT  960
GGCAAAGCCT TTCTCAAGAA ATCACGGCTC AACATACATC AGAAAACACA TACCGGAGAG 1020
AAACCCTATA TATGCAGTGA ATGTGGAAAA GGCTTCATCC AGAAAGGAAA TCTCATTGTA 1080
CACCAGCGAA TTCATACAGG TGAGAAACCT TATATATGCA ATGAATGTGG AAAAGGCTTC 1140
ATTCAGAAGA CGTGTCTCAT AGCACATCAG AGATTTCACA CAGGAAAGAC GCCCTTTGTG 1200
TGCAGTGAAT GTGGAAAATC CTGTTCTCAG AAATCAGGTC TCATTAAACA TCAAAGAATT 1260
CACACAGGAG AGAAACCCTT TGAATGTAGT GAATGTGGGA AAGCCTTTAG CACAAAGCAA 1320
AAGCTCATTG TCCATCAAAG GACTCATACA GGAGAGAGAC CCTATGGCTG TAACGAGTGT 1380
GGGAAAGCGT TTGCGTATAT GTCGTGTCTG GTTAAGCATA AGAGAATACA CACAAGGGAG 1440
AAACAAGAGG CAGCCAAGGT GGAAAATCCT CCTGCAGAGA GGCACAGCTC ATTACACACC 1500
AGTGATGTCA TGCAGGAGAA AAACTCTGCT AACGGGGCGA CTACACAAGT GCCTTCTGTG 1560
GCCCCTCAGA CATCATTAAA CATCAGCGGC CTCCTCGCAA ACAGGAACGT AGTCCTTGTG 1620
GGACAGCCAG TGGTCAGATG TGCAGCCTCA GGAGATAACA GAGGATTTGC ACAGGACAGA 1680
AACCTTGTGA ATGCAGTGAA TGTGGTTGTG CCTTCCGTGA TCAATTATGT CTTATTTTAT 1740
GTTACAGAAA ACCCATAG
```

Seq ID NO: 214 Protein sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MMGSHVAQAG LELLGSSDPP ALASESAGIT GLLLQESITL EDVAVDFTWE EWQLLGAAQK   60
DLYRDVMLEN YSNLVAVGYQ ASKPDALFKL EQGEQLWTIE DGIHSGACSG SPKVPFSIFS  120
SVPFTLQNCL HSNIWKVDHV LERLQSESLV NRRKPCHEHD AFENIVHCSK SQFLLGQNHD  180
IFDLRGKSLK SNLTLVNQSK GYEIKNSVEF TGNGDSFLHA NHERLHTAIK FPASQKLIST  240
```

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KSQFISPKHQ KTRKLEKHHV CSECGKAFIK KSWLTDHQVM HTGEKPHRCS LCEKAFSRKF   300
MLTEHQRTHT GEKPYECPEC GKAFLKKSRL NIHQKTHTGE KPYICSECGK GFIQKGNLIV   360
HQRIHTGEKP YICNECGKGF IQKTCLIAHQ RFHTGKTPFV CSECGKSCSQ KSGLIKHQRI   420
HTGEKPFECS ECGKAFSTKQ KLIVHQRTHT GERPYGCNEC GKAFAYMSCL VKHKRIHTRE   480
KQEAAKVENP PAERHSSLHT SDVMQEKNSA NGATTQVPSV APQTSLNISG LLANRNVVLV   540
GQPVVRCAAS GDNRGFAQDR NLVNAVNVVV PSVINYVLFY VTENP
```

Seq ID NO: 215 DNA sequence
Nucleic Acid Accession #: NM_032190.1
Coding sequence: 502..1332

```
1          11         21         31         41         51
|          |          |          |          |          |
GATTCCGTGT TCTTGGCCAT GTTAGCCATA ATATCCTGTG CAGTATGTTT TTCCTGTGCA    60
GAGGCAAAAA CATATTGGGC ATATGTTCCC AAGCCCCCAG CAGTATGACC CATACTTTGG   120
AGTGACACTC CTCCTAAGAT TTATCATGAT TAAGGAGCAT GGGCTCCAGG ACCCCTAACT   180
CCACCTGACA TAGAACAGTT AGACTCTCAG AATAATGTCA TTAATTATAC CGCTCCATTG   240
GAAGGACTTC CTTTGTGTGT CACCACAAAG ACATCACTCA GCCATAGCTG TCTTACAGTT   300
CAAGCTCACA CATGGTTGAG TCACTATGGG AAAATCATGT ACTTATTAAG TCTTGGTTAT   360
ATTAATGTAA CCGGTGTGCT AACCAACCAT TCCTGGCCCA ATCGCCTTCA TTGTGCTGAC   420
TATACAGAAT GGATTCCCTT CAATAGTTCC TACCCCCCTC CATAGACCCA GTGTCTTGGC   480
CCACTGGCTA GAAAACAATC TATGTTAACT GGAGACATTG TGGATTGGGG ACCTAAAGGC   540
CAATTAGATG GAAAAGAAGA AAATCAGAAA TCGTGGCACA AACTTTGCTG GCATTGGTGG   600
CAAGCTTTTA ATGCTTCTTC TTTATATAAC ACTGGGATCC AATCCCAGTC GGCCGCCCAG   660
ATTGCTTGGC ATGGAGCAGG CTTTAGCCCG CCTCTTCCTC AGTGGCATTA TCTAGGGAGG   720
AAAGGACCAA TTCAAAAGAT GATATGGAAG GCAGCATTCC CATTTATGAA TGGCAACATC   780
TGGGTTGCCA TAATACTATC CAATAATAGC AATAGTAAGC AACACAGTCT TAATGTTACA   840
TTTGTAAAGA ATATCACCAC TCAATTTACA GTTTGTGTTT TTAATCCTTA TGTGTTTTTG   900
GCAGCTAAGA AGGACCAGCT CCAGGTAAAC AATACCCAAT TGACCTGTAA ATCTTGCCAG   960
TTATATCACT GCATTAATCA TAGCACATTG CAAACACATA ATATCTCTAC TTTGATGATT  1020
TTAGGTTGCA TCCCTGGGCT ATGGATTCCT GTTAATCTGT CTGAGCCATG GGCTGCCACA  1080
ATTGCTTTAC ATTTTGTGAA ACTTCTTCTA ACTCAGTTTA CTCATTGTGT CCGTAGAGGC  1140
TTAGGCATGA TAATTTTTGC TATTGTTTAC TTCGTCACAC TAATAATTTC TGTTGTGATG  1200
TCCTCTGTAG CTTTGCATAG TTCTATTCAA ACAGCTCAGT ATGTGGAGAA CTGGACACGC  1260
ACAGTCAACC AAGGGTGGCT ACTTGAGAAT AAAATTAACA CTGAGTTACA AACTGAAGTG  1320
GCAGTGTTAT AATCCACGAT TCTATGGTTA GGGGAACAAG TACAAAGCTT GCAATTGCAG  1380
CAGTAATTGT GTTGTCATTT TAATCACACT CATATTTGTG TAACCAACTT AGAATATAAC  1440
CAAAGTGAGT ATCCATGGGA TCTTGTGAAA GCCCATTTGC AGGGAGCTTT CACATCCGAC  1500
ATCACCTTTG ATATTGGTGA ATTACAAAAC AAAATTCTTG ATTTAAATAA ACAAATTCCA  1560
GAGTTTCAGC CTTCTTTAGA AGACTGGACT GAATTCCAGC AAGGCCTGGA GAGCGTCAAC  1620
CCTTGGACCT ATCTAAAGCA CCACATTAAC ATCTTATATA TAGTTCTTGG AATAATGTTG  1680
TTTTGTCTCT GTCTTCTGTT CATAGTCTGT AAAATCGGAT GGACTGCCAA TCGGAGAATG  1740
AAAGCTACCC AGCCTGGCCT TACATTCTTT CACTTAATAC ATAAACAAGA AGGGGGAAAT  1800
GTTGGGAGCC AAAAAGGCCA AAGGGATGGT GACCAACTCA GCATTCCACT GGAGGCTACA  1860
TGATCAAACA GCAAACTGTT TATCATGAAT ACAGAATGTG GGCAAACTCG CTTCTGTGCC  1920
TGCCCAGAAG GTTTGCTGAG GGCCATCGCT CCCTGGCCCC GGCTCCTTGA GGTTATCTAC  1980
TGGGACATCT AGAGCCTATT GTTCGAGGAA TGCAGTCTTG CAAGCCTACT CTGGACCGAG  2040
CAGCTGACCT CTTCTTCCAC ACCCCTTCTC ACTATCTCTT TTGCCTAATA AATATGGAGG  2100
GCTGTGTAAA GCTCAGGGCC CTTGTCCACT AGAGGCAAGG TGTCCCCTGA CCCTTCTTCC  2160
AAACAT
```

Seq ID NO: 216 Protein sequence
Protein Accession #: NP_115566.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLTGDIVDWG PKGQLDGKEE NQKSWHKLCW HWWQAFNASS LYNTGIQSQS AAQIAWHGAG    60
FSPPLPQWHY LGRKGPIQKM IWKAAFPFMN GNIWVAIILS NNSNSKQHSL NVTFVKNITT   120
QFTVCVFNPY VFLAAKKDQL QVNNTQLTCK SCQLYHCINH STLQTHNIST LMILGCIPGL   180
WIPVNLSEPW AATIALHFVK LLLTQFTHCV RRGLGMIIFA IVYLVTLIIS VVMSSVALHS   240
SIQTAQYVEN WTRTVNQGWL LENKINTELQ TEVAVL
```

Seq ID NO: 217 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1566

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGTGAACC CCAAATCCAC TTCCTCCCTC TTCAGGTTAT GTTTTTTGCT CCTGAGGAGT    60
CAGAACCTGT GGGTTGAAGA GCAAATTCAA TGCAAAAACA TATTGGGCAT ATGTTCCCAA   120
TCCCCCAGCA GTATGGCCTA TACTTTGGAG CTCACTCCTC CTGAGATTTA TCACGATCAG   180
GGAGAGTGGG CTCCAGGACC CCTAACTCCC CGTGACATAG AAAAGTTAGA CTCTCAGAAC   240
AATGTCATTA ATTATACCAC TCCACTGGAA GGACTCCCTT TGTTTATCAC CACAAAGACG   300
TCGCTCAGCC ATAGCTGTCT TGCAATTCAA GCTCAAACAT GGTTGAGTCA CTATGGAAAA   360
ATTATGTACT TATTAGGTCT TGGTTCTATT AATGTAACTG GTGTGCTAAC CAATCATTCC   420
CAGTCCAGTC ACCCTAATTG TGCTGATTAT ACAGAATGGA TTCCATTCAA TAGTTCCTAC   480
CCCACTCTGT GGACCCAGTG TCTTGATCCA CTGGCTAGTA AACAATATAT GTCAACTGAA   540
GACACTGTGG ATTGGGAACC TAAAGGTCAA TTAGATGGAA AAGGTGAAAG TCAGAAATCA   600
TGGCACAAAC TTCACTGGCA TTGGCGGCAA GCTTTTAATG CTTCTTCTTT ATACAACAGC   660
AGAATCCAAT CCCAGTCTGC TGCTCAGATT GCTTGGCATG GAGCAGGCTT TAGCCCACCT   720
CTTCCTCAGT TGCATTATCT GGGGAGGAAA GGACCAATTC AAGAAACTAT ATGGAAGGCA   780
GCACTCCCAT TTATGAATGG CAACATCTGG ATTGGAACAC TGTCTAATAA TAGCAATAGT   840
AAGCAACACA GTCTTAATGT TGCATTTGTA AAGAATATCA CCACTCAGTT TACAGTTTGT   900
GTTTTTAATC CTTATGCCTT TTTGGCAGCT AAGAAGAACC AGCTTCAGGT GGAGAACTGG   960
```

```
ACACGCACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT  1020
GAAGTGGCAA TGTTGAAATC CATGGTTCTG TGGTTAGGAG AACAGGTACA AAGCTTGCAG  1080
TTGCAGCAGC AATTGCGTCA TCATTTTAAT CACATTCATA TTTGCGTAAC TAACTCAGAA  1140
TATAACCAAA GTGAGTATCC GTGGGACCTT GTGAAAGCCC ATTTGCAAGG AGCTTTCACA  1200
TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAACAAAA TTATTGATTT AAATAGGCAA  1260
ACTCAAGAAT TTCAGCCTTC TTTAGAAGAC TGGACCGAAT TCCAGGAAGG CCTGGAGAGC  1320
CTCAACCCTT GGACCTATCT AAGGCACCAC ATTAACATCT TATATGTAGT TCTTGGAATA  1380
ATGTTGTTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG  1440
AGAATGAGAG CCTCCCAGCC CAGCCTTACA TTCTTTCAAT TAATACATAA ACAGAAAGGG  1500
GGATATGCAG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATTCT GCTGGAGGCT  1560
ATATGA
```

Seq ID NO: 218 Protein sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MVNPKSTSSL FRLCFLLLRS QNLWVEEQIQ CKNILGICSQ SPSSMAYTLE LTPPEIYHDQ    60
GEWAPGPLTP RDIEKLDSQN NVINYTTPLE GLPLFITTKT SLSHSCLAIQ AQTWLSHYGK   120
IMYLLGLGSI NVTGVLTNHS QSSHPNCADY TEWIPFNSSY PTLWTQCLDP LASKQYMSTE   180
DTVDWEPKGQ LDGKGESQKS WHKLHWHWRQ AFNASSLYNS RIQSQSAAQI AWHGAGFSPP   240
LPQLHYLGRK GPIQETIWKA ALPFMNGNIW IGTLSNNSNS KQHSLNVAFV KNITTQFTVC   300
VFNPYAFLAA KKNQLQVENW TRTADQARLL QNKINTELQT EVAMLKSMVL WLGEQVQSLQ   360
LQQQLRHHFN HIHICVTNSE YNQSEYPWDL VKAHLQGAFT SNITFDIGEL QNKIIDLNRQ   420
TQEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLFCLCLRFI VCKIGWTTNW   480
RMRASQPSLT FFQLIHKQKG GYAGSQRPVG RDQLSILLEA I
```

Seq ID NO: 219 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..900

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC    60
CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC   120
GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC   180
CGGCCCACTG CGCTGGACAC CTTCTCTGGT ACGTACGTTC AATCGCCCGT GCGGCCGCGT   240
GGCTGCGGCG GGGCTGTGCA CCGGGGAGCT GGGGCGGGCG TCTCGGCGGG AGGGCGCAGA   300
GGACCCCGGG GAGGAGACTG GAGCAGGCCC CGAGGTGGCG CTGGTGCGGC CCAGGACGCT   360
CTTCCTAACT CAGGCTCTCC CCGCCCCGCC CCTGCAGTGC AAGTCCTGGT GGATGGAGCT   420
CCGGTGCGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTTCC   480
CTTTGCTACC CGGATACCGA TGTCTTCCTG GCGTGCTTCA GCGTGGTGCA GCCCAGCTCC   540
TTTCAAAACA TCACAGAGAA ATGGCTGCCC GAGATCCGCA CGCACAACCC CCAGGCGCCT   600
GTGCTGCTGG TGGGCACCCA GGCCGACCTG AGGGACGATG TCAACGTACT AATTCAGCTG   660
GACCAGGGGG GCCGGGAGGG CCCCGTGCCC CAACCCCAGG CTCAGGGTCT GGCCGAGAAG   720
ATCCGAGCCT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAGTA   780
TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT   840
GCCAAAGGTG TGCGCACCCT CTCCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCGTTTGA
```

Seq ID NO: 220 Protein sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY    60
RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA   120
LPNSGSPRPA PAVQVLVDGA PVRIELWDTA GQEDFDRLRS LCYPDTDVFL ACFSVVQPSS   180
FQNITEKWLP EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGPVP QPQAQGLAEK   240
IRACCYLECS ALTQKNLKEV FDSAILSAIE HKARLEKKLN AKGVRTLSRC RWKKFFCFV
```

Seq ID NO: 221 DNA sequence
Nucleic Acid Accession #: XM_063832.2
Coding sequence: 1..711

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC    60
CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC   120
GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC   180
CGGCCCACTG CGCTGGACAC CTTCTCTGTG CAAGTCCTGG TGGATGGAGC TCCGGTGCGC   240
ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTC CCTTTGCTAC   300
CCGGATACCG ATGTCTTCCT GGCGTGCTTC AGCGTGGTGC AGCCCAGCTC CTTTCAAAAC   360
ATCACAGAGA AATGGCTGCC CGAGATCCGC ACGCACAACC CCCAGGCGCC TGTGCTGCTG   420
GTGGGCACCC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTCAGCT GGACCAGGGG   480
GGCCGGGAGG GCCCCGTGCC CCAACCCCAG GCTCAGGGTC TGGCCGAGAA GATCCGAGCC   540
TGCTGCTACC TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG   600
GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAAACTGAA TGCCAAAGGT   660
GTGCGCACCC TCTCCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTCGTTTG A
```

Seq ID NO: 222 Protein sequence
Protein Accession #: XP_063832.1

```
1          11         21         31         41         51
|          |          |          |          |          |
```

```
MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY    60
RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLRSLCY PDTDVFLACF SVVQPSSFQN   120
ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQPQ AQGLAEKIRA   180
CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAKG VRTLSRCRWK KFFCFV
```

Seq ID NO: 223 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1161

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG    60
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT   120
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCTGGAAA   180
TCCAGCCGGA TTTTCCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG   240
CCGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA AGTTTGGGGA CATCCCTTGC   300
CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG   360
GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC   420
AATTGGACAG CAGCCATCAT CTCTTGCCTT CTGTGGGGCA TCACTGTTGG CCTAACAGTC   480
CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC   540
AGCATCTGCC ATACCTTCCG GTGGCACGAA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC   600
CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GACACAAATG   660
GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT   720
GTCATCTGCT TCCTTCCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT   780
TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC   840
AGCTTCACCT ACATGAACAG CATGCTGGAC CCCGTGGTGT ACTACTTCTC CAGCCCATCC   900
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG   960
CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC  1020
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCCTCTTA TCTGGGCCCA  1080
ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTCACCAAG AACCAGCATC TCTGGAGAAA  1140
CAGTTGGGAT GTTGCATCGA G
```

Seq ID NO: 224 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MNRHHLQDHF LEIDKKNCCV FRDDFIAKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK    60
SSRIFLFNLA VADFLLIICL PFVMDYYVRR SDWKFGDIPC RLVLFMFAMN RQGSIIFLTV   120
VAVDRYFRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKKLLIQ NGPANVCISF   180
SICHTFRWHE AMFLLEFLLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF   240
VICFLPSVVV RIRIFWLLHT SGTQNCEVYR SVDLAFFITL SFTYMNSMLD PVVYYFSSPS   300
FPNFFSTLIN RCLQRKMTGE PDNNRSTSVE LTGDPNKTRG APEALMANSG EPWSPSYLGP   360
TSNNHSKKGH CHQEPASLEK QLGCCIE
```

Seq ID NO: 225 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1092

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG    60
TTCCGAGATG ACTTCATTGT CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTC   120
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCTGGAAA   180
TCCAGCCGGA TTTTCCTGTT CAACCTGGCA GTGGCTGACT TTCTACTGAT CATCTGCCTG   240
CCCTTCCTGA TGGACAACTA TGTGAGGCGT TGGGACTGGA AGTTTGGGGA CATCCCTTGC   300
CGGCTGATGC TCTTCATGTT GGCTATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG   360
GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC   420
AATCGGACAG CAGCCATCAT CTCTTGCCTT CTGTGGGGCA TCACTATTGG CCTGACAGTC   480
CACCTCCTGA AGAAGAAGAT GCCGATCCAG AATGGCGGTG CAAATTTGTG CAGCAGCTTC   540
AGCATCTGCC ATACCTTCCA GTGGCACGAA GCCATGTTCC TCCTGGAGTT CTTCCTGCCC   600
CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG   660
GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT   720
GTCATCTGCT TCCTTCCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT   780
TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC   840
AGCTTCACCT ACATGAACAG CATGCTGGAC CCCGTGGTGT ACTACTTCTC CAGCCCATCC   900
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG   960
CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC  1020
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCCTCTTA TCTGGGCCCA  1080
```

Seq ID NO: 226 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MNRHHLQDHF LEIDKKNCCV FRDDFIVKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK    60
SSRIFLFNLA VADFLLIICL PFLMDNYVRR WDWKFGDIPC RLMLFMLAMN RQGSIIFLTV   120
VAVDRYFRVV HPHHALNKIS NRTAAIISCL LWGITIGLTV HLLKKKMPIQ NGGANLCSSF   180
SICHTFQWHE AMFLLEFFLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF   240
VICFLPSVVV RIRIFWLLHT SGTQNCEVYR SVDLAFFITL SFTYMNSMLD PVVYYFSSPS   300
FPNFFSTLIN RCLQRKMTGE PDNNRSTSVE LTGDPNKTRG APEALMANSG EPWSPSYLGP   360
TSP
```

Seq ID NO: 227 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 61..1224

```
1          11         21         31         41         51
|          |          |          |          |          |
CGCCACTTTG CTGGAGCATT CACTAGGCGA GGCGCTCCAT CGGACTCACT AGCCGCACTC    60
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG   120
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT   180
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCTGGAAA   240
TCCAGCCGGA TTTTCCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG   300
CCGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC   360
CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG   420
GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC   480
AATTGGACAG CAGCCATCAT CTCTTGCCTT CTGTGGGGCA TCACTGTTGG CCTAACAGTC   540
CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC   600
AGCATCTGCC ATACCTTCCG GTGGCACGAA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC   660
CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG   720
GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT   780
GTCATCTGCT TCCTTCCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT   840
TCGGGCACGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC   900
AGCTTCACCT ACATGAACAG CATGCTGGAC CCCGTGGTGT ACTACTTCTC CAGCCCATCC   960
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG  1020
CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC  1080
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCCTCTTA TCTGGGCCCA  1140
ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTCACCAAG AACCAGCATC TCTGGAGAAA  1200
CAGTTGGGCT GTTGCATCGA GTAATGTCAC TGGACTCGGC CTAAGGTTTC CTGGAACTTC  1260
CAGATTCAGA GAATCTGATT TAGGGAAACT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG  1320
GTGTGACCAC AGGAATCCTG GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAAACTTGC  1380
TTCATCTCTG ACGCTCGCAG GACTGAAGAT GGGCAAATTG TAGGCGTTTC TGCTGAGCAG  1440
AGTTGGAGCC AGAGATCTAC TTGTGACTTG TTGGCCTTCT TCCCACATCT GCCTCAGACT  1500
GGGGGGGGCT CAGCTCCTCG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG  1560
GAGAGCTGAG ATTGGAGGGA ATTGTGTTGC TCCTGGAGGA AGCCCAGGCA TCATTAAACA  1620
AGCCAGTAGG TCACCTGGCT TCCGTGGACC AATTCATCTT TCAGACAAGC TTTAGAGAAA  1680
TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTTCCGG TGGGTGTAAT  1740
AGGGGATTAC CCCCAGAAGG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAAATGGCA  1800
TTGCTGCTTT CAACCAGCGA CTAATGCAAT CCATTCCTCT CTTGTTTATA GTAATCTAAG  1860
GGTTGAGCAG TTAAAACGGC TTCAGGATAG AAAGCTGTTT CCCACCTGTT TCGTTTTACC  1920
ATTAAAAGGG AAACGTGCCT CTGCCCCACG GGTAGAGGGG GTGCACGTTC CTCCTGGTTC  1980
CTTCGCTTGT GTTTCTGTAC TTACCAAAAA TCTACCACTT CAATAAATTT TGATAGGAGA  2040
CAAAAAAAAA A
```

Seq ID NO: 228 Protein sequence
Protein Accession #: NP_006009.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MNRHHLQDHF LEIDKKNCCV FRDDFIAKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK    60
SSRIFLFNLA VADFLLIICL PFVMDYYVRR SDWNFGDIPC RLVLFMFAMN RQGSIIFLTV   120
VAVDRYFRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKKLLIQ NGPANVCISF   180
SICHTFRWHE AMFLLEFLLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF   240
VICFLPSVVV RIRIFWLLHT SGTQNCEVYR SVDLAFFITL SFTYMNSMLD PVVYYFSSPS   300
FPNFFSTLIN RCLQRKMTGE PDNNRSTSVE LTGDPNKTRG APEALMANSG EPWSPSYLGP   360
TSNNHSKKGH CHQEPASLEK QLGCCIE
```

Seq ID NO: 229 DNA sequence
Nucleic Acid Accession #: NM_014398.1
Coding sequence: 64..1314

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCACCGATT CGGGGCCTGC CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC    60
ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG   120
CACGATGGCA GTCAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT   180
ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACCAGC TAAGCAAGCA   240
CCTCACCAAA CTTTAGCAGC AAGATTCATG GATGGTCATA TCACCTTTCA AACAGCGGCC   300
ACAGTAAAAA TTCCAACAAC TACCCCAGCA ACTACAAAAA ACACTGCAAC CACCAGCCCA   360
ATTACCTACA CCCTGGTCAC AACCCAGGCC ACACCCAACA ACTCACACAC AGCTCCTCCA   420
GTTACTGAAG TTACAGTCGG CCCTAGCTTA GCCCCTTATT CACTGCCACC CACCATCACC   480
CCACCAGCTC ATACAGCTGG AACCAGTTCA TCAACCGTCA GCCACACAAC TGGGAACACC   540
ACTCAACCCA GTAACCAGAC CACCCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC   600
ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAACGGC AGCTGCCCAC   660
AATACCACCC GCACAGCTGC ACCTGCCTCC ACGGTTCCTG GGCCCACCCT TGCACCTCAG   720
CCATCGTCAG TCAAGACTGG AATTTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA   780
GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA   840
TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC   900
AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA   960
TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC  1020
CAAGGAATCA AACATGCGGT GGTGATGTTC CAGACAGCAG TCGGGCATTC CTTCAAGTGC  1080
GTGAGTGAAC AGAGCCTCCA GTTGTCAGCC CACCTGCAGG TGAAAACAAC CGATGTCCAA  1140
CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCGTCTGAC  1200
TACACAATTG TGCTTCCTGT GATTGGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG  1260
GGTGTCTATA AAATCCGCCT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG  1320
CCCGGGGGGA ATGAAAATAA TGGAATTTAG AGAACTCTTT CATCCCTTCC AGGATGGATG  1380
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TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA  1440
AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT  1500
GTTTATTTTA TGAAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA  1560
GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA  1620
AGCCTTCAAA TTATAAACCA AGGGTCAATT GTAACTAATA CTACTGTGTG TGCATTGAAG  1680
ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCTTTG TTATCAAATG GACTTTCAGT  1740
GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA  1800
ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTTGAGAC GGAGTTTCAC TCTTGTCACC  1860
CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCCGCCTCC CGGGTTCAAG  1920
TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCACGCCTG  1980
GCTAATTTTT GTATTTTTAT TATAGACGGG TTTCACCATG TTGGCCAGAC TGGTCTTGAA  2040
CTCTTGACCT CAGGTGATCC ACCCACCTCA GCCTCCCAAA GTGCTGGGAT TACAGGCATG  2100
AGCCATTGCG CCCGGCCTTA AATGTTTTTT TTAATCATCA AAAAGAACAA CATATCTCAG  2160
GTTGTCTAAG TGTTTTTATG TAAAACCAAC AAAAAGAACA AATCAGCTTA TATTTTTTAT  2220
CTTGATGACT CCTGCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA  2280
CTAAACAATA AGCAAGAGAC AATAATAATG GCCCTTAATT ATTAACAAAG TGCCAGAGTC  2340
TAGGCTAAGC ACTTTATCTA TATCTCATTT CATTCTCACA ACTTATAAGT GAATGAGTAA  2400
ACTGAGACTT AAGGGAACTG AATCACTTAA ATGTCACCTG GCTAACTGAT GGCAGAGCCA  2460
GAGCTTGAAT TCATGTTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA  2520
CCTACAAGAA CAATGACACC ACACTCTGCC TGAAGGCTCA CACCTCATAC CAGCATACGC  2580
TCACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG  2640
AGCTTTGCAG ATAACAAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC  2700
TGAGGGGCTT TGTAAAACAT TAGTCAGTTG CTCATTTTTA TGGGATTGCT TAGCTGGGCT  2760
GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTTAA ATTTTTTTGA TAATAGAGAA  2820
ACTTCGCTAA CCAACTGTTC TTTCTTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC  2880
TTCTGCACTT CATATCCATA TTTCCTATTG TTCACTTTAT TCTGTAGAGC AGCCTGCCAA  2940
GAATTTTATT TCTGCTGTTT TTTTTGCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAC  3000
AGAAAAGTCC ACATAACCCT AGAATTCTTA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA  3060
CCATGTTGAC TTTCCTCATG TGTTTCCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT  3120
TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG
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Seq ID NO: 230 Protein sequence
Protein Accession #: NP_055213.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPRQLSAAAA LFASLAVILH DGSQMRAKAF PETRDYSQPT AAATVQDIKK PVQQPAKQAP    60
HQTLAARFMD GHITFQTAAT VKIPTTTPAT TKNTATTSPI TYTLVTTQAT PNNSHTAPPV   120
TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNTT QPSNQTTLPA TLSIALHKST   180
TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTGIYQV LNGSRLCIKA   240
EMGIQLIVQD KESVFSPRRY FNIDPNATQA SGNCGTRKSN LLLNFQGGFV NLTFTKDEES   300
YYISEVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTTDVQL   360
QAFDFEDDHF GNVDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRCQS SGYQRI
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Seq ID NO: 231 DNA sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

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1          11         21         31         41         51
|          |          |          |          |          |
TTCCTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG    60
CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC   120
TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC   180
TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC   240
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT   300
AAAGGACAAC GATGCCTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT   360
GAAAGAAAGA ATTTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA   420
AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG   480
AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT   540
GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA   600
CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT   660
GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTTGTATT ATACATTCAT   720
GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT   780
GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT   840
CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG   900
CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAAATACAC ACTTCTTTCC   960
CCAAATATCA TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT  1020
TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA  1080
TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT  1140
GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC  1200
TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTTGAAA  1260
TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTTGAAAAA TAAGCAAATG TATACCTAGC  1320
AATCACTTTT ACTTTTTGTA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT  1380
TTGTTCATGC CTATATACTG TAAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA  1440
GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTTCTTTT TTAAAAAAAA AAA
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Seq ID NO: 232 Protein sequence
Protein Accession #: NP_005400.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI    60
EVIITLKENK GQRCLNPKSK QARLIIKKVE RKNF
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Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: NM_000577.1
Coding sequence: 41..520

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGG GAAGACCTCC TGTCCTATCA GGCCCTCCCC ATGGCTTTAG AGACGATCTG    60
CCGACCCTCT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAACCA   120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAATGT   180
CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT   240
CCATGGAGGG AAGATGTGCC TGTCCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT   300
GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT   360
CATCCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCCGCCTGCC CCGGTTGGTT   420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG   480
CGTCATGGTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCCAG GCCTGCCTGT   540
TCCCATTCTT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCG   600
GCTATGGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA   660
CCTGGTCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG   720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCCTGCA CAAAGCCCTT CCATGTCGCC   780
TCTGCATTCA GGATCAAACC CCGACCACCT GCCCAACCTG CTCTCCTCTT GCCACTGCCT   840
CTTCCTCCCT CATTCCACCT TCCCATGCCC TGGATCCATC AGGCCACTTG ATGACCCCCA   900
ACCAAGTGGC TCCCACACCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT   960
TTTAAGGGTT TGTGGAAAAT GAAAATTAGG ATTTCATGAT TTTTTTTTTT CAGTCCCCGT  1020
GAAGGAGAGC CCTTCATTTG GAGATTATGT TCTTTCGGGG AGAGGCTGAG GACTTAAAAT  1080
ATTCCTGCAT TTGTGAAATG ATGGTGAAAG TAAGTGGTAG CTTTTCCCTT CTTTTTCTTC  1140
TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAAGTTAT GGTACTATGT TAGCCCCATA  1200
ATTTTTTTTT TCCTTTTAAA ACACTTCCAT AATCTGGACT CCTCTGTCCA GGCACTGCTG  1260
CCCAGCCTCC AAGCTCCATC TCCACTCCAG ATTTTTTACA GCTGCCTGCA GTACTTTACC  1320
TCCTATCAGA AGTTTCTCAG CTCCCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGGTTCTT  1380
TCTTCCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACTTGGAG  1440
ACTTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCCC ACCAGGCTGG GAGCTCTGCA  1500
GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG  1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAAGT TCCCTACTTC  1620
CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAAAAT GCCTAAAAAA AAAAAAAAAA  1680
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA
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Seq ID NO: 234 Protein sequence
Protein Accession #: NP_000568.1

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1          11         21         31         41         51
|          |          |          |          |          |
MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGPNVNLE EKIDVVPIEP    60
HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSENRK QDKRFAFIRS DSGPTTSFES   120
AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE
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Seq ID NO: 235 DNA sequence
Nucleic Acid Accession #: NM_001840.1
Coding sequence: 149..1567

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1          11         21         31         41         51
|          |          |          |          |          |
GGGGACTACG GAGAGCTCTG CAGGGAGCCG AGGCCCCCGC CCGGGCCAAG GGAGCTTCTG    60
TCCCGAGGAC CAGGGGATGC GAAGGGATTG CCCCCTGTGG GTCACTTTCT CAGTCATTTT   120
GAGCTCAGCC TAATCAAAGA CTGAGGTTAT GAAGTCGATC CTAGATGGCC TTGCAGATAC   180
CACCTTCCGC ACCATCACCA CTGACCTCCT GTACGTGGGC TCAAATGACA TTCAGTACGA   240
AGACATCAAA GGTGACATGG CATCCAAATT AGGGTACTTC CCACAGAAAT TCCCTTTAAC   300
TTCCTTTAGG GGAAGTCCCT TCCAAGAGAA GATGACTGCG GGAGACAACC CCCAGCTAGT   360
CCCAGCAGAC CAGGTGAACA TTACAGAATT TTACAACAAG TCTCTCTCGT CCTTCAAGGA   420
GAATGAGGAG AACATCCAGT GTGGGGAGAA CTTCATGGAC ATAGAGTGTT TCATGGTCCT   480
GAACCCCAGC CAGCAGCTGG CCATTGCAGT CCTGTCCCTC ACGCTGGGCA CCTTCACGGT   540
CCTGGAGAAC CTCCTGGTGC TGTGCGTCAT CCTCCACTCC CGCAGCCTCC GCTGCAGGCC   600
TTCCTACCAC TTCATCGGCA GCCTGGCGGT GGCAGACCTC CTGGGGAGTG TCATTTTTGT   660
CTACAGCTTC ATTGACTTCC ACGTGTTCCA CCGCAAAGAT AGCCGCAACG TGTTTCTGTT   720
CAAACTGGGT GGGGTCACGG CCTCCTTCAC TGCCTCCGTG GGCAGCCTGT TCCTCACAGC   780
CATCGACAGG TACATATCCA TTCACAGGCC CCTGGCCTAT AAGAGGATTG TCACCAGGCC   840
CAAGGCCGTG GTGGCGTTTT GCCTGATGTG GACCATAGCC ATTGTGATCG CCGTGCTGCC   900
TCTCCTGGGC TGGAACTGCG AGAAACTGCA ATCTGTTTGC TCAGACATTT TCCCACACAT   960
TGATGAAACC TACCTGATGT TCTGGATCGG GGTCACCAGC GTACTGCTTC TGTTCATCGT  1020
GTATGCGTAC ATGTATATTC TCTGGAAGGC TCACAGCCAC GCCGTCCGCA TGATTCAGCG  1080
TGGCACCCAG AAGAGCATCA TCATCCACAC GTCTGAGGAT GGGAAGGTAC AGGTGACCCG  1140
GCCAGACCAA GCCCGCATGG ACATTAGGTT AGCCAAGACC CTGGTCCTGA TCCTGGTGGT  1200
GTTGATCATC TGCTGGGGCC CTCTGCTTGC AATCATGGTG TATGATGTCT TTGGGAAGAT  1260
GAACAAGCTC ATTAAGACGG TGTTTGCATT CTGCAGTATG CTCTGCCTGC TGAACTCCAC  1320
CGTGAACCCC ATCATCTATG CTCTGAGGAG TAAGGACCTG CGACACGCTT TCCGGAGCAT  1380
GTTTCCCTCT TGTGAAGGCA CTGCGCAGCC TCTGGATAAC AGCATGGGGG ACTCGGACTG  1440
CCTGCACAAA CACGCAAACA ATGCAGCCAG TGTTCACAGG GCCGCAGAAA GCTGCATCAA  1500
GAGCACGGTC AAGATTGCCA AGGTAACCAT GTCTGTGTCC ACAGACACGT CTGCCGAGGC  1560
TCTGTGAGCC TGATGCCTCC CTGGCAGCAC AGGAAAAGAA TTTTTTTTTT TAAGCTCAAA  1620
ATCTAGAAGA GTCTATTGTC TCCTTGGTTA TATTTTTTTA ACTTTACCAT GCTCAATGAA  1680
AAGGTGATTG CCACATGTCA CTTATTTGCT TAGTTTCCGT TTGGGCTAAT CTTCCGGGGT  1740
TCGTAGGAAA CCTTT
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Seq ID NO: 236 Protein sequence
Protein Accession #: NP_001831.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKSILDGLAD TTFRTITTDL LYVGSNDIQY EDIKGDMASK LGYFPQKFPL TSFRGSPFQE    60
KMTAGDNPQL VPADQVNITE FYNKSLSSFK ENEENIQCGE NFMDIECFMV LNPSQQLAIA   120
VLSLTLGTFT VLENLLVLCV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF VYSFIDFHVF   180
HRKDSRNVFL FKLGGVTASF TASVGSLFLT AIDRYISIHR PLAYKRIVTR PKAVVAFCLM   240
WTIAIVIAVL PLLGWNCEKL QSVCSDIFPH IDETYLMFWI GVTSVLLLFI VYAYMYILWK   300
AHSHAVRMIQ RGTQKSIIIH TSEDGKVQVT RPDQARMDIR LAKTLVLILV VLIICWGPLL   360
AIMVYDVFGK MNKLIKTVFA FCSMLCLLNS TVNPIIYALR SKDLRHAFRS MFPSCEGTAQ   420
PLDNSMGDSD CLHKHANNAA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL
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Seq ID NO: 237 DNA sequence
Nucleic Acid Accession #: NM_016083.2
Coding sequence: 64..1482

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1          11         21         31         41         51
|          |          |          |          |          |
GATTGCCCCC TGTGGGTCAC TTTCTCAGTC ATTTTGAGCT CAGCCTAATC AAAGACTGAG    60
GTTATGAAGT CGATCCTAGA TGGCCTTGCA GATACCACCT TCCGCACCAT CACCACTGAC   120
CTCCTGTACG TGGGCTCAAA TGACATTCAG TACGAAGACA TCAAAGGTGA CATGGCATCC   180
AAATTAGGGT ACTTCCCACA GAAATTCCCT TTAACTTCCT TTAGGGGAAG TCCCTTCCAA   240
GAGAAGATGA CTGCGGGAGA CAACCCCCAG CTAGTCCCAG CAGACCAGGT GAACATTACA   300
GAATTTTACA ACAAGTCTCT CTCGTCCTTC AAGGAGAATG AGGAGAACAT CCAGTGTGGG   360
GAGAACTTCA TGGACATAGA GTGTTTCATG GTCCTGAACC CCAGCCAGCA GCTGGCCATT   420
GCAGTCCTGT CCCTCACGCT GGGCACCTTC ACGGTCCTGG AGAACCTCCT GGTGCTGTGC   480
GTCATCCTCC ACTCCCGCAG CCTCCGCTGC AGGCCTTCCT ACCACTTCAT CGGCAGCCTG   540
GCGGTGGCAG ACCTCCTGGG GAGTGTCATT TTTGTCTACA GCTTCATTGA CTTCCACGTG   600
TTCCACCGCA AAGATAGCCG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT CACGGCCTCC   660
CTCACTGCCT CCGTGGGCAG CCTGTTCCTC ACAGCCATCG ACAGGTACGT ATCCATTCAC   720
AGGCCCCTGG CCTATAAGAG GATTGTCACC AGGCCCAAGG CCGTGGTGGC GTTTTGCCTG   780
ATGTGGACCA TAGCCATTGC GATCGCCGTG CTGCCTCTCC TGGGCTGGAA CTGCGAGAAA   840
CTGCAATCTG TTTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT GATGTTCTGG   900
ATCGGGGTCA CCAGCGTACT GCTTCTGTTC ATCGTGTATG CGTACATGTA TATTCTCTGG   960
AAGGCTCACA GCCACGCCGT CCGCATGATT CAGCGTGGCA CCCAGAAGAG CATCATCATC  1020
CACACGTCTG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG CATGGACATT  1080
AGGTTAGCCA AGACCCTGGT CCTGATCCTG GTGGTGTTGA TCATCTGCTG GGGCCCTTTG  1140
CTTGCAATCA TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTAA GACGGTGTTT  1200
GCATTCTGCA GTATGCTCTG CCTGCTGAAC TCCACCGTGA ACCCCATCAT CTATGCTCTG  1260
AGGAGTAAGG ACCTGCGACA CGCTTTCCGG AGCATGTTTC CCTCTTGTGA AGGCACTGCG  1320
CAGCCTCTGG ATAACAGCAT GGGGGACTCG GACTGCCTGC ACAAACACGC AAACAATGCA  1380
GCCAGTGTTC ACAGGGCCGC AGAAAGCTGC ATCAAGAGCA CGGTCAAGAT TGCCAAGGTA  1440
ACCATGTCTG TGTCCACAGA CACGTCTGCC GAGGCTCTGT GAGCCTGATG CCTCCCTGGC  1500
AGCACAGGAA AAGAATTTTT TTTTTTAAGC TCAAAATCTA GAAGAGTCTA TTGTCTCCTT  1560
GGTTATATTT TTTTAACTTT ACCATGCTCA ATGAAAAGGT GATTGTCACC ATGATCACTT  1620
ATCAGTTTGC TAATGTTTCC ATAGTTTAGG TACTCAAACT CCATTCTCCA GGGGTTTACA  1680
GTGAAGAAAG CCTGTTGTTT AAGTGACTGA ACGATCCTTC AAAGTCTCAA TGAAATAGGA  1740
GGGAAACCTT TGGCTACACA ATTGGAAGTC TAAGAACCCA TGGAAAAATG CCATCAAATG  1800
AATAATGCCT TTGTAACCAC AACTTTCACT ATAATGTGAA ATGTAACTGT CCGTAGTATC  1860
AGAGATGTCC ATTTTTACAA GTTATAGTAC TAGAGATATT TTGTAAAATG TATTATGTCC  1920
TGTGACATGT GTATCAGTGT TTATGTGCTA TTAATATTTG TTTAGTTCAG CAAAACTGAA  1980
AGGTAGACTT TTATGAGAAC AATGGACAAG CAGTGGATAC GTGTCAATGT GTGCACTTTT  2040
TTTCTATATT ATTGCCCATG ATATAACTTT AGAAATAAAC CTTAATATTT CTTCAAATAT  2100
CTCTATTTAA TTTTGACACT GAAATAACCG TAAAGGTTTA TTTTTCTGTT ACCTCAACAA  2160
GAAGAATTTG AAGACTTCAA AATATTGAGC AGAATTCATT CATACTTAAA AATTTATTAG  2220
CCCTGCATTT TCATAGGAAG ACACATTATC TTCTGGACTA TAGCTGTTCT AATGGATTAT  2280
AATCAGAATG GAAGAGAGAA AGCATATTGA CTTTTTTTGA GCGACATCTC TGACTTTCTT  2340
TAGTCTTTAG CTATTACTGG ATCTCTTAAG ACAGCATGTG TTAATCTTAA TGTATATCGT  2400
TATCACTGTG CAGTTGCTGT TTACTTGAAT AGTATTGTGT TCCTATATTC CAGGTTTAAG  2460
TAGATTTCAT GCCTGGGTGG CCAAACAACA GTCTTCATTT TTTTTAATTG AAAAGAAGTA  2520
GTGTCTGGAT CAGTAAAATT ATACTGTGTG TGAGTGTGAA TATAAATGTG TGTATGTGTG  2580
TTTCTGTCCG TAACTGTTAC AGTAATGTCA TAAAGTGAGA AAACTGTGAC CAAGTATAAA  2640
CTTTTACCAC TTGCTGCACT CTTGCACATG GATTCAGTTT CTAAAATTGA GTTCTTCCTG  2700
TAATCTTGTT GATAAAAATA CTGACTCCAA CCATTCAAAA ATTTCACCCC ATCCCTCCTT  2760
AAGAGATTGG ATCAAGTATT ACTAAATTGA CCTTTAGGTA TTACACAAGA CCAGTGCTTA  2820
GCAAAAAATA ATGACAGGCA TCCAAGGAAG GGATGTATTT GTAGTGTTAT TGCCAGGAAA  2880
GGAGAGTACT TTGGTTTCTG AGCACCGAAT ATTGAGCAAT ATGTCAGTCA CTAAAAGGAA  2940
GACAGTTCTA CAGAAAAACA AATGGTAACA TTTTTCAATA GCGTGTGTAG ATAGTATGCA  3000
CTATATACAT CACGTTAAAG TAGGACTATC ACACCCAGCC CATGTGGCTA AAAAAGCTGA  3060
ATCAGACAGT GGATGAGACA CACAACGGCA GTGAAGAACC GATACACTTG GCATTGACGT  3120
CTAGCTATGC TGTATCTGTG CTTTGCCCAC ATGCCCTTGG TGACAGCTGA GCACCCAGCT  3180
CTGTCTTGGT AGGTTTGGGC TAAGGAACAA ATCTCTCCTT TGCTCGTGGT TAGCAAGATA  3240
CACTCAAGCA TGAAGATAAA CACAGCTGCT TTCTTCTTAC ACCCCGGTCT CATGCTCCTT  3300
AATGGCGCCA TGGGTGCTTG TTGGGCCTTT TTCCAGTAAG GAATGATATT GCTGAAGAAT  3360
CTACTTAACC CTGACAAATT TTAATTATAA TCTCTTCTTA TACAGATAAA ACATGACTCC  3420
TACAAGGCCC CAAGGTTTAC ATAGTCTGAA GTGAAGTACA GAGCTGGCAT CTATCTGGTG  3480
ATTTCTAGCT CTCGAGATAC CCAAGCAGCC TGATGGGGCA GTTCCCCTTC TTACGGTTCA  3540
CGCTCTAAGG CAGGATGTGG CTTATGAGAT ACTTTGCATT GTCTGTCTGC ACACCTTGAA  3600
TCTGCCTGCT GGCTCCCTTA CTTTACCTCT CTGTCATGTG CAGATGAAGG CTCAGGGTGC  3660
TAGAGGATTA GTAAGATCTC TTTCTAAAGA CAGGAGAGAT TATTTACAAG AAGAACTCAC  3720
CAGGGTTTAG TTTGCATTTA AGAATTGCCA GTCTTTTGTC CTGCATCATC TTGAACATTA  3780
ATCCACATGT TTCAGAGCTC ACCAGGCAGT ACCAATGCTC TTTTCACAGC TATGAAGAGC  3840
TAGAGAAATT CTTGTTATGG TAGAAAAATT TCACGGTTCA TTTTTGAAAC TGCATTTGTG  3900
CGTATGCAGT GTAGATTTTA TAGTGTGTTG TGCTTTCAAG ATCTAAATCA TATATAATAA  3960
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ATTAAGGGAC AATGGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA  4020
TCTGTGAAAT ATCATCACGT ATGTTATACA ACCTTCATTT AAAAAGGTTT AAAACTAGTT  4080
AGATTCACTT TGACACTTTT CATATCATTT CTTAACCCAA GTGACGAAAA CATTGTCCCC  4140
AATGAATATA CTCATTAGAA TTACCATTTG TTAATATCAC TCATTAATTA ACCCCATAAT  4200
TAGATCCATT AATTTAAATG ATTTAAATTT AAGTAAGTTT TATAAGGTCT GACATCAGAG  4260
GTATCTTACT TTCCTCTGAG GATGATGTAC TTGCCCTGAC CATGCATTTT ACCATCACAC  4320
ATGTTCAGAA AGGGCCAAAT TCCCAACCTG CTCATTTTTT TTTTTATCAG AGTCATGATG  4380
AATCAGTCCT AGAATGTTTC ATTTGCACAA GTAGGGCTGC CTCCAAGAGG AACCTCTGAT  4440
TTATTTTGTA TGAAATATAT GTGAAAGGAT ATGAATCTGA GAGATGCTGT AGACATCTGT  4500
CCTACACTTG AGATGATTTC CAAGCCTCTC TGGCACTTTG AGTTAAGTCT ATCTGGTATT  4560
AAATGCCAAG GACCTTTTGC TGCCTAAATC CACTCTGCAG GAAATAGGCC CAACCACCAG  4620
ATGAGAATTA GGCCCTGGAT GAGTAGCGCT ATAGTTACTG TCCTGTTGAT TAATTTCTGC  4680
CATTTCATGT CCATAAAAGA GACCACCCAT ATCATGCACA CAATTAGATT TCTCACACTC  4740
TAACTGTATA TTTGTATGAT ATTTTAAAAT CTCCTAAATG CTGGGCAATG GCTATTAACA  4800
ATTAATTGTC TTGCACTGGC CTTCTGATGA AATGTTAACA ATGCCTATTG TAATATAGAA  4860
AAAAACATTC TATCTACTGA TTTGGGCTGA ATGTATGTAA ATAGGTTTCT AAAAAGTCAG  4920
ATGTTTGAGC AGTGGCCTAC AAATCAGTAA TTTTCGGGTG GGAGAGTTTC TTTACATTGC  4980
CGTGGCATCT TAAAAGCTAT CTTCATGTAA ATTGACTGTA CTAGGCCTAC TGGGGATCAG  5040
AGTTCCCAAG AAAGGAAACC TTTTCTTGTA TCTGGATTCA AATTTATTTC CAATGTTTCA  5100
AGCGGGAAAC ATGACTCTTT ATTGTCTGTA AATCTAACAT TATTACTTTT CCTCTTAGAA  5160
GAATATTGTA TTGTTAGATG TTTGTTGAGC TGGTAACATC GTTGCAACCA CTGCAATATC  5220
TTCGTTAGTA ATCTGTATAA TACTTTGTAT ACAAGTACTG GTAAGATTGT TATTAAATGT  5280
AGCTTCAGTC ATTAAATTAC TATAGCAAAG TAGTACTTCT TCTGTAATAT TTACAATGTA  5340
TTAAGCCCAC AGTATATTTT ATTTCAATGT AATTAAACTG TTAACTTATT CAAAGAGAAA  5400
ACATCTCATC ATGTCTATTG TCCAAAGTTA CCTGGAATCA AATAAAAATT CTAGATTACC  5460
ATGAAGAACA TA
```

Seq ID NO: 238 Protein sequence
Protein Accession #: NP_057167.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKSILDGLAD TTFRTIITDL LYVGSNDIQY EDIKGDMASK LGYFPQKFPL TSFRGSPFQE    60
KMTAGDNPQL VPADQVNITE FYNKSLSSFK ENEENIQCGE NFMDIECFMV LNPSQQLAIA   120
VLSLTLGTFT VLENLLVLCV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF VYSFIDFHVF   180
HRKDSRNVFL FKLGGVTASL TASVGSLFLT AIDRYVSIHR PLAYKRIVTR PKAVVAFCLM   240
WTIAIAIAVL PLLGWNCEKL QSVCSDIFPH IDETYLMFWI GVISVLLLFI VYAYMYILWK   300
AHSHAVRMIQ RGTQKSIIIH TSEDGKVQVT RPDQARMDIR LAKTLVLILV VLIICWGPLL   360
AIMVYDVFGK MNKLIKTVFA FCSMLCLLNS TVNPIIYALR SKDLRHAFRS MFPSCEGTAQ   420
PLDNSMGDSD CLHKHANNAA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL
```

Seq ID NO: 239 DNA sequence
Nucleic Acid Accession #: NM_033181.1
Coding sequence: 17..1252

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAAGTCGA TCCTAGATGG CCTTGCAGAT ACCACCTTCC GCACCATCAC CACTGACCTC    60
CTGTACGTGG GCTCAAATGA CATTCAGTAC GAAGACATCA AAGGAGAATG AGGAGAACAT   120
CCAGTGTGGG GAGAACTTCA TGGACATAGA GTGTTTCATG GTCCTGAACC CCAGCCAGCA   180
GCTGGCCATT GCAGTCCTGT CCCTCACGCT GGGCACCTTC ACGGTCCTGG AGAACCTCCT   240
GGTGCTGTGC GTCATCCTCC ACTCCCGCAG CCTCCGCTGC AGGCCTTCCT ACCACTTCAT   300
CGGCAGCCTG GCGGTGGCAG ACCTCCTGGG GAGTGTCATT TTTGTCTACA GCTTCATTGA   360
CTTCCACGTG TTCCACCGCA AAGATAGCCG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT   420
CACGGCCTCC TTCACTGCCT CCGTGGGCAG CCTGTTCCTC ACAGCCATCG ACAGGTACAT   480
ATCCATTCAC AGGCCCCTGG CCTATAAGAG GATTGTCACC AGGCCCAAGG CCGTGGTGGC   540
GTTTTGCCTG ATGTGGACCA TAGCCATTGT GATCGCCGTG CTGCCTCTCC TGGGCTGGAA   600
CTGCGAGAAA CTGCAATCTG TTTGCTCAGA CATTTCCCA CACATTGATG AAACCTACCT   660
GATGTTCTGG ATCGGGGTCA CCAGCGTACT GCTTCTGTTC ATCGTGTATG CGTACATGTA   720
TATTCTCTGG AAGGCTCACA GCCACGCCGT CCGCATGATT CAGCGTGGCA CCCAGAAGAG   780
CATCATCATC CACACGTCTG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG   840
CATGGACATT AGGTTAGCCA AGACCCTGGT CCTGATCCTG GTGGTGTTGA TCATCTGCTG   900
GGGCCCTCTG CTTGCAATCA TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTAA   960
GACGGTGTTT GCATTCTGCA GTATGCTCTG CCTGCTGAAC TCCACCGTGA ACCCCATCAT  1020
CTATGCTCTG AGGAGTAAGG ACCTGCGACA CGCTTTCCGG AGCATGTTTC CCTCTTGTGA  1080
AGGCACTGCG CAGCCTCTGG ATAACAGCAT GGGGGACTCG GACTGCCTGC ACAAACACGC  1140
AAACAATGCA GCCAGTGTTC ACAGGGCCGC AGAAAGCTGC ATCAAGAGCA CGGTCAAGAT  1200
TGCCAAGGTA ACCATGTCTG TGTCCACAGA CACGTCTGCC GAGGCTCTGT GA
```

Seq ID NO: 240 Protein sequence
Protein Accession #: NP_149421.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MALQIPPSAP SPLTSCTWAQ MTFSTKTSKE NEENIQCGEN FMDIECFMVL NPSQQLAIAV    60
LSLTLGTFTV LENLLVLCVI LHSRSLRCRP SYHFIGSLAV ADLLGSVIFV YSFIDFHVFH   120
RKDSRNVFLF KLGGVTASFT ASVGSLFLTA IDRYISIHRP LAYKRIVTRP KAVVAFCLMW   180
TIAIVIAVLP LLGWNCEKLQ SVCSDIFPHI DETYLMFWIG VTSVLLLFIV YAYMYILWKA   240
HSHAVRMIQR GTQKSIIIHT SEDGKVQVTR PDQARMDIRL AKTLVLILVV LIICWGPLLA   300
IMVYDVFGKM NKLIKTVFAF CSMLCLLNST VNPIIYALRS KDLRHAFRSM FPSCEGTAQP   360
LDNSMGDSDC LHKHANNAAS VHRAAESCIK STVKIAKVTM SVSTDTSAEA L
```

Seq ID NO: 241 DNA sequence
Nucleic Acid Accession #: NM_003596.1

Coding sequence: 82..1194

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1           11          21          31          41          51
|           |           |           |           |           |
GTAGACTGTC CATGGCCTGA ACATTTTCCG AAAATCATTT TGAGCAAAAT ATCTGTTTAA    60
TAACAAGATA ACCACATCAA GATGGTTGGA AAGCTGAAGC AGAACTTACT ATTGGCATGT   120
CTGGTGATTA GTTCTGTGAC TGTGTTTTAC CTGGGCCAGC ATGCCATGGA ATGCCATCAC   180
CGGATAGAGG AACGTAGCCA GCCAGTCAAA TTGGAGAGCA CAAGGACCAC TGTGAGAACT   240
GGCCTGGACC TCAAAGCCAA CAAAACCTTT GCCTATCACA AAGATATGCC TTTAATATTT   300
ATTGGRGGTG TGCCTCGGAG TGGAACCACA CTCATGAGGG CCATGCTGGA CGCACATCCT   360
GACATTCGCT GTGGAGAGGA AACCAGGGTC ATTCCCCGAA TCCTGGCCCT GAAGCAGATG   420
TGGTCACGGT CAAGTAAAGA GAAGATCCGC CTGGATGAGG CTGGTGTTAC TGATGAAGTG   480
CTGGATTCTG CCATGCAAGC CTTCTTACTA GAAATTATCG TTAAGCATGG GGAGCCAGCC   540
CCTTATTTAT GTAATAAAGA TCCTTTTGCC CTGAAATCTT TAACTTACCT TTCTAGGTTA   600
TTCCCCAATG CCAAATTTCT CCTGATGGTC CGAGATGGCC GGGCATCAGT ACATTCAATG   660
ATTTCTCGAA AAGTTACTAT AGCTGGATTT GATCTGAACA GCTATAGGGA CTGTTTGACA   720
AAGTGGAATC GTGCTATAGA GACCATGTAT AACCAGTGTA TGGAGGTTGG TTATAAAAAG   780
TGCATGTTGG TTCACTATGA ACAACTTGTC TTACATCCTG AACGGTGGAT GAGAACACTC   840
TTAAAGTTCC TCCAGATTCC ATGGAACCAC TCAGTATTGC ACCATGAAGA GATGATTGGG   900
AAAGCTGGGG GAGTGTCTCT GTCAAAAGTG GAGAGATCTA CAGACCAAGT AATCAAGCCA   960
GTCAATGTAG GAGCTCTATC AAAATGGGTT GGGAAGATAC CGCCAGATGT TTTACAAGAC  1020
ATGGCAGTGA TTGCTCCTAT GCTTGCCAAG CTTGGATATG ACCCATATGC CAACCCACCT  1080
AACTACGGAA AACCTGATCC CAAAATTATT GAAAACACTC GAAGGGTCTA TAAGGCAGAA  1140
TTCCAACTAC CTGACTTTCT TAAAGAAAAA CCACAGACTG AGCAAGTGGA GTAGCAGAAC  1200
CAGGAGCCTC TTCCATACAT GAGGAAAGAT TGCTGCCTTT TCAGCAGAAG GGAAATTCCT  1260
AGGATTGGCT GTCCCCTGCC AAGCTTGGTG GAGCGTCTGC ACCTTGGCTG CGCCGCCTGT  1320
GCATTTGCCA GTTTCCTCCC ACTGAGAGGA TGGAGGTGTC CGCACAGCTT TGGGCCTCGT  1380
GAGGGATCTG CCTCCTGAGC AAAGAGCTCT TGATCCCGAT TTCATGCACA GCCCTGCAGT  1440
AAGGAGCCCA GAAGGAACAT GTGTTTCCTG TTAAAACTCC TCTTGTTCTC TTTTCTTACA  1500
TTATGACGTT TGTTTTCAAG GAGAGGGTTT AAAAATGGGA TCCTGTAAGC AGACTTGGGC  1560
AGTCTCCTTT TGAAATAGGT TGTCTGTACA TGTTCTAATG TTTTGTAGAA CACGTGTGCC  1620
TGTTTAAGTG TATTGATGTG AATAATATTA AATATCCTAA TTATTTAATT CATTGTATTG  1680
TTTCTGAGAA GTTGGGAAAT TACCATTATA CATTTACAAC CTAATGACTT TTGTATTTTA  1740
TTTTTCAAAA TAAAAGCTTT CAATGTGA
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Seq ID NO: 242 Protein sequence
Protein Accession #: NP_003587.1

```
1           11          21          31          41          51
|           |           |           |           |           |
MVGKLKQNLL LACLVISSVT VFYLGQHAME CHHRIEERSQ PVKLESTRTT VRTGLDLKAN    60
KTFAYHKDMP LIFIGGVPRS GTTLMRAMLD AHPDIRCGEE TRVIPRILAL KQMWSRSSKE   120
KIRLDEAGVT DEVLDSAMQA FLLEIIVKHG EPAPYLCNKD PFALKSLTYL SRLFPNAKFL   180
LMVRDGRASV HSMISRKVTI AGFDLNSYRD CLTKWNRAIE TMYNQCMEVG YKKCMLVHYE   240
QLVLHPERWM RTLLKFLQIP WNHSVLHHEE MIGKAGGVSL SKVERSTDQV IKPVNVGALS   300
KWVGKIPPDV LQDMAVIAPM LAKLGYDPYA NPPNYGKPDP KIIENTRRVY KGEFQLPDFL   360
KEKPQTEQVE
```

Seq ID NO: 243 DNA sequence
Nucleic Acid Accession #: NM_001492.3
Coding sequence: 1395..2513

```
1           11          21          31          41          51
|           |           |           |           |           |
ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCACGGCGGG    60
CGAGCGGGCG GTATGGCGGC GGCGGGGCCC GCGGCGGGGC CGACGGGGCC CGAGCCCATG   120
CCGAGCTACG CGCAGCTAGT GCAGCGCGGC TGGGGCAGCG CGCTGGCGGC GGCGCCGGGC   180
TGCACGGACT GCGGCTGGGG GCTGGCGCGT CGCGGCCTGG CTGAGCACGC GCACCTGGCG   240
CCGCCCGAGC TGCTGCTGCT GGCGCTCGGC GCGCTGGGCT GGACCGCGCT GCGCTCCGCG   300
GCCACTGCGC GCCTCTTTCG GCCCCTGGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC   360
GCCAAGATGC CCGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCAGCTG GAGCTACAGT   420
GCCTACCTGC TGTTTGGCAC CGACTACCCC TTCTTCCATG ACCCACCATC TGTCTTCTAC   480
GACTGGACGC CGGGCATGGC AGTGCCACGG GACATTGCAG CCGCCTACCT GCTCCAGGGA   540
AGCTTCTATG GCCACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG   600
GTGGTCATGC TGCTCCACCA CGTGGTCACT CTCATCCTCA TCGTCTCCTC CTACGCCTTC   660
CGGTACCACA ATGTGGGCAT CCTTGTGCTC TTCCTGCACG ATATCAGTGA CGTGCAGCTT   720
GAGTTCACCA AGCTCAACAT TTACTTCAAG TCCCGCGGCG GCTCCTACCA TCGGCTGCAT   780
GCCTTGGCAG CAGACTTGGG CTGCCTCAGC TTCGGCTTCA GCTGGTTCTG GTTCCGCCTC   840
TACTGGTTCC CGCTCAAGGT CCTGTATGCC ACCAGTCACT GCAGTCTGCG CACGGTGCCT   900
GACATCCCCT TCTACTTCTT CTTCAATGCG CTCCTGCTGC TGCTCACCCT TATGAACCTC   960
TACTGGTTCC TGTACATCGT GGCGTTTGCA GCCAAGGTGT TGACAGGCCA GGTGCACGAG  1020
CTGAAGGACC TGCGGGAGTA TGACACAGCC GAGGCCCAGA GCCTGAAGCC CAGCAAAGCC  1080
GAGAAGCCAC TGAGGAACGG CCTGGTGAAG GACAAGCGCT TCTGAACCCC TCGGCCCCGC  1140
CCCCGTGGAC CCGGCCCCAC CCCGAATACC CCGGCCACGC TCCCCGTCCT TGGCCCCCCC  1200
TCCACCCCCT CCAACTCTGC TCCTCTAGGG CCGCCGCCAC CTCCCCTGGG ACCCCGCCCC  1260
CTCATCCTGC CTCCATTTCC CGGCCACGCC CCCCAGGACC CCTGCCCCTC CGGGGACACC  1320
GGCCCCGCCC TCAGCCCACT GGTCCCGGGC CGCCGCGGAC CCTGCGCACT CTCTGGTCAT  1380
CGCCTGGGAG GAAGATGCCA CCGCCGCAGC AAGGTCCCTG CGGCCACCAC CTCCTCCTCC  1440
TCCTGGCCCT GCTGCTGCCC TCGCTGCCCC TGACCCGCGC CCCCGTGCCC CCAGGCCCAG  1500
CCGCCGCCCT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGGTGCC CCCAGGCTCC  1560
GGCCGGTTCC CCCGGTCATG TGGCGCCTGT TTCGACGCCG GGACCCCCAG GAGACCAGGT  1620
CTGGCTCGCG GCGGACGTCC CCAGGGGTCA CCCTGCAACC GTGCCACGTG GAGGAGCTGG  1680
GGGTCGCCGG AAACATCGTG CGCCACATCC CGGACCGCGG TGCGCCCACC CGGGCCTCGG  1740
AGCCTGTCTC GGCCGCGGGG CATTGCCCTG AGTGGACAGT CGTCTTCGAC CTGTCGGCTG  1800
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TGGAACCCGC TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG  1860
CGGCAGCCCC GGAGGGCGGC TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GGCGCGGGCG  1920
CGGACCCCGG GCCGGTGCTG CTCCGCCAGT TGGTGCCCGC CCTGGGGCCG CCAGTGCGCG  1980
CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCCTCATG GCCGCGCAGC CTCCGCCTGG  2040
CGCTGGCGCT ACGCCCCCGG GCCCCTGCCG CCTGCGCGCG CCTGGCCGAG GCCTCGCTGC  2100
TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCCTGGC CCGGCCGCGG CGCGACGCCG  2160
AACCCGTGTT GGGCGGCGGC CCCGGGGGCG CTTGTCGCGC GCGGCGGCTG TACGTGAGCT  2220
TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCCGCG CGGCTTCCTG GCCAACTACT  2280
GCCAGGGTCA GTGCGCGCTG CCCGTCGCGC TGTCGGGGTC CGGGGGGCCG CCGGCGCTCA  2340
ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCCGCCCC GGGAGCCGCC GACCTGCCCT  2400
GCTGCGTGCC CGCGCGCCTG TCGCCCATCT CCGTGCTCTT CTTTGACAAC AGCGACAACG  2460
TGGTGCTGCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCGC TAACCCGGGG  2520
CGGGCAGGGA CGCGGGCCCA ACAATAAATG CCGCGTGGTC TGCTC
```

Seq ID NO: 244 Protein sequence
Protein Accession #: NP_001483.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MPPPQQGPCG HHLLLLLALL LPSLPLTRAP VPPGPAAALL QALGLRDEPQ GAPRLRPVPP    60
VMWRLFRRRD PQETRSGSRR TSPGVTLQPC HVEELGVAGN IVRHIPDRGA PTRASEPVSA   120
AGHCPEWTVV FDLSAVEPAE RPSRARLELR FAAAAAAAPE GGWELSVAQA GQGAGADPGP   180
VLLRQLVPAL GPPVRAELLG AAWARNASWP RSLRLALALR PRAPAACARL AEASLLLVTL   240
DPRLCHPLAR PRRDAEPVLG GGPGGACRAR RLYVSFREVG WHRWVIAPRG FLANYCQGQC   300
ALPVALSGSG GPPALNHAVL RALMHAAAPG AADLPCCVPA RLSPISVLFF DNSDNVVLRQ   360
YEDMVVDECG CR
```

Seq ID NO: 245 DNA sequence
Nucleic Acid Accession #: NM_021267.1
Coding sequence: 17..1125

```
1          11         21         31         41         51
|          |          |          |          |          |
ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCACGGCGGG    60
CGACCGGGCG GTATGGCGGC GGCGGGGCCC GCGGCGGGGC CGACGGGGCC CGAGCCCATG   120
CCGAGCTACG CGCAGCTAGT GCAGCGCGGC TGGGGCAGCG CGCTGGCGGC GGCGCGGGGC   180
TGCACGGACT GCGGCTGGGG GCTGGCGCGT CGCGGCCTGG CTGAGCACGC GCACCTGGCG   240
CCGCCCGAGC TGCTGCTGCT GGCGCTCGGC GCGCTGGGCT GGACCGCGCT GCGCTCCGCG   300
GCCACTGCGC GCCTCTTTCG GCCCCTGGCG AAGCCGTGCT GCCTCCAGCC CAGAGATGCC   360
GCCAAGATGC CCGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCAGCTG GAGCTACAGT   420
GCCTACCTGC TGTTTGGCAC CGACTACCCC TTCTTCCATG ACCCACCATC TGTCTTCTAC   480
GACTGGACGC CGGGCATGGC AGTGCCACGG GACATTGCAG CCGCCTACCT GCTCCAGGGA   540
AGCTTCTATG GCCACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG   600
GTGGTCATGC TGCTCCACCA CGTGGTCACT CTCATCCTCA TCGTCTCCTC CTACGCCTTC   660
CGGTACCACA ATGTGGGCAT CCTTGTGCTC TTCCTGCACG ATATCAGTGA CGTGCAGCTT   720
GAGTTCACCA AGCTCAACAT TTACTTCAAG TCCCGCGGCG GCTCCTACCA TCGGCTGCAT   780
GCCTTGGCAG CAGACTTGGG CTGCCTCAGC TTCGGCTTCA GCTGGTTCTG GTTCCGCCTC   840
TACTGGTTCC CGCTCAAGGT CCTGTATGCC ACCAGTCACT GCAGTCTGCG CACGGTGCCT   900
GACATCCCCT TCTACTTCTT CTTCAATGCG CTCCTGCTGC TGCTCACCCT TATGAACCTC   960
TACTGGTTCC TGTACATCGT GGCGTTTGCA GCCAAGGTGT TGACAGGCCA GGTGCACGAG  1020
CTGAAGGACC TGCGGGAGTA TGACACAGCC GAGGCCCAGA GCCTGAAGCC CAGCAAAGCC  1080
GAGAAGCCAC TGAGGAACGG CCTGGTGAAG GACAAGCGCT TCTGAACCCC TCGGCCCCGC  1140
CCCCGTGGAC CCGGCCCCAC CCCGAATACC CCGGCCACGC TCCCCGTCCT TGGCCGCCCC  1200
TCCACCCCCT CCAACTCTGC TCCTCTAGGG CCGCCGCCAC CTCCCCTGGG ACCCCGCCCC  1260
CTCATCCTGC CTCCATTTCC CGGCCACGCC CCCCAGGACC CCTGCCCCTC CGGGGACACC  1320
GGCCCCGCCC TCAGCCCACT GGTCCCGGGC CGCCGCGGAC CCTGCGCACT CTCTGGTCAT  1380
CGCCTGGGAG GAAGATGCCA CCGCCGCAGC AAGGTCCCTG CGGCCACCAC CTCCTCCTCC  1440
TCCTGGCCCT GCTGCTGCCC TCGCTGCCCC TGACCCGCGC CCCCGTGCCC CCAGGCCCAG  1500
CCGCCGCCCT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGGTGCC CCCAGGCTCC  1560
GGCCGGTTCC CCCGGTCATG TGGCGCCTGT TTCGACGCCG GGACCCCCAG GAGACCAGGT  1620
CTGGCTCGCG GCGGACGTCC CCAGGGGTCA CCCTGCAACC GTGCCACGTG GAGGAGCTGG  1680
GGGTCGCCGG AAACATCGTG CGCCACATCC CGGACCGCGG TGCGCCCACC CGGGCCTCGG  1740
AGCCTGTCTC GGCCGCGGGG CATTGCCCTG AGTGGACAGT CGTCTTCGAC CTGTCGGCTG  1800
TGGAACCCGC TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG  1860
CGGCAGCCCC GGAGGGCGGC TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GGCGCGGGCG  1920
CGGACCCCGG GCCGGTGCTG CTCCGCCAGT TGGTGCCCGC CCTGGGGCCG CCAGTGCGCG  1980
CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCCTCATG GCCGCGCAGC CTCCGCCTGG  2040
CGCTGGCGCT ACGCCCCCGG GCCCCTGCCG CCTGCGCGCG CCTGGCCGAG GCCTCGCTGC  2100
TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCCTGGC CCGGCCGCGG CGCGACGCCG  2160
AACCCGTGTT GGGCGGCGGC CCCGGGGGCG CTTGTCGCGC GCGGCGGCTG TACGTGAGCT  2220
TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCCGCG CGGCTTCCTG GCCAACTACT  2280
GCCAGGGTCA GTGCGCGCTG CCCGTCGCGC TGTCGGGGTC CGGGGGGCCG CCGGCGCTCA  2340
ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCCGCCCC GGGAGCCGCC GACCTGCCCT  2400
GCTGCGTGCC CGCGCGCCTG TCGCCCATCT CCGTGCTCTT CTTTGACAAC AGCGACAACG  2460
TGGTGCTGCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCGC TAACCCGGGG
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Seq ID NO: 246 Protein sequence
Protein Accession #: NP_067090.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAAAGPAAGP TGPEPMPSYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL    60
LLLALGALGW TALRSAATAR LFRPLAKRCC LQPRDAAKMP ESAWKFLFYL GSWSYSAYLL   120
FGTDYPFFHD PPSVFYDWTP GMAVPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML   180
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LHHVVTLILI VSSYAFRYHN VGILVLFLHD ISDVQLEFTK LNIYFKSRGG SYHRLHALAA   240
DLGCLSFGFS WFWFRLYWFP LKVLYATSHC SLRTVPDIPF YFFFNALLLL LTLMNLYWFL   300
YIVAFAAKVL TGQVHELKDL REYDTAEAQS LKPSKAEKPL RNGLVKDKRF
```

Seq ID NO: 247 DNA sequence
Nucleic Acid Accession #: NM_002081.1
Coding sequence: 222..1898

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCGCGCCGC CGCCGCCGCC    60
GGCTTTTGTT GTCTCCGCCT CCTCGGCCGC CGCCGCCTCT GGACCGCGAG CCGCGCGCGC   120
CGGGACCTTG GCTCTGCCCT TCGCGGGCGG GAACTGCGCA GGACCCGGCC AGGATCCGAG   180
AGAGGCGCGG GCGGGTGGCC GGGGGCGCCG CCGGCCCCGC CATGGAGCTC CGGGCCCGAG   240
GCTGGTGGCT GCTATGTGCG GCCGCAGCGC TGGTCGCCTG CGCCCGCGGG GACCCGGCCA   300
GCAAGAGCCG GAGCTGCGGC GAGGTCCGCC AGATCTACGG AGCCAAGGGC TTCAGCCTGA   360
GCGACGTGCC CCAGGCCGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA   420
CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA   480
CCGCGCTCCG GGACAGCAGC CGCGTCCTGC AGGCCATGCT TGCCACCCAG CTGCGCAGCT   540
TCGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC   600
CCGGCGCCTT CGGAGAGCTG TACACGCAGA ACGCGAGGGC CTTCCGGGAC CTGTACTCAG   660
AGCTGCGCCT GTACTACCGC GGTGCCAACC TGCACCTGGA GGAGACGCTG GCCGAGTTCT   720
GGGCCCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCCTGATG   780
ACTACCTGGA CTGCCTGGGC AAGCAGGCCG AGGCGCTGCG GCCCTTCGGG GAGGCCCCGA   840
GAGAGCTGCG CCTGCGGGCC ACCCGTGCCT TCGTGGCTGC TCGCTCCTTT GTGCAGGGCC   900
TGGGCGTGGC CAGCGACGTG GTCCGGAAAG TGGCTCAGGT CCCCCTGGGC CCGGAGTGCT   960
CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCCT GGGAGTCCCC GGCGCCAGGC  1020
CCTGCCCTGA CTATTGCCGA AATGTGCTCA AGGGCTGCCT TGCCAACCAG GCCGACCTGG  1080
ACGCCGAGTG GAGGAACCTC CTGGACTCCA TGGTGCTCAT CACCGACAAG TTCTGGGGTA  1140
CATCGGGTGT GGAGAGTGTC ATCGGCAGCG TGCACACGTG GCTGGCGGAG GCCATCAACG  1200
CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCAT CCAGGGCTGC GGGAACCCCA  1260
AGGTCAACCC CCAGGGCCCT GGGCCTGAGG AGAAGCGGCG CCGGGGCAAG CTGGCCCCGC  1320
GGGAGAGGCC ACCTTCAGGC ACGCTGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC  1380
GCGACGTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC  1440
TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCCGG TACCTCCCCG  1500
AGGTCATGGG TGACGGCCTG GCCAACCAGA TCAACAACCC CGAGGTGGAG GTGGACATCA  1560
CCAAGCCGGA CATGACCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCGGC  1620
TGCGCAGCGC CTACAACGGC AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGGCAGCG  1680
GCTCGGGCAG CGGTGATGGC TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA  1740
GCTCCAGCTC CCGGACGCCC TTGACCCATG CCCTCCCAGG CCTGTCAGAG CAGGAAGGAC  1800
AGAAGACCTC GGCTGCCAGC TGCCCCCAGC CCCCGACCTT CCTCCTGCCC CTCCTCCTCT  1860
TCCTGGCCCT TACAGTAGCC AGGCCCCGGT GGCGGTAACT GCCCCAAGGC CCCAGGGACA  1920
GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGACG ATATTTAATT CACCTCAGCC  1980
TGGAGAGGCC TGGGGTGGGA CAGGGAGGGC CGGCGGCTCT GAGCAGGGGC AGGCGCAGAG  2040
GTCCCAGCCC CAGGCCTGGC CTCGCCTGCC TTTCTGCCTT TTAATTTTGT ATGAGGTCCT  2100
CAGGTCAGCT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCACC  2160
TCCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGCACCGCCG CAGAAGCAGC CCCTCGAGGC  2220
CTACAGAGGA GGCCTCAAAG CAACCCGCTG GAGCCCACAG CGAGCCTGTG CCTTCCTCCC  2280
CGCCTCCTCC CACTGGGACT CCCAGCAGAG CCCACCAGCC AGCCCTGGCC CACCCCCCAG  2340
CCTCCAGAGA AGCCCCGCAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC  2400
TCTGAGATGA TGCATGATGC CCTCCCCTCA GCGCAGGCTG CAGAGCCCGG CCCCACCTCC  2460
CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGACGCC TGAGACAGCA CCACTGCTGA  2520
GGAGTCTGAG GACTGTCCTC CCACAGACCC TGCAGTGAGG GGCCCTCCAT GCGCAGATGA  2580
GGGGCCACTG ACCCACCTGC GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCCAG  2640
GGAGGCAGCG TGGGCTCTGC CAATGTGGGC TGCCCCTCGC ACACAGGGCT CACAGGGCAG  2700
GCCTTGCTGG GGTCCAGGGC TGTTGGAGGA CCCCGAGGGC TGAGGAGCAG CCAGGACCCG  2760
CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCCTCC CTGTTCACGG TGACACAGGT  2820
CAGGGCTCAG AGTGACCCTC GGCTGTCACC TGCTCACAGG GATCCTGGTG GCTGGTGAGA  2880
CCCCGCACTG CACACGGGAA TGCCTAGGTC CCTTCCCGAC CCAGCCAGCT GCACTGCAGG  2940
GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAAACATGC ATCCATTTAC TGACACTTCC  3000
TGTCCTTGTT CATGGAGAGC TGTTCGCTCC TCCCAGATGG CTTCGGAGGC CCGCAGGGCC  3060
CACCTTGGAC CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC  3120
CTGGACGGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG  3180
TGTGGTGTTG GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG  3240
TCCTGAACCG ACTGACCCTG AGGAGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCGTCC  3300
CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC  3360
CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA  3420
CCCTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG  3480
CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCCAC CCTACGCTCA  3540
TCTCTGGAAG GGGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT  3600
CCTTCCTCCA CAAGGTCCCC CCACCGCTCA GTGTCAGCGG GTGACGTGTG TTCTTTTGAG  3660
TCCTTGTATG AATAAAAGGC TGGAAACCTA AA
```

Seq ID NO: 248 Protein sequence
Protein Accession #: NP_002072.1

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1          11         21         31         41         51
|          |          |          |          |          |
MELRARGWWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSDVP QAEISGEHLR    60
ICPQGYTCCT SEMEENLANR SHAELETALR DSSRVLQAML ATQLRSFDDH FQHLLNDSER   120
TLQATFPGAF GELYTQNARA FRDLYSELRL YYRGANLHLE ETLAEFWARL LERLFKQLHP   180
QLLLPDDYLD CLGKQAEALR PFGEAPRELR LRATRAFVAA RSFVQGLGVA SDVVRKVAQV   240
PLGPECSRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVLI   300
TDKFWGTSGV ESVIGSVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR   360
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WO03042661 [file://E:/WO03042661.pcl]


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RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA   420
RGRYLPEVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD   480
ASDDGSGSGS
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Seq ID NO: 249 DNA sequence
Nucleic Acid Accession #: NM_001492.3
Coding sequence: 8..1864

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1          11         21         31         41         51
|          |          |          |          |          |
GAAGGCCATG GTCTCCCCAC GGATGTCCGG GCTCCTCTCC CAGACTGTGA TCCTAGCGCT    60
CATTTTCCTC CCCCAGACAC GGCCCGCTGG CGTCTTCGAG CTGCAGATCC ACTCTTTCGG   120
GCCGGGTCCA GGCCCTGGGG CCCCGCGGTC CCCCTGCAGC GCCCGGCTCC CCTGCCGCCT   180
CTTCTTCAGA GTCTGCCTGA AGCCTGGGCT CTCAGAGGAG GCCGCCGAGT CCCCGTGCGC   240
CCTGGGCGCG GCGCTGAGTG CGCGCGGACC GGTCTACACC GAGCAGCCCG GAGCGCCCGC   300
GCCTGATCTC CCACTGCCCG ACGGGCTCTT GCAGGTGCCC TTCCGGGACG CCTGGCCTGG   360
CACCTTCTCT TTCATCATCG AAACCTGGAG AGAGGAGTTA GGAGACCAGA TTGGAGGGCC   420
CGCCTGGAGC CTGCTGGCGC GCGTGGCTGG CAGGCGGCGC TTGGCAGCCG GAGGCCCGTG   480
GGCCCGGGAC ATTCAGCGCG CAGGCGCCTG GGAGCTGCGC TTCTCGTACC GCGCGCGCTG   540
CGAGCCGCCT GCCGTCGGGA CCGCGTGCAC GCGCCTCTGC CGTCCGCGCA GCGCCCCCTC   600
GCGGTGCGGT CCGGGACTGC GCCCCTGCGC ACCGCTCGAG GACGAATGTG AGGCGCCGCT   660
GGTGTGCCGA GCAGGCTGCA GCCCTGAGCA TGGCTTCTGT GAACAGCCCG GTGAATGCCG   720
ATGCCTAGAG GGCTGGACTG GACCCCTCTG CACGGTCCCT GTCTCCACCA GCAGCTGCCT   780
CAGCCCCAGG GGCCCGTCCT CTGCTACCAC CGGATGCCTT GTCCCTGGGC CTGGGCCCTG   840
TGACGGGAAC CCGTGTGCCA ATGGAGGCAG CTGTAGTGAG ACACCCAGGT CCTTTGAATG   900
CACCTGCCCG CGTGGGTTCT ACGGGCTGCG GTGTGAGGTG AGCGGGGTGA CATGTGCAGA   960
TGGACCCTGC TTCAACGGCG GCTTGTGTGT CGGGGGTGCA GACCCTGACT CTGCCTACAT  1020
CTGCCACTGC CCACCTGGTT TCCAAGGCTC CAACTGTGAG AAGAGGGTGG ACCGGTGCAG  1080
CCTGCAGCCA TGCCGCAATG GCGGACTCTG CCTGGACCTG GGCCACGCCC TGCGCTGCCG  1140
CTGCCGCGCC GGCTTCGCGG GTCCTCGCTG CGAGCACGAC CTGGACGACT GCGCGGGCCG  1200
CGCCTGCGCT AACGGCGGCA CGTGTGTGGA GGGCGGCGGC GCGCACCGCT GCTCCTGCGC  1260
GCTGGGCTTC GGCGGCCGCG ACTGCCGCGA GCGCGCGGAC CCGTGCGCCG CGCGCCCCTG  1320
TGCTCACGGC GGCCGCTGCT ACGCCCACTT CTCCGGCCTC GTCTGCGCTT GCGCTCCCGG  1380
CTACATGGGA GCGCGGTGTG AGTTCCCAGT GCACCCCGAC GGCGCAAGCG CCTTGCCCGC  1440
GGCCCCGCCG GGCCTCAGGC CCGGGGACCC TCAGCGCTAC CTTTTGCCTC CGGCTCTGGG  1500
ACTGCTCGTG GCCGCGGGCG TGGCCGGCGC TGCGCTCTTG CTGGTCCACG TGCGCCGCCG  1560
TGGCCACTCC CAGGATGCTG GGTCTCGCTT GCTGGCTGGG ACCCCGGAGC CGTCAGTCCA  1620
CGCACTCCCG GATGCACTCA ACAACCTAAG GACGCAGGAG GGTTCCGGGG ATGGTCCGAG  1680
CTCGTCCGTA GATTGGAATC GCCCTGAAGA TGTAGACCCT CAAGGGATTT ATGTCATATC  1740
TGCTCCTTCC ATCTACGCTC GGGAGGTAGC GACGCCCCTT TTCCCCCCGC TACACACTGG  1800
GCGCGCTGGG CAGAGGCAGC ACCTGCTTTT TCCCTACCCT TCCTCGATTC TGTCCGTGAA  1860
ATGAATTGGG TAGAGTCTCT GGAAGGTTTT AAGCCCATTT TCAGTTCTAA CTTACTTTCA
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Seq ID NO: 250 Protein sequence
Protein Accession #: NP_058637.1

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1          11         21         31         41         51
|          |          |          |          |          |
MVSPRMSGLL SQTVILALIF LPQTRPAGVF ELQIHSFGPG PGPGAPRSPC SARLPCRLFF    60
RVCLKPGLSE EAAESPCALG AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDAWPGTF   120
SFIIETWREE LGDQIGGPAW SLLARVAGRR RLAAGGPWAR DIQRAGAWEL RFSYRARCEP   180
PAVGTACTRL CRPRSAPSRC GPGLRPCAPL EDECEAPLVC RAGCSPEHGF CEQPGECRCL   240
EGWTGPLCTV PVSTSSCLSP RGPSSATTGC LVPGPGPCDG NPCANGGSCS ETPRSFECTC   300
PRGFYGLRCE VSGVTCADGP CFNGGLCVGG ADPDSAYICH CPPGFQGSNC EKRVDRCSLQ   360
PCRNGGLCLD LGHALRCRCR AGFAGPRCEH DLDDCAGRAC ANGGTCVEGG GAHRCSCALG   420
FGGRDCRERA DPCAARPCAH GGRCYAHFSG LVCACAPGYM GARCEFPVHP DGASALPAAP   480
PGLRPGDPQR YLLPPALGLL VAAGVAGAAL LLVHVRRRGH SQDAGSRLLA GTPEPSVHAL   540
PDALNNLRTQ EGSGDGPSSS VDWNRPEDVD PQGIYVISAP SIYAREVATP LFPPLHTGRA   600
GQRQHLLFPY PSSILSVK
```

Seq ID NO: 251 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
GAAATATAAC CATTGCAATT AGAAAATATC CAAAATAGCC TGTTATCTTC CACGTGGCCT    60
AGATTATTGA CAATCCCAAA TATACAATTT TTCTTTAAAA GTAGTACAAT TTCCTTTGTA   120
GCTTCAATTC CTTATATGAC TTCAGACTGG AGAAGCCTGT TAAACCACTG TTAGTTTCAG   180
TTAGAAAGTC TGAGAGACTT TATACATAAA TTCTCAATTT GGCTGCTGTA CACGTGCCAG   240
AGTTTTACTA CTGTAGTGAC CGTTGAGAAG ACCCTTGTTT ATTTACATTT GAAGCACTGT   300
TTGTGCAAAC AACCTTTCAT TGTTAAGTGC CTGTATTCCT TTCATTTACT TCATGTCCAG   360
GGGTGCTATT TACCTAGAAC CATTGTCTAC TACAATTAAC ATTTACATTA CAAAGTGTGT   420
GGTTTTCTTT TTCAACGAGG TTCAATTAAG GCAATAAGAT GTTTGCTGGA GAAACCTATT   480
GTTTACTGAA AGCACTCAAT GAAGTCAAAT TACTGAAGCT TTTGCCTACA TCTTGGTCTT   540
TTATGTAAAT ATGTTAAATA TAACATCTAA GGAAAATAAA CAATATTATA ATTATGTGTT   600
TGCCATTGTC ATATCAAACT TGCTTTGTAT CATACTAATG TTACATAACT TATCGATCAA   660
TAAAAATACA TTTCAATGTT AAAAAAAAAA AAAAAAAA
```

Seq ID NO: 252 DNA sequence
Nucleic Acid Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
AGGTACTGCC AGAAAGGATC AGGACCTGGA GTCTGGCAAG AGGAAGACAG AGGCCTGTGT    60
```

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GGGAAGCGAG TTGTTATCTT TGGTTATCTA GCTGTATGAG TGTATTGGTC TTCATAAAGC   120
TAGATAACCG AAAGTAAAAA CTTCTTCAAG ATCGCCGGGG AGCGTGTGAG AATGAAAGAC   180
TACAGCCGAG AGACAGTAAA AACCAGAAAG GTCAGGAATA CTTATTGAAT CTAACTTTGT   240
TTTTGTTTTG TTTTTTTCCT TATGATTAAA GGTGGGATGA GAGAAAATTA AATGACACAC   300
ACATGCTAAA ATATCAAGGT TCCAGATATG TCTTGAGAGG GGTTGTTGCA GCTGCAAAGG   360
AGAAGTGTAT AGTGATAATG AGTAAAGATG CATGTGCAGT TTGTTCTATT TTAAGGCAAA   420
AGTTATATCA GGGATTTTTT TCTTAGAAAG GTGTTGCAGA GATGTCTGGT ACCTAGTTTA   480
AAAATGATTC CATAATATGT AGACTTGGGC AGTTCCTTTG GGAGGCACCT CCCTCTCAAA   540
ATTTGAAGAT TGTGCTTGGA AATTACTTTA CATGTATTTG GGCTGTATGT CAATTTGTAC   600
GAAATTAGAC TTTCAGAAAA GTTTATACTG GAAGGTTAAT AATTTGTATC TACTGAGGAC   660
TTAGAGCTAG CAGGCAAAAT GAAAAAAAAA AAAAAAAARG CAAGGGCTGA TTTTTATTCT   720
TCTATTCAAA ATACAAGGAC AGATGCTTCT CTGTTCCAAG AGGGTTTCCT TGAGGAAGCT   780
ACTGAAGCAG AAAGACATGA TGGAGACGAG ATCGCCTCCC CTCTTGTCAA AGTGTTAAAA   840
AAATGTTCTG TCTTACTCTG CGCCTAGCAT TGGAAATGAA AGTGACATTT ACGCCACAAC   900
CCACGTGTGC GCCTCCTCTC TTTTTGTTTA AGGATGATCA GGTCTATCCA GGAAACAGCT   960
CTGGCATCCC AAACTGAAAT AATTAGGACG TATATAGACC TGACAAAAAT GGAAAGGGGG  1020
TGGGGAATCT GAGGGTCTGT CTTGCCTAAT TGATTCCGCT AAACGGAATG CAGGAGATGT  1080
GAACGGCAGG ACGCTCCGAT TCCCACGCTC GGGGGCAAGT GATAAAGCGG GGCCGGGCAG  1140
CCTATGACAG ACAGCCCTGT TGGGGGGTGG GGGTATGAAA AAAACATCAA GTGCACACAC  1200
CATACTCATC TCCATCGCTT AAGAAAGTAA AGGCATTTCC CACCCACAGC CATCTGCAGC  1260
TTCCCAAATG GCAGCACCAA CTGGTCTGTA GCTGCTACAT AGTCTGCTTC TGTTAATTTT  1320
TTAACCACTG TTTAATCTGG CCATAATTAA GTTTGGCTTT CTTCGTTGTT TGAGATTTTC  1380
AGAATTCAAG GCAAGCTAGT AGAAAGCAAT TCCAAGAAAG TCCCATGACT GCCTGCCCCT  1440
AATGTCAAAA TCTCAGTCCA TGAGATTATG GCCTTGTGAC CACATTTTTG CTTTGTTTT   1500
GGGTGGGCAA ATGTGTATAG AGATAAAATA CATATCTCTA TATAACAGTC GTTATTATAA  1560
TTTCATGAGG CTTTTTACCT CTTAACATGA TACATCTAGG AACTTGGTCT AATTGTGCTA  1620
GTAGATATAC ACTAGAAGTA AAACTATAAA GTCATTAGCC TGTAGAAAGT TGATTATGAT  1680
AACAATATGA TAAAAAGTTT GTTTTGGAAT AGTCTCAGCT AGATGGGTCT AAATAGCCAT  1740
TTTAATGTAA TCTAAAAATA ACACTATGCC TAGCAGAAAC TTTGGCGCTT TGGAGGTCCC  1800
CATTGTCGCC TTTTCATAAA AGTCCTTAAG TTTTCCATAT GTCACCAAGC AAACATTTGT  1860
ATAGGCATTT ACACAGAAAT ATAACCATTG CAATTAGAAA ATATCCAAAA TAGCCTGTTA  1920
TCTTCCACGT GGCCTAGATT ATTGACAATC CCAAATATAC AATTTTTCTT TAAAAGTAGT  1980
ACAATTTCCT TTGTAGCTTC AATTCCTTAT ATGACTTCAG ACTGGAGAAG CCTGTTAAAC  2040
CACTGTTAGT TTCAGTTAGA AAGTCTGAGA GACTTTATAC ATAAATTCTC AATTTGGCTG  2100
CTGTACACGT GCCAGAGTTT TACTACTGTA GTGACCGTTG AGAAGACCCT TGTTTATTTA  2160
CATTTGAAGC ACTGTTTGTG CAAACAACCT TTCATTGTTA AGTGCCTGTA TTCCTTTCAT  2220
TTACTTCATG TCCAGGGGTG CTATTTACCT AGAACCATTG TCTACTACAA TTAACATTTA  2280
CATTACAAAG TGTGTGGTTT TCTTTTTCAA GGAGGTTCAA TTAAGGCAAT AAGATGTTTG  2340
CTGGAGAAAC CTATTGTTTA CTGAAAGCAC TCAATGAAGT CAAATTACTG AAGCTTTTGC  2400
CTACATCTTG GTCTTTTATG TAAATATGTT AAATATAACA TCTAAGGAAA ATAAACAATA  2460
TTATAATTAT GTGTTTGCCA TTGTCATATC AAACTTGCTT TGTATCATAC TAATGTTACA  2520
TAACTTATCG ATCAATAAAA ATACATTTCA ATGTT
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Seq ID NO: 253 DNA sequence
Nucleic Acid Accession #: NM_001650.2
Coding sequence: 40.1011

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1          11         21         31         41         51
|          |          |          |          |          |
GGGGCAGGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCCACAGCA    60
AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCTTTCAAA   120
GGGGTCTGGA CTCAAGCTTT CTGGAAAGCA GTCACAGCGG AATTTCTGGC CATGCTTATT   180
TTTGTTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG   240
GTCGACATGG TTCTCATCTC CCTTTGCTTT GGACTCAGCA TTGCAACCAT GGTGCAGTGC   300
TTTGGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGGCCAT GGTGTGCACC   360
AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC   420
ATTGGAGCAG GAATCCTCTA TCTGGTCACA CCTCCCAGTG TGGTGGGAGG CCTGGGAGTC   480
ACCATGGTTC ATGGAAATCT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA   540
TTTCAATTGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACGGACTGA TGTCACTGGC   600
TCAATAGCTT TAGCAATTGG ATTTTCTGTT GCAATTGGAC ATTTATTTGC AATCAATTAT   660
ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG   720
GAAAACCATT GGATATATTG GGTTGGGCCC ATCATAGGAG CTGTCCTCGC TGGTGGCCTT   780
TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC   840
AAAGCTGCCC AGCAAACAAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA   900
GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCATG TGATTGACGT TGACCGGGGA   960
GAGGAGAAGA AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTCAGTATG ACTAGAAGAT  1020
CGCACTGAAA GCAGACAAGA CTCCTTAGAA CTGTCCTCAG ATTTCCTTCC ACCCATTAAG  1080
GAAACAGATT TGTTATAAAT TAGAAATGTG CAGGTTTGTT GTTTCATGTC ATATTACTCA  1140
GTCTAAACAA TAAATATTTC ATAATTTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT  1200
TCCAAATCTA AAAAAAGAAA TATTTTTAAG ATGTTCTTAA GCAAATATAT ACCTATTTTA  1260
TCTAGTTACC TTTCATTAAC AACCAATTTT AACCGTGTGT CAAGATTTGG TTAAGTCTTG  1320
CCTGACAGAA CTCAAAGACA CGTCTATCAG CTTATTCCTT CTCTACTGGA ATATTGGTAT  1380
AGTCAATTCT TATTTGAATA TTTATTCTAT TAAACTGAGT TTAACAATGG C
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Seq ID NO: 254 Protein sequence
Protein Accession #: NP_001641.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSDRPTARRW GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG    60
GTEKPLPVDM VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA   120
AQCLGAIIGA GILYLVTPPS VVGGLGVTMV HGNLTAGHGL LVELIITFQL VFTIFASCDS   180
KRTDVTGSIA LAIGFSVAIG HLFAINYTGA SMNPARSFGP AVIMGNWENH WIYWVGPIIG   240
AVLAGGLYEY VFCPDVEFKR RFKEAFSKAA QQTKGSYMEV EDNRSQVETD DLILKPGVVH   300
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VIDVDRGEEK KGKDQSGEVL SSV

Seq ID NO: 255 DNA sequence
Nucleic Acid Accession #: U26742.1
Coding sequence: 325..1449

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1          11         21         31         41         51
|          |          |          |          |          |
CAGGAAACCC TGGTACTGGC AGCAGCCAGC CTCTGCTGTG CCCACATGAC CCACAACTCT    60
GGCAGCGGAC CCGGCACTTC CAACATTATT AAATAATAAG AAAGCGGCTC CTACTCCAGG   120
CTCAAACCTC CCTGCAGACC AATGGACACC TTCTAAGAGT TTGGCGAGTC AGTGACTGAA   180
GCGCCCGTCC ATTCCAAGAT AAATAGGATT TACCAATCCT TGGATGAAGT GCTTGGGAAG   240
TCTTTAAGTG CCATAATCAA CTGCCATTTC AAAGAATATA GATGGTTTTG AAAAGTTCAT   300
GCTGTCCCTT CATTGAATTT TAGAATGATT GAAGATAGTG GGAAAAGAGG AAATACCATG   360
GCAGAAAGAA GACAGCTGTT TGCAGAGATG AGGGCTCAAG ATCTGGATCG CATCCGACTC   420
TCCACCTACA GAACAGCATG CAAGCTTAGG TTTGTTCAGA AGAAATGCAA TTTGCACCTG   480
GTGGACATAT GGAATGTCAT AGAAGCATTG CGGGAAAATG CTCTGAACAA CCTGGACCCA   540
AACACTGAAC TCAACGTGTC CCGCTTAGAG GCTGTGCTCT CCACTATTTT TTACCAGCTC   600
AACAAACGGA TGCCAACCAC TCACCAAATC CATGTGGAGC AGTCCATCAG CCTCCTCCTT   660
AACTTCCTGC TTGCAGCGTT TGATCCGGAA GGCCATGGTA AAATTTCAGT ATTTGCTGTC   720
AAAATGGCTT TAGCCACATT GTGTGGAGGG AAGATCATGG ACAAATTAAG ATATATTTTC   780
TCAATGATTT CTGACTCCAG TGGGGTGATG GTTTATGGAC GATATGACCA ATTCCTTCGG   840
GAAGTTCTCA AACTACCCAC GGCAGTTTTT GAAGGTCCTT CATTTGGTTA CACAGAACAG   900
TCAGCCAGAT CCTGTTTCTC CCAACAGAAA AAAGTCACGT TAAATGGTTT CTTGGACACG   960
CTTATGTCAG ATCCTCCCCC GCAGTGTCTG GTCTGGTTGC CTCTTCTGCA TCGACTAGCA  1020
AATGTGGAAA ATGTCTTCCA TCCGGTTGAG TGTTCCTACT GCCACAGTGA GAGTATGATG  1080
GGATTTCGCT ACCGATGCCA ACAGTGTCAC AATTACCAGC TCTGTCAGGA CTGCTTCTGG  1140
AGGGGACATG CCGGTGGTTC TCATAGCAAC CAGCACCAAA TGAAAGAGTA CACGTCATGG  1200
AAATCACCTG CTAAGAAGCT GACTAATGCA TTAAGCAAGT CCCTGAGCTG TGCTTCCAGC  1260
CGTGAACCTT TGCACCCCAT GTTCCCAGAT CAGCCTGAGA AGCCACTCAA CTTGGCTCAC  1320
ATCGTTGATA CTTGGCCTCC CAGACCTGTA ACCAGCATGA ACGACACCCT GTTCTCCCAC  1380
TCTGTTCCCT CCTCAGGAAG TCCTTTTATT ACCAGGAGCT CGGACGGTGC TTTTGGTGGA  1440
TGCGTCTAGA TGGATAACAT GACTTCTTCT ACCCTAAAAT ATTCCTATAA TACTTTGAGC  1500
TGTTCTGGTT CCTCCAGGGT GCATGGTACC CATTAACCCA AAATATGATT ATTTCCCTTT  1560
TTTCCCATTT TCAGTCATTT TGGAATGTTC TCTGTGAACC ACAGTTGGGT TGTTTAAAGC  1620
TCACATTTCT TTCTGTCACC ACAGAGATTG GCCTACGGTT TCTGTTTTGA GGGTGCTGTT  1680
CAATAAAGCT GTGTACACTA AATGTCC
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Seq ID NO: 256 Protein sequence
Protein Accession #: AAC50424.1

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1          11         21         31         41         51
|          |          |          |          |          |
MIEDSGKRGN TMAERRQLFA EMRAQDLDRI RLSTYRTACK LRFVQKKCNL HLVDIWNVIE    60
ALRENALNNL DPNTELNVSR LEAVLSTIFY QLNKRMPTTH QIHVEQSISL LLNFLLAAFD   120
PEGHGKISVF AVKMALATLC GGKIMDKLRY IFSMISDSSG VMVYGRYDQF LREVLKLPTA   180
VFEGPSFGYT EQSARSCFSQ QKKVTLNGFL DTLMSDPPPQ CLVWLPLLHR LANVENVFHP   240
VECSYCHSES MMGFRYRCQQ CHNYQLCQDC FWRGHAGGSH SNQHQMKEYT SWKSPAKKLT   300
NALSKSLSCA SSREPLHPMF PDQPEKPLNL AHIVDTWPPR PVTSMNDTLF SHSVPSSGSP   360
FITRSSDGAF GGCV
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Seq ID NO: 257 DNA sequence
Nucleic Acid Accession #: NM_004172.1
Coding sequence: 179..1807

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1          11         21         31         41         51
|          |          |          |          |          |
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CACCCCTTAC AAAATCAGAA AAGTTGTGTT TTCTAATACC AAAGAGGAGG TTTGGCTTTC   120
TGTGGGTGAT TCCCAGACAC TGAAGTGCAA AGAAGAGACC CTCCTAGAAA AGTAAAATAT   180
GACTAAAAGC AATGGAGAAG AGCCCAAGAT GGGGGGCAGG ATGGAGAGAT TCCAGCAGGG   240
AGTCCGTAAA CGCACACTTT TGGCCAAGAA GAAAGTGCAG AACATTACAA AGGAGGATGT   300
TAAAAGTTAC CTGTTTCGGA ATGCTTTTGT GCTGCTCACA GTCACCGCTG TCATTGTGGG   360
TACAATCCTT GGATTTACCC TCCGACCATA CAGAATGAGC TACCGGGAAG TCAAGTACTT   420
CTCCTTTCCT GGGGAACTTC TGATGAGGAT GTTACAGATG CTGGTCTTAC CACTTATCAT   480
CTCCAGTCTT GTCACAGGAA TGGCGGCGCT AGATAGTAAG GCATCAGGGA AGATGGGAAT   540
GCGAGCTGTA GTCTATTATA TGACTACCAC CATCATTGCT GTGGTGATTG GCATAATCAT   600
TGTCATCATC ATCCATCCTG GGAAGGGCAC AAAGGAAAAC ATGCACAGAG AAGGCAAAAT   660
TGTACGAGTG ACAGCTGCAG ATGCCTTCCT GGACTTGATC AGGAACATGT TCCCTCCAAA   720
TCTGGTAGAA GCCTGCTTTA AACAGTTTAA AACCAACTAT GAGAAGAGAA GCTTTAAAGT   780
GCCCATCCAG GCCAACGAAA CGCTTGTGGG TGCTGTGATA AACAATGTGT CTGAGGCCAT   840
GGAGACTCTT ACCCGAATCA CAGAGGAGCT GGTCCCAGTT CCAGGATCTG TGAATGGAGT   900
CAATGCCCTG GGTCTAGTTG TCTTCTCCAT GTGCTTCGGT TTTGTGATTG GAAACATGAA   960
GGAACAGGGG CAGGCCCTGA GAGAGTTCTT TGATTCTCTT AACGAAGCCA TCATGAGACT  1020
GGTAGCAGTA ATAATGTGGT ATGCCCCCGT GGGTATTCTC TTCCTGATTG CTGGGAAGAT  1080
TGTGGAGATG GAAGACATGG GTGTGATTGG GGGGCAGCTT GCCATGTACA CCGTGACTGT  1140
CATTGTTGGC TTACTCATTC ACGCAGTCAT CGTCTTGCCA CTCCTCTACT TCTTGGTAAC  1200
ACGGAAAAAC CCTTGGGTTT TTATTGGAGG GTTGCTGCAA GCACTCATCA CCGCTCTGGG  1260
GACCTCTTCA AGTTCTGCCA CCCTACCCAT CACCTTCAAG TGCCTGGAAG AGAACAATGG  1320
CGTGGACAAG CGCGTCACCA GATTCGTGCT CCCCGTAGGA GCCACCATTA ACATGGATGG  1380
GACTGCCCTC TATGAGGCTT TGGCTGCCAT TTTCATTGCT CAAGTTAACA ACTTTGAACT  1440
GAACTTCGGA CAAATTATTA CAATCAGCAT CACAGCCACA GCTGCCAGTA TTGGGGCAGC  1500
TGGAATTCCT CAGGCGGGCC TGGTCACTAT GGTCATTGTG CTGACATCTG TCGGCCTGCC  1560
CACTGACGAC ATCACGCTCA TCATCGCGGT GGACTGGTTC CTGGATCGCC TCCGGACCAC  1620
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CACCAACGTA CTGGGAGACT CCCTGGGAGC TGGGATTGTG GAGCACTTGT CACGACATGA  1680
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ACCATATCAA CTGATTGCAC AGGACAATGA AACTGAGAAA CCCATCGACA GTGAAACCAA  1800
GATGTAGACT AACATAAAGA AACACTTTCT TGAGCACCAG GTGTTAAAAA CCATTATAAA  1860
ATCTTTCCAT CTCATTACAG CTCATTCGCT CCAGCAAGCC CGTCATCTTC CCTTTCCTCC  1920
CTTCTGATAA GACTGGAAAA TAGTCCTCCA AAACACAAGG GAGGATTTTG GGTGGCCAAA  1980
GTGTACAATT TTCATCCCAC AATTGAAATT TTTAAATCAT TTCATGTTAG TCTTACCGAA  2040
TAAGGTACCA AGATCACAAA TAGTGTTGAT CAGATCTTAC AAGTTTATGT GGCACACAAT  2100
TCCTATAAAT GTGATTTTTT TATATAAGTT AAAGAGACAA ATAGTAGGCT AAAAACATTT  2160
TAAAATCAAC TTTTGAAATT TAAAAATCTT TCAGAATACA ATTCAGTTTT AGTTTCAAAA  2220
TGTTAACAAC TTGAATTACA ACCGGTTATC AGTTGGACAG TAAGATTTTA TCCCTTTCTC  2280
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GGCCTCAGTG TCCTCATCTA TAAAATGAGG GACTTCCCTA GAAGTCTTCA TGGTCTCTTC  2460
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CCCAGTTCAT CCCAATGGGG GAAGTATTCC CTTCTTTCCT ACTCTGGGAA GAATGTCTCC  2760
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AATCATTCCC CCCGTGAAGT CTGCTTACCA AAACATAAGA CGACTTATAT ATTTGAAAGA  3060
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Seq ID NO: 258 Protein sequence
Protein Accession #: NP_004163.1

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GTILGFTLRP YRMSYREVKY FSFPGELLMR MLQMLVLPLI ISSLVTGMAA LDSKASGKMG   120
MRAVVYYMTT TIIAVVIGII IVIIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFPP   180
NLVEACFKQF KTNYEKRSFK VPIQANETLV GAVINNVSEA METLTRITEE LVPVPGSVNG   240
VNALGLVVFS MCFGFVIGNM KEQGQALREF FDSLNEAIMR LVAVIMWYAP VGILFLIAGK   300
IVEMEDMGVI GGQLAMYTVT VIVGLLIHAV IVLPLLYFLV TRKNPWVFIG GLLQALITAL   360
GTSSSSATLP ITFKCLEENN GVDKRVTRFV LPVGATINMD GTALYEALAA IFIAQVNNFE   420
LNFGQIITIS ITATAASIGA AGIPQAGLVT MVIVLTSVGL PTDDITLIIA VDWFLDRLRT   480
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Seq ID NO: 259 DNA sequence
Nucleic Acid Accession #: NM_021948.1
Coding sequence: 48..2783

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TGGAAGGAGA CAGCTCAGAG GACCGCGCTT TTCGCGTGCG CATCGCGGGC GACGCGCCAC   180
TGCAGGGCGT GCTCGGCGGC GCCCTCACCA TCCCTTGCCA CGTCCACTAC CTGCGGCCAC   240
CGCCGAGCCG CCGGGCTGTG CTGGGCTCTC CGCGGGTCAA GTGGACTTTC CTGTCCCGGG   300
GCCGGGAGGC AGAGGTGCTG GTGGCGCGGG GAGTGCGCGT CAAGGTGAAC GAGGCCTACC   360
GGTTCCGCGT GGCACTGCCT GCGTACCCAG CGTCGCTCAC CGACGTCTCC CTGGCGCTGA   420
GCGAGCTGCG CCCCAACGAC TCAGGTATCT ATCGCTGTGA GGTCCAGCAC GGCATCGATG   480
ACAGCAGCGA CGCTGTGGAG GTCAAGGTCA AAGGGGTCGT CTTTCTCTAC CGAGAGGGCT   540
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CCTCCAACCC AGCCTCCAAC CCAGCCTCTG ATGGACTAGA GGCTATCGTC ACAGTGACAG  1200
AGACCCTGGA GGAACTGCAG CTGCCTCAGG AAGCCACAGA GAGTGAATCC CGTGGGGCCA  1260
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CAGAGGCCCC TAGGACGCTC CTAGAATTTG AAACACAATC CATGGTACCG CCCACGGGGT  1380
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Seq ID NO: 260 Protein sequence
Protein Accession #: NP_068767.1

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SLALSELRPN DSGIYRCEVQ HGIDDSSDAV EVKVKGVVFL YREGSARYAF SFSGAQEACA   180
RIGAHIATPE QLYAAYLGGY EQCDAGWLSD QTVRYPIQTP REACYGDMDG FPGVRNYGVV   240
DPDDLYDVYC YAEDLNGELF LGDPPEKLTL EEARAYCQER GAEIATTGQL YAAWDGGLDH   300
CSPGWLADGS VRYPIVTPSQ RCGGGLPGVK TLFLFPNQTG FPNKHSRFNV YCFRDSAQPS   360
AIPEASNPAS NPASDGLEAI VTVTETLEEL QLPQEATESE SRGAIYSIPI MEDGGGGSST   420
PEDPAEAPRT LLEFETQSMV PPTGFSEEEG KALEEEEKYE DEEEKEEEEE EEEVEDEALW   480
AWPSELSSPG PEASLPTEPA AQEESLSQAP ARAVLQPGAS PLPDGESEAS RPPRVHGPPT   540
ETLPTPRERN LASPSPSTLV EAREVGEATG GPELSGVPRG ESEETGSSEG APSLLPATRA   600
PEGTRELEAP SEDNSGRTAP AGTSVQAQPV LPTDSASRGG VAVVPASGDC VPSPCHNGGT   660
CLEEEEGVRC LCLPGYGGDL CDVGLRFCNP GWDAFQGACY KHFSTRRSWE EAETQCRMYG   720
AHLASISTPE EQDFINNRYR EYQWIGLNDR TIEGDFLWSD GVPLLYENWN PGQPDSYFLS   780
GENCVVMVWH DQGQWSDVPC NYHLSYTCKM GLVSCGPPPE LPLAQVFGRP RLRYEVDTVL   840
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Seq ID NO: 261 DNA sequence
Nucleic Acid Accession #: NM_004386.1
Coding sequence: 2..3967

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CTTTACCCTG CAGCCACGGC CAAGCGCAGC CCGAGATGCC CCTCGGATAA AGTGGACCAA   240
GGTGCGGACT GCGTCGGGCC AGCGACAGGA CTTGCCCATC CTGGTGGCCA AGGACAATGT   300
CGTGAGGGTG GCCAAAAGCT GGCAGGGACG AGTGTCACTG CCTTCCTACC CCCGGCGCCG   360
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TGTGTTCCAC TACCGATCAG CCCGGGACCG CTATGCACTG ACCTTCGCTG AGGCCCAGGA   540
GGCCTGCCGT CTCAGCTCAG CCATCATTGC AGCCCCTCGG CATCTACAGG CTGCCTTTGA   600
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TCTGCGTGTG CCATGTGCGT GGCACGCATA TGAGTGTGTG TGCGTGTGAA CGGCTTTGGG  6180
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Seq ID NO: 262 Protein sequence
Protein Accession #: NP_004377.1

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WO03042661 [file:///E:/WO03042661.pcp]


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LDQCDPGWLA DGSVRYPIQT PRRRCGGPAP GVRTVYRFAN RTGFFSPAER FDAYCFRAHH   360
PTSQHGDLET PSSGDEGEIL SAEGPPVREL EPTLEEEEVV TPDFQEPLVS SGEEETLILE   420
EKQESQQTLS PTPGDPMLAS WPTGEVWLST VAPSPSDMGA GTAASSHTEV APTDPMPRRR   480
GRFKGLNGRY FQQQEPEPGL QGGMEASAQP PTSEAAVNQM EPPLAMAVTE MLGSGQSRSP   540
WADLTNEVDM PGAGSAGGKS SPEPWLWPPT MVPPSISGHS RAPVLELEKA EGPSARPATP   600
DLFWSPLEAT VSAPSPAPWE AFPVATSPDL PMMAMLRGPK EWMLPHPTPI STEANRVEAH   660
GEATATAPPS PAAETKVYSL PLSLTPTGQG GEAMPTTPES PRADFRETGE TSPAQVNKAE   720
HSSSSPWPSV NRNVAVGFVP TETATEPTGL RGIPGSESGV FDTAESPTSG LQATVDEVQD   780
PWPSVYSKGL DASSPSAPLG SPGVFLVPKV TPNLEPWVAT DEGPTVNPMD STVTPAPSDA   840
SGIWEPGSQV PEEAESTTLS PQVALDTSIV TPLTTLEQGD KVGVPAMSTL GSSSSQPHPE   900
PEDQVETQGT SGASVPPHQS SPLGKPAVPP GTPTAASVGE SASVSSGEPT VPWDPSSTLL   960
PVTLGIEDFE LEVLAGSPGV ESFWEEVASG EEPALPGTPM NAGAEEVHSD PCENNPCLHG  1020
GTCNANGTMY GCSCDQGFAG ENCEIDIDDC LCSPCENGGT CIDEVNGFVC LCLPSYGGSF  1080
CEKDTEGCDR GWHKFQGHCY RYFAHRRAWE DAEKDCRRRS GHLTSVHSPE EHSFINSFGH  1140
ENTWIGLNDR IVERDFQWTD NTGLQFENWR ENQPDNFFAG GEDCVVMVAH ESGRWNDVPC  1200
NYNLPYVCKK GTVLCGPPPA VENASLIGAR KAKNNVHATV RYQCNEGFAQ HHVVTIRCRS  1260
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Seq ID NO: 263 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 7..2085

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ACGCGGACCC TGCAGGCCCT CAGCTCGGAG AAGAAGGCCA AGAAGGCGCG CTTCTACCGG   240
AACGGGGACC GCTACTTCAA GGGCCTGGTG TTTGCCATCT CCAGCGACCG CTTCCGGTCC   300
TTCGATGCGC TCCTCATAGA GCTCACCCGC TCCCTGTCGG ACAACGTGAA CCTGCCCCAG   360
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Seq ID NO: 264 Protein sequence
Protein Accession #: Eos sequence

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SSVKSEVKES KDFIKPKLVT VIRSGVKPRK AVRILLNKKT AHSFEQVLTD ITEAIKXASG   240
VVKRLCTLDG KQVRVTCVHL PDFFGDDDVF IACGPEKFRY AQDDFVLDHS ECRVLKSSYS   300
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YKIGKVIGDG NFAVVKECID RSTGKEFALK IIDKAKCCGK EHLIENEVSI LRRVKHPNII   420
MLVEEMETAT ELFLVMELVK GGDLFDAITS STKYTERDGS AMVYNLANAL RYLHGLSIVH   480
RDIKPENLLV CEYPDGTKSL KLGDFGLATV VEGPLYTVCG TPTYVAPXII AETGYGLKVD   540
IWAAGVITYI LLCGFPPFRS ENNLQEDLFD QILAGKLEFP APYWDNITDS AKELISQMLQ   600
VNVEARCTAG QILSHPWVSD DASQENNMQA EVTGKLKQHF NNALPKQNST TTGVSVIMVS   660
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Seq ID NO: 265 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

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TGCTTGCTTT TATGTTGCTG TAATTTTTAT TTTAAATGGA CTAATGATGG CATTATTCTT   240
CATATATGGC ACATATTTAA GTGGCAGCCG ATTAGGAGGC CTGGTTACAG TGTTGTGCTT   300
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Seq ID NO: 266 Protein sequence
Protein Accession #: BAA74900.1

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GYIDICKLRK IIYIHMISLA LCFVLMFGNS MLLTSYYASS LVIIWGILAM KPHFLKINVS   240
ELSLWVIQGC FWLPGTVILK YLTSKIFGIA DDAHIGNLLT SKFFSYKDFD TLLYTCAAEF   300
DPMEKETPLR YTKTLLLPVV LVVFVAIVRK IISDMWGVLA KQQTHVRKHQ FDHGELVYHA   360
LQLLAYTALG ILIMRLKLFL TPHMCVMASL ICSRQLFGWL FCKVHPGAIV FAILAAMSIQ   420
GSANLQTQWN IVGEFSNLPQ EELIEWIKYS TKPDAVFAGA MPTMASVKLS ALRPIVNHPH   480
YEDAGLRART KIVYSMYSRK AAEEVKRELI KLKVNYYILE ESWCVRRSKP GCSMPEIWDV   540
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Seq ID NO: 267 DNA sequence
Nucleic Acid Accession #: U26744.1
Coding sequence: 59..1600

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Seq ID NO: 268 Protein sequence
Protein Accession #: AAC50426.1

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Seq ID NO: 269 DNA sequence
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Coding sequence: 127..1278

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TGCTCTGCAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT   240
GGGAGCTGCT TCCCAGATGC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT   300
GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGGA ATGATGTGAC GCTCTACGGC   360
ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTTGTC TGTCGGAGGA   420
TGGAACTTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT   480
TTCATCAAGT CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC   540
TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCCTAATCAA GGAAATGAAG   600
GCCGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG CGCAGCACTG   660
TCTGCGGGGA AGGTCACCAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG   720
GATTTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GGCGTGGGAC CACAGGCCAT   780
CACAGTCCCC TGTTCCGAGG TCAGGAGGAT GCAAGTCCTG ACAGATTCAG CAACACTGAC   840
TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC   900
CCCACCTTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTTGG AGCCCCAATC   960
TCAGGACCGG GAATTCCAGG CCGGTTCACC AAGGAGGCAG GGACCCTTGC CTACTATGAG  1020
ATCTGTGACT TCCTCCGCGG AGCCACAGTC CATAGAACCC TCGGCCAGCA GGTCCCCTAT  1080
GCCACCAAGG GCAACCAGTG GGTAGGATAC GACGACCAGG AAAGCGTCAA AAGCAAGGTG  1140
CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC  1200
TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT  1260
GCACTCGCTG CAACGTAGCC CTCTGTTCTG CACACAGCAC GGGGGCCAAG GATGCCCCGT  1320
CCCCCTCTGG CTCCAGCTGG CCGGGAGCCT GATCACCTGC CCTGCTGAGT CCCAGGCTGA  1380
GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA  1440
GCCCTGGTGG GCAGAGAGGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA  1500
GACTCGGGAT TAGTACACAC TTGTTGATGA TTAATGGAAA TGTTTACAGA TCCCCAAGCC  1560
TGGCAAGGGA ATTTCTTCAA CTCCCTGCCC CCTAGCCCTC CTTATCAAAG GACACCATTT  1620
TGGCAAGCTC TATCACCAAG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA  1680
TACCCCCTGC AAAGCCAGCT TGAAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT  1740
ACTTCCCCTT CCTAATTCCA CAGCTGCTCA ATAAAGTACA AGAGTTTAAC AGTGTGTTGG  1800
CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCCCCCATC  1860
TCTTCTGGGT TCCTTCCTCT GAGCCTTGGG ACCCCTGAGC TTGCAGAGAT GAAGGCCGCC  1920
ATGTT
```

Seq ID NO: 270 Protein sequence
Protein Accession #: NP_001267.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGVKASQTGF VVLVLLQCCS AYKLVCYYTS WSQYREGDGS CFPDALDRFL CTHIIYSFAN    60
ISNDHIDTWE WNDVTLYGML NTLKNRNPNL KTLLSVGGWN FGSQRFSKIA SNTQSRRTFI   120
KSVPPFLRTH GFDGLDLAWL YPGRRDKQHF TTLIKEMKAE FIKEAQPGKK QLLLSAALSA   180
GKVTIDSSYD IAKISQHLDF ISIMTYDFHG AWRGTTGHHS PLFRGQEDAS PDRFSNTDYA   240
VGYMLRLGAP ASKLVMGIPT FGRSFTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC   300
DFLRGATVHR TLGQQVPYAT KGNQWVGYDD QESVKSKVQY LKDRQLAGAM VWALDLDDFQ   360
GSFCGQDLRF PLTNAIKDAL AAT
```

Seq ID NO: 271 DNA sequence
Nucleic Acid Accession #: NM_006474.1
Coding sequence: 181..669

```
1          11         21         31         41         51
|          |          |          |          |          |
GCTGCCTAGG GTCTGGAAAG CTCGGGCACC CTCCCTCTCC GGGGCTCCTG CTCCCACCCC    60
TCCGGCCCCC CCACCGTCGC GCTCCTCCAG GCTGGGCCTG TGGCCGCGGT GCTTTTAATT   120
TTCCCCCAGC TCAGAATCTT GCTGCTCGGC CCCCAGGAGA GCAACAACTC AACGGGAACG   180
ATGTGGAAGG TGTCAGCTCT GCTCTTCGTT TTGGGAAGCG CGTCGCTCTG GGTCCTGGCA   240
GAAGGAGCCA GCACAGGCCA GCCAGAAGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC   300
GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAGCGA AGACCGCTAT   360
AAGTCTGGCT TGACAACTCT GGTGGCAACA AGTGTCAACA GTGTAACAGG CATTCGCATC   420
GAGGATCTGC CAACTTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA   480
GCCTCAAACG TGGCCACCAG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACAACA   540
GTTGAGAAAG ATGGTTTGTC AACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA   600
GCCATCGGTT TCATTGGTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGGAAGGTAC   660
TCGCCCTAAA GAGCTGAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT   720
TTCTGACTCT GTGGCCCTGT CCCTGAGCTC GTGGGGAGAA GATGACCCTG GGAACATTTG   780
CGGGCCCATT CAGATTCCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT   840
```

TCACCAGATT TGGTTCTTAA ACTTT

Seq ID NO: 272 Protein sequence
Protein Accession #: NP_006465.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MWKVSALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSEDRY    60
KSGLTTLVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVATSHST EKVDGDTQTT   120
VEKDGLSTVT LVGIIVGVLL AIGFIGGIIV VVMRKMSGRY SP
```

Seq ID NO: 273 DNA sequence
Nucleic Acid Accession #: CAT cluster

```
1          11         21         31         41         51
|          |          |          |          |          |
GCGGCCGCCA GCTTGCAAAG CCGAAGTCTG GCCGCGCTCT TCGACTCGCT GCGCCACGTC    60
CCCGGGGGTG CCGAGCCGGC GGGGGGTGAG GTGGCTGCGC CGGCGGCCGG GCTAGGAGGT   120
GCGGGCACTG GGGGCGCGGG AGGGGACGTG GCAGGCCCCG CGGGGGCCAC GGCGATCCCA   180
GGGGCCAGGA AGGTCCCGCT GCGGGCACGC AATCTGCCTC CGTCCTTCTT CACGGAGCCG   240
TCCCGGGCAG GCGGCGGCGG GTGTGGCCCG TCGGGGCCGG ACGTGAGCTT GGGCGACCTG   300
GAGAAGGGCG CGGAGGCCGT GGAGTTCTTT GAGCTGCTGG GGCCCGACTA CGGCGCCGGC   360
ACGGAGGCGG CAGTCTTGCT TGCCGCCGAG CCTCTCGACG TGTTCCCCGC CGGAGCCTCC   420
GTACTGCGGG GACCCCCGGA GCTGGAGCCC GGCCTCTTTG AGCCGCCGCC GGCAGTGGTG   480
GGAAACCTAC TGTACCCCGA GCCCTGGAGC GTCCCGGGCT GCTCCCCGAC CAAAAAGAGC   540
CCCTTGACTG CCCTCCGCGG CGGGTTGACC TTGAACGAGC CCTTGAGCCC CCTGTACCCC   600
GCCGCTGCGA ATTTCTCCCG GCGGGGAGGA CGGGCCGGGC CATTTGGCTT CTTTCGCCCC   660
CTTCTTTCCA GACTGCGCTT TGC
```

Seq ID NO: 274 DNA sequence
Nucleic Acid Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
CAAAGAGGCC GGGCTCCAGC TCCGGGGGTC CCCGCAGTAC GGAGGCTCCG GCGGGGAACA    60
CGTCGAGAGG CTCGGCGGCA AGCAAGACTG CCGCCTCCGT GCCGGCGCCG TAGTCGGGCC   120
CCAGCAGCTC AAAGAACTCC ACGGCCTCCG CGCCCTTCTC CAGGTCGCCC AAGCTCACGT   180
CCGGCCCCGA CGGGCCACAC CCGCCGCCGC CTGCCCGGGA CGGCTCCGTG AACAAGGACG   240
GAGGCAGATT GCGTGCCCGC AGCGGGACCT TCCTGGCCCC TGGGATCGCC GTGGCCCCCG   300
CGGGGCCTGC CACGTCCCCT CCCGCGCCCC CAGTGCCCGC ACCTCCTAGC CCGGCCGCCG   360
GCGCAGCCAC CTCACCCCCC GCCGGCTCGG CACCCCCGGG GACGTGGCGC AGCGAGTCGA   420
AGAGCGCGGC CAGACTTCGG CTTTGCAAGC TGGCGGCCGC
```

Seq ID NO: 275 DNA sequence
Nucleic Acid Accession #: NM_001118.1
Coding sequence: 74..1651

```
1          11         21         31         41         51
|          |          |          |          |          |
AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG    60
GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG   120
TCCGTGGGGC CGGGGCAGAC TCCGCAAAGG ACGCGCAGCC TGCAAGTCCG CGGCCCAGAG   180
ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCAAGAAG   240
TGTCATGGCT GGTGTCGTGC ACGTTTCCCT GGCTGCTCTC CTCCTGCTGC CTATGGCCCC   300
TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCCTGG AGAAGATCCA   360
GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCCTCTCCA GGCTGTCCTG GGATGTGGGA   420
CAACATCACG TGTTGGAAGC CCGCCCATGT GGGTCAGATG GTCCTGGTCA GCTGCCCTGA   480
GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCATTG GAGAGTCTGA   540
TTTTGGTGAC AGTAACTCCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAACTGCAC   600
GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTACTTTGAT GCCTGTGGGT TTGATGAATA   660
TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCCC TCTACACGGT   720
TGGCTACAGC ACATCCCTCG TCACCCTCAC CACTGCCATG GTCATCCTTT GTCGCTTCCG   780
GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTCGT TCATGCTGAG   840
GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG   900
CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTC TTCCACTACT GTGTTGTGTC   960
CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT  1020
CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGCTGGGGGA CCCCAACTGT  1080
GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT  1140
GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT  1200
TAACTTTGTG CTTTTTATTG GCATTATCGT CATCCTTGTG CAGAAACTTC AGTCTCCAGA  1260
CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT  1320
CCCACTATTC GGAATCCACT ACACAGTATT TGCCTTCTCC CCAGAGAATG TCAGCAAAAG  1380
GGAAAGACTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCTTTGTGG TGGCTGTTCT  1440
CTACTGTTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAAATGGC GAAGCTGGAA  1500
GGTGAACCGT TACTTCGCTG TGGACTTCAA GCACCGACAC CCGTCTCTGG CCAGCAGTGG  1560
GGTGAATGGG GGCACCCAGC TCTCCATCCT GAGCAAGAGC AGCTCCCAAA TCCGCATGTC  1620
TGGCCTCCCT GCTGACAATC TGGCCACCTG AGCCATGCTC CCCT
```

Seq ID NO: 276 Protein sequence
Protein Accession #: NP_001109.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAGVVHVSLA AHCGACPWGR GRLRKGRAAC KSAAQRHIGA DLPLLSVGGQ WCWPRSVMAG    60
```

```
VVHVSLAALL LLPMAPAMHS DCIFKKEQAM CLEKIQRANE LMGFNDSSPG CPGMWDNITC   120
WKPAHVGEMV LVSCPELFRI FNPDQVWETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW   180
SEPFPHYFDA CGFDEYESET GDQDYYYLSV KALYTVGYST SLVTLTTAMV ILCRFRKLHC   240
TRNFIHMNLF VSFMLRAISV FIKDWILYAE QDSNHCFIST VECKAVMVFF HYCVVSNYFW   300
LFIEGLYLFT LLVETFFPER RYFYWYTIIG WGTPTVCVTV WATLRLYFDD TGCWDMNDST   360
ALWWVIKGPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGGN ESSIYLRLAR STLLLIPLFG   420
IHYTVFAFSP ENVSKRERLV FELGLGSFQG FVVAVLYCFL NGEVQAEIKR KWRSWKVNRY   480
FAVDFKHRHP SLASSGVNGG TQLSILSKSS SQIRMSGLPA DNLAT
```

Seq ID NO: 277 DNA sequence
Nucleic Acid Accession #: NM_004000.1
Coding sequence: 36..1193

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1          11         21         31         41         51
|          |          |          |          |          |
AGAAGAAGCT GGCCAAGGAT ATGGGAGCAA CCACCATGGA CCAGAAGTCT CTCTGGGCAG    60
GTGTAGTGGT CTTGCTGCTT CTCCAGGGAG GATCTGCCTA CAAACTGGTT TGCTACTTTA   120
CCAACTGGTC CCAGGACCGG CAGGAACCAG GAAAATTCAC CCCTGAGAAT ATTGACCCCT   180
TCCTATGCTC TCATCTCATC TATTCATTCG CCAGCATCGA AAACAACAAG GTTATCATCA   240
AGGACAAGAG TGAAGTGATG CTCTACCAGA CCATCAACAG TCTCAAAACC AAGAATCCCA   300
AACTGAAAAT TCTCTTGTCC ATTGGAGGGT ACCTGTTTGG TTCCAAAGGG TTCCACCCTA   360
TGGTGGATTC TTCTACATCA CGCTTGGAAT TCATTAACTC CATAATCCTG TTTCTGAGGA   420
ACCATAACTT TGATGGACTG GATGTAAGCT GGATCTACCC AGATCAGAAA GAAAACACTC   480
ATTTCACTGT GCTGATTCAT GAGTTAGCAG AAGCCTTTCA GAAGGACTTC ACAAAATCCA   540
CCAAGGAAAG GCTTCTCTTG ACTGCGGGCG TATCTGCAGG GAGGCAAATG ATTGATAACA   600
GCTATCAAGT TGAGAAACTG GCAAAAGATC TGGATTTCAT CAACCTCCTG TCCTTTGACT   660
TCCATGGGTC TTGGGAAAAG CCCCTTATCA CTGGCCACAA CAGCCCTCTG AGCAAGGGGT   720
GGCAGGACAG AGGGCCAAGC TCCTACTACA ATGTGGAATA TGCTGTGGGG TACTGGATAC   780
ATAAGGGAAT GCCATCAGAG AAGGTGGTCA TGGGCATCCC CACATATGGG CACTCCTTCA   840
CACTGGCCTC TGCAGAAACC ACCGTGGGGG CCCCTGCCTC TGGCCCTGGA GCTGCTGGAC   900
CCATCACAGA GTCTTCAGGC TTCCTGGCCT ATTATGAGAT CTGCCAGTTC CTGAAAGGAG   960
CCAAGATCAC GCGCCTCCAG GATCAGCAGG TTCCCTACGC AGTCAAGGGG AACCAGTGGG  1020
TGGGCTATGA TGATGTGAAG AGTATGGAGA CCAAGGTTCA GTTCTTAAAG AATTTAAACC  1080
TGGGAGGAGC CATGATCTGG TCTATTGACA TGGATGACTT CACTGGCAAA TCCTGCAACC  1140
AGGGCCCTTA CCCTCTTGTC CAAGCAGTCA AGAGAAGCCT TGGCTCCTTG TGAAGGATTA  1200
ACTTACAGAG AAGCAGGCAA GATGACCTTG CTGCCTGGGG CCTGCTCTCT CCCAGGAATT  1260
CTCATGTGGG ATTCCCCTTG CCAGGCTGGC CTTTGGATCT CTCTTCCAAG CCTTTCCTGA  1320
CTTCCTCTTA GATCATAGAT TGGACCTGGT TTTGTTTTCC TGCAGCTGTT GACTTGTTGC  1380
CCTGAAGTAC AATAAAAAAA ATTCATTTTG CTCCAGTA
```

Seq ID NO: 278 Protein sequence
Protein Accession #: NP_003991.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDQKSLWAGV VVLLLLQGGS AYKLVCYFTN WSQDRQEPGK FTPENIDPFL CSHLIYSFAS    60
IENNKVIIKD KSEVMLYQTI NSLKTKNPKL KILLSIGGYL FGSKGFHPMV DSSTSRLEFI   120
NSIILFLRNH NFDGLDVSWI YPDQKENTHF TVLIHELAEA FQKDFTKSTK ERLLLTAGVS   180
AGRQMIDNSY QVEKLAKDLD FINLLSFDFH GSWEKPLITG HNSPLSKGWQ DRGPSSYYNV   240
EYAVGYWIHK GMPSEKVVMG IPTYGHSFTL ASAETTVGAP ASGPGAAGPI TESSGFLAYY   300
EICQFLKGAK ITRLQDQQVP YAVKGNQWVG YDDVKSMETK VQFLKNLNLG GAMIWSIDMD   360
DFTGKSCNQG PYPLVQAVKR SLGSL
```

Seq ID NO: 279 DNA sequence
Nucleic Acid Accession #: NM_015166.1
Coding sequence: 116..1249

```
1          11         21         31         41         51
|          |          |          |          |          |
TGCTGGAAGT CCCTCACCCA GAGACCAGTG CTCCCAACGG CAGAGCAGCG GGGGAGATAA    60
AGAACTGGTG ACACGTGGCT GTACATTCAG CACAGCTGTG GTGTCCCCAA GTGCCATGAC   120
CCAGGAGCCA TTCAGAGAGG AGCTGGCCTA TGACCGGATG CCCACGCTGG AGCGGGGCCG   180
GCAAGACCCC GCCAGCTATG CCCCAGACGC GAAGCCGAGC GACCTGCAGC TGTCGAAGAG   240
ACTGCCCCCC TGCTTCAGCC ACAAGACGTG GGTCTTCTCT GTGCTGATGG GGAGCTGCCT   300
CCTGGTGACC TCGGGGTTTT CGCTGTACCT GGGGAACGTG TTCCCGGCTG AGATGGATTA   360
CTTGCGCTGT GCTGCAGGCT CTTGCATCCC CTCGGCAATT GTGAGCTTCA CCGTCTCCAG   420
GAGGAACGCC AATGTGATTC CCAACTTTCA GATATTGTTT GTTTCCACGT TTGCTGTGAC   480
CACTACGTGT TTAATTTGGT TTGGATGCAA ACTAGTCCTG AACCCATCAG CAATAAACAT   540
CAACTTCAAC CTCATCCTGC TGCTCCTGCT GGAGCTGCTC ATGGCGGCCA CGGTGATCAT   600
CGCTGCACGG TCCAGCGAGG AGGACTGCAA GAAAAAGAAG GGCTCCATGT CTGACAGCGC   660
CAACATTCTG GACGAAGTGC CATTTCCTGC TCGGGTCCTG AAATCTTACT CAGTCGTCGA   720
GGTAATCGCA GGCATCTCTG CCGTCCTCGG GGGGATCATT GCCCTGAACG TGGATGACTC   780
AGTTTCAGGC CCACACCTCT CAGTGACGTT CTTTTGGATC CTAGTGGCCT GCTTTCCAAG   840
TGCCATTGCC AGTCATGTGG CAGCAGAGTG TCCCAGCAAG TGTCTGGTGG AGGTCCTGAT   900
TGCCATAAGC AGCCTCACGT CTCCGCTGCT GTTCACAGCC TCTGGATATC TGTCATTCAG   960
CATCATGAGA ATCGTGGAGA TGTTTAAGGA TTACCCGCCA GCCATAAAAC CATCCTACGA  1020
TGTGCTGCTG CTGCTGCTGC TGCTAGTGCT CCTGCTGCAG GCCGGCCTCA ACACGGGCAC  1080
CGCCATCCAG TGCGTGCGCT TCAAGGTCAG TGCAAGGCTG CAGGGTGCAT CCTGGGACAC  1140
CCAGAACGGC CCGCAGGAGC GCCTGGCTGG GGAGGTGGCC AGGAGCCCCC TGAAGGAGTT  1200
CGACAAGGAG AAAGCCTGGA GAGCCGTCGT GGTGCAAATG GCCCAGTGAC CCCCAGACGC  1260
GGAAACCGGG TGGCAGCGCC CAGCCTGGCC CCAAGCATGG AAACGCACAA CCCCTAATCG  1320
CCCTGAGCTA CTGCTTCTAA CACCTCTTTT CCCTTGTGTG AGGGCAAACC AGGCTGCAGG  1380
TGGGGTTTTC ACTTCCTAGG GTAGTTTAAT TTTAAAATAG GCCAATGTTG GCTAGTCTGT  1440
GCCTCAGTGA GATCAGTCAG CTCCGAGTGG CTCCCGTGTC GTAACAGCAG GAGCATGGCC  1500
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GCAACTTCCC AGGCCGAGGA AGGGCCCCCG GCTCGGCCTC TTGAGAGCCC CACCCCTGAA  1560
CTGGCCCCAG CTCCTCTTCC TGCCTCTCTC ATGGCTTGGG CTGGAGTGGG CTCTCTGGAC  1620
CTGACCAGAC TGTGGGTCCC TGCGTCTCCT GCCCACTCTG ACCGGGCTTC CTCCCTCCAC  1680
GCTTAGGGTC TGTCCCGGGT ACTCAGTCAG CCCAGTGGGA TCTTACCCAC TTCCCTGCAA  1740
GGTGCACCTG CCCCAGGCTC AGGCTGCCCA GCGGCTCTTC CTGGACAGTG AGAGCAGGGC  1800
TTGGCGCCTC TGTCCTGGCC CGGGAGCCGC AGGGGCCCCT CCTCCAGAGC CTGGGCGCAA  1860
GCGACACAGG CTGCCGCTGC TCTCCCAGGT GAAATCCACA CCAGTCCACG CCGGGTCGCC  1920
TGCCCTGTCT CCCTACTTAG ACCCAGTCAT TCTAGAGGGA TCCACCGCCA CACTGGCCGG  1980
CCCACGTCCT GGGTGCTGTC ATGCCCAGCT TGGAGTGCCA CGTGGCCGCT GCCCACGTCC  2040
CGGGCACTGT CATGCCCAGC TTGGAGTGCC ACATGGCCGC TGCCCACGTC CCGGGCACTG  2100
TCATGCCCAG CTTGGAGTGC CACGTGGCCG CTGCTGTGAC AGGCAGTGTT CTTGGGGGTG  2160
GGGCTGCATC CAAGGCTTTG TAAACCGGCT GGACCACGTC TCCCTGGCCC CAGTGACCGG  2220
GGGAAGCTGA GCCCCTCCCT CCTGTGTTTG CTCCCATTAC TCAAAATGCA GGACAGATCA  2280
GGTCAGAGCC CAGGAATTCT CACAGGTTCA CCCAGCGCCC TCTACCTCCT AGCAAGTACT  2340
TTGTCTTGAT CCTCACTGAG AAGGCCCCAG GGCAGCGGTC TTCTCCATCT CCGCTGTTTT  2400
GGGGTCTTAG GGTACAGCCC AGGCGGTCAC TGCCCACCTG CCAGGCTGCA GGGACAGTTG  2460
GGTGTGAGAA TAACACTGGC TTTGGGTAGT GCCATGGCCA GGAGTGGGTT TCCCTGCGTC  2520
TCCTCGTCCC GAGGGCGCCT GGGTCCTCCC AGCTGACGGC AGTAAATCCA CAGTGAGTTG  2580
GGGCGACTGT GAAACTGGAA TGCTGTTACT TTGATAATTA CTTTCCAGCA GGTGTTTTCC  2640
TTCACAATGG TTTTGTTTCT TTCCTTCTGA TCTGAGAAGA CATGAACGTT TTCTCTTCAC  2700
CGCCGTGGGG TGTATTGACT GGTCCCCCAT GGGCTGCTGG AAAGGCCCGG AGATGCATCT  2760
GTGGCCTGGG GCCATCAAGA TCAAAGAACC AGGAGGCCTG GGAGATGCAG CTGGATGGGG  2820
CGGCCTGCAG ACCCTGCCAG GGGGTTTGAG GACCCTCCCA GGTTTCCCAC TGCGGAACAG  2880
GAGTGACTCT GGCTGCCAAG ATACCTTCAT GGTGTTCATG ACAAGTGGAA TCATTATTTT  2940
CAACCATTGA AGGGGGATGC AGGCAAGACA CCTTCCCAGC TGCTCCTAGA GGGGACAAGC  3000
CAGGCCCTCT CTGCAGTCCT CGGCAGCTCC GGAAGGACAC AGTCAGGGGC CGGGCAAACA  3060
CTTTGGCCAC AGCCCCAAAC AAGCGCCACC GTGGGAGAGG AGAGGCTGCT GTCACTGGTA  3120
CCGGATGCAG ACCCCACCCT GTCTGCAGGC CACCCCCACC TCCCTGCAGC TTTGAGGCTG  3180
GCGGGGTCTG CTCCTGGGAA TGGGGTGGGA GCCACAGGGA CGACCCGGGG CGGGCTGATG  3240
TCTTCTTGGG GGCAGACCAG AGAGCTCAAG TTTCAGAGTC AGAATTAGGC ACTTGGAACG  3300
TTTTTGCTGG CTTGCACTTT CTTATTTTCT TATTTTAGAG CGCTTAAAAA ATCCGGAAAA  3360
ATGGGGTTTA AAAGAACTGT CTCTTTCAGT CTACATTTTT GTTTAATACG CTTGAGCAAT  3420
AAACGCTGAC TTGCAGACGT G
```

Seq ID NO: 280 Protein sequence
Protein Accession #: NP_055981.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTQEPFREEL AYDRMPTLER GRQDPASYAP DAKPSDLQLS KRLPPCFSHK TWVFSVLMGS    60
CLLVTSGFSL YLGNVFPAEM DYLRCAAGSC IPSAIVSFTV SRRNANVIPN FQILFVSTFA   120
VTTTCLIWFG CKLVLNPSAI NINFNLILLL LLELLMAATV IIAARSSEED CKKKKGSMSD   180
SANILDEVPF PARVLKSYSV VEVIAGISAV LGGIIALNVD DSVSGPHLSV TFFWILVACF   240
PSAIASHVAA ECPSKCLVEV LIAISSLTSP LLFTASGYLS FSIMRIVEMF KDYPPAIKPS   300
YDVLLLLLLL VLLLQAGLNT GTAIQCVRFK VSARLQGASW DTQNGPQERL AGEVARSPLK   360
EFDKEKAWRA VVVQMAQ
```

Seq ID NO: 281 DNA sequence
Nucleic Acid Accession #: NM_004518.1
Coding sequence: 43..2577

```
1          11         21         31         41         51
|          |          |          |          |          |
GCTGAGCCTG AGCCCGACCC GGGGCGCCTC CCGCCAGGCA CCATGGTGCA GAAGTCGCGC    60
AACGGCGGCG TATACCCCGG CCCGAGCGGG GAGAAGAAGC TGAAGGTGGG CTTCGTGGGG   120
CTGGACCCCG GCGCGCCCGA CTCCACCCGG GACGGGGCGC TGCTGATCGC CGGCTCCGAG   180
GCCCCCAAGC GCGGCAGCAT CCTCAGCAAA CCTCGCGCGG GCGGCGCGGG CGCCGGGAAG   240
CCCCCCAAGC GCAACGCCTT CTACCGCAAG CTGCAGAATT TCCTCTACAA CGTGCTGGAG   300
CGGCCGCGCG GCTGGGCGTT CATCTACCAC GCCTACGTGT TCCTCCTGGT TTTCTCCTGC   360
CTCGTGCTGT CTGTGTTTTC CACCATCAAG GAGTATGAGA AGAGCTCGGA GGGGGCCCTC   420
TACATCCTGG AAATCGTGAC TATCGTGGTG TTTGGCGTGG AGTACTTCGT GCGGATCTGG   480
GCCGCAGGCT GCTGCTGCCG GTACCGTGGC TGGAGGGGGC GGCTCAAGTT TGCCCGGAAA   540
CCGTTCTGTG TGATTGACAT CATGGTGCTC ATCGCCTCCA TTGCGGTGCT GGCCGCCGGC   600
TCCCAGGGCA ACGTCTTTGC CACATCTGCG CTCCGGAGCC TGCGCTTCCT GCAGATTCTG   660
CGGATGATCC GCATGGACCG GCGGGGAGGC ACCTGGAAGC TGCTGGGCTC TGTGGTCTAT   720
GCCCACAGCA AGGAGCTGGT CACTGCCTGG TACATCGGCT TCCTTTGTCT CATCCTGGCC   780
TCGTTCCTGG TGTACTTGGC AGAGAAGGGG GAGAACGACC ACTTTGACAC CTACGCGGAT   840
GCACTCTGGT GGGGCCTGAT CACGCTGACC ACCATTGGCT ACGGGGACAA GTACCCCCAG   900
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CGGGGCCCAG CGATCACGGA CAAGGACCGC ACCAAGGGCC CGGCCGAGGC GGAGCTGCCC  1800
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TCTAACAGAT TAGCTGAGAT ATTAACTTAC TCACACGGAC AGGTTGATGC CAGAGCCGTA  7260
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Seq ID NO: 282 Protein sequence
Protein Accession #: NP_004509.1

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SSEGALYILE IVTIVVFGVE YFVRIWAAGC CCRYRGWRGR LKFARKPPCV IDIMVLIASI   180
AVLAAGSQGN VFATSALRSL RFLQILRMIR MDRRGGTWKL LGSVVYAHSK ELVTAWYIGF   240
LCLILASFLV YLAEKGENDH FDTYADALWW GLITLTTIGY GDKYPQTWNG RLLAATFTLI   300
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QYYERTVTVP MYRLIPPLNQ LELLRNLKSK SGLAFRKDPP PEPSPSQKVS LKDRVFSSPR   420
GVAAKGKGSP QAQTVRRSPS ADQSLEDSPS KVPKSWSFGD RSRARQAFRI KGAASRQNSE   480
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QVLSMEKKLD PLVNIYMQRM GIPPTETEAY FGAKEPEPAP PYHSPEDSRE HVDRHGCIVK   660
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ERSLSAYGGG NRASMEFLRQ EDTPGCRPPE GTLRDSDTSI SIPSVDHEEL ERSFSGFSIS   780
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Seq ID NO: 2838 DNA sequence
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Coding sequence: 1..2391

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GCGAGGGGGG CCCAAGTTGT GTCCAAAGGG AACAAACAGC ATTTTCAGCT CAGTCATCAG   240
ACAGGTGATT TGCTCCTGAA TGAGAAATTG GACCGGGAGG AGCTATGCGG CCCCACAGAA   300
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CTCCGTATCA TAGATGTAAA TGACCATTCT CCGGTATTCT TTGAAAATGA AATGCATCTG   420
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CTCACTCGCA GTCGTAGGGA CGGAAGGAAG TACCCGGAAC TAGTACTGGA TAAAGCGCTC   600
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Seq ID NO: 284 Protein sequence
Protein Accession #: AAD43757.1

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MQLVKYLNFE AINSYEVDIE AKDGGGLSGK STVIVQVVDV NDNPPELTLS SVNSPIPENS   360
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GTNAQVTYSL LPPQDPHLPL SSLVSINADN GHLFALRSLD YEALQAFEFR VGATDRGSPA   540
LSSEALVRVL VLDANDNSPF VLYPLQNGSA PCTELVPRAA EPGYLVTKVV AVDGDSGQNA   600
WLSYQLLKAT EPGLFGVWAH NGEVRTARLL SERDAAKHRL VVLVKDNGEP PRSATATLHV   660
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Seq ID NO: 285 DNA sequence
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Coding sequence: 15..2765

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Seq ID NO: 286 Protein sequence
Protein Accession #: NP_001785.2

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1          11         21         31         41         51
|          |          |          |          |          |
MTAGAGVLLL LLSLSGALRA HNEDLTTRET CKAGFSEDDY TALISQNILE GEKLLQVKFS    60
SCVGTKGTQY ETNSMDFKVG ADGTVPATRE LQVPSEQVAF TVTAWDSQTA EKWDAVVRLL   120
VAQTSSPHSG HKPQKGKKVV ALDPSPPPKD TLLPWPQHQN ANGLRRRKRD WVIPPINVPE   180
NSRGPFPQQL VRIRSDKDND IPIRYSITGV GADQPPMEVF SIDSMSGRMY VTRPMDREEH   240
ASYHLRAHAV DMNGNKVENP IDLYIYVIDM NDNRPEFINQ VYNGSVDEGS KPGTYVMTVT   300
ANDADDSTTA NGMVRYRIVT QTPQSPSQNM FTINSETGDI VTVAAGLDRE KVQQYTVIVQ   360
```

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ATDMEGNLNY GLSNTATAII TVTDVNDNPP EFTASTFAGE VPENRVETVV ANLTVMDRDQ   420
PHSPNWNAVY RIISGDPSGH FSVRTDPVTN EGMVTVVKAV DYELNRAFML TVMVSNQAPL   480
ASGIQMSFQS TAGVTISIMD INEAPYFPSN HKLIRLEEGV PPGTVLTTFS AVDPDRFMQQ   540
AVRYSKLSDP ASWLHINATN GQITTAAVLD RESLYTKNNV YEATFLAADN GIPPASGTGT   600
LQIYLIDIND NAPELLPKEA QICEKPNLNA INITAADADV DPNIGPYVFE LPFVPAAVRK   660
NWTITRLNGD YAQLSLRILY LEAGMYDVPI IVTDSGNPPL SNTSIIKVKV CPCDDNGDCT   720
TIGAVAAAGL GTGAIVAILI CILILLTMVL LFVMWMKRRE KERHTKQLLI DPEDDVRDNI   780
LKYDEEGGGE EDQDYDLSQL QQPEAMGHVP SKAPGVRRVD ERPVGAEPQY PIRPMVPHPG   840
DIGDFINEGL RAADNDPTAP PYDSLLVFDY EGSGSTAGSV SSLNSSSSGD QDYDYLNDWG   900
PRFKKLADMY GGGEED
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Seq ID NO: 287 DNA sequence
Nucleic Acid Accession #: AF152495.1
Coding sequence: 1..2397

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1          11         21         31         41         51
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ATGGAGGCCG GAGAGGGGAA GGAGCGCGTT CCGAAACAAA GGCAAGTCCT GATATTCTTT    60
GTTTTGCTGG GCATAGCTCA GGCTAGTTGC CAGCCTAGGC ACTATTCAGT GGCCGAGGAA   120
ACGGAGAGTG GCTCCTTTGT GGCCAATTTG TTAAAAGACC TGGGGCTGGA GATAGGAGAA   180
CTTGCTGTGA GGGGGGCCAG GGTCGTTTCC AAAGGAAAAA AAATGCATTT GCAGTTCGAT   240
AGGCAGACCG GGGATTTGTT GTTAAATGAG AAATTGGACC GGGAGGAGCT GTGCGGCCCC   300
ACAGAGCCCT GTGTCCTACC TTTCCAGGTG TTACTAGAAA ATCCCTTGCA GTTTTTTCAG   360
GCGGAGCTAC GGATTAGGGA CGTAAATGAT CATTCCCCAG TTTTCCTAGA CAAAGAAATA   420
CTTTTGAAAA TTCCAGAAAG TATCACTCCT GGAACTACTT TCTTAATAGA ACGTGCCCAG   480
GACTTGGATG TAGGAACCAA CAGTCTCCAA AATTACACAA TCAGTCCCAA TTTCCACTTT   540
CATCTTAATT TACAAGACAG TCTCGATGGC ATAATATTAC CACAGCTGGT GCTGAACAGA   600
GCCCTGGATC GCGAGGAGCA GCCTGAGATC AGGTTAACCC TCACAGCGCT AGATGGCGGG   660
AGTCCACCCA GGTCCGGCAC GGCCCTGGTA CGGATTGAAG TTGTGGACAT CAATGACAAC   720
GTCCCAGAGT TTGCAAAGCT GCTCTATGAG GTGCAGATCC CGGAGGACAG CCCCGTTGGA   780
TCCCAGGTTG CCATCGTCTC TGCCAGGGAT TTAGACATTG GAACTAATGG AGAAATATCT   840
TATGCATTTT CCCAAGCATC TGAAGACATT CGCAAAACGT TTCGATTAAG TGCAAAATCC   900
GGAGAACTGC TTTTAAGACA GAAACTGGAT TTCGAATCCA TCCAGACATA CACAGTAAAT   960
ATTCAGGCCA CAGATGGTGG GGGCCTATCT GGAACTTGTG TGGTATTTGT CCAAGTGATG  1020
GATTTGAATG ACAATCCTCC GGAACTAACT ATGTCGACAC TTATCAATCA GATCCCAGAA  1080
AACTTGCAGG ACACCCTCAT TGCTGTATTC AGCGTTTCAG ATCCTGACTC CGGAGACAAC  1140
GGAAGGATGG TGTGCTCCAT CCAAGATGAT CTTCCTTTTT TCTTGAAACC TTCTGTTGAG  1200
AACTTTTACA CTCTGGTGAT AAGCACGGCC CTGGACCGGG AGACCAGATC CGAATACAAC  1260
ATCACCATCA CCGTCACCGA CTTCGGGACA CCCAGGCTGA AAACCGAGCA CAACATAACC  1320
GTGCTGGTCT CCGACGTCAA TGACAACGCC CCCGCCTTCA CCCAAACCTC CTACACCCTG  1380
TTCGTCCGCG AGAACAACAG CCCCGCCCTG CACATCGGCA GCGTCAGCGC CACAGACAGA  1440
GACTCGGGCA CCAACGCCCA GGTCACCTAC TCGCTGCTGC CGCCCCAGGA CCCGCACCTG  1500
CCCCTCGCCT CCCTGGTCTC CATCAACGCG GACAACGGCC ACCTGTTCGC TCTCCAGTCG  1560
CTGGACTACG AGGCCCTGCA GGCGTTCGAG TTCCGCGTGG GCGCCGCAGA CCGCGGCTCC  1620
CCGGCGTTGA GCAGCGAGGC GCTGGTGCGC GTGCTGGTGC TGGACGCCAA CGACAACTCG  1680
CCCTTCGTGC TGTACCCGCT GCAGAACGGC TCCGCGCCCT GCACCGAGCT GGTGCCCCGG  1740
GCGGCCGAGC CGGGCTACCT GGTGACCAAG GTGGTGGCGG TGGACGGCGA CTCGGGCCAG  1800
AACGCCTGGC TGTCGTACCA GCTGCTCAAG GCCACGGAGC CCGGGCTGTT CGGCGTGTGG  1860
GCGCACAATG GCGAGGTGCG CACCGCCAGG CTGCTGAGGG AGCGCGACGC TGCCAAGCAG  1920
AGGCTGGTGG TGCTGGTCAA GGACAATGGC GAGCCTCCGC GCTCGGCCAC CGCCACGCTG  1980
CACGTGCTCC TGGTGGACGG CTTCTCCCAG CCCTACCTGC TGCTCCCGGA GGCGGCACCG  2040
GCCCAGGCCC AGGCCGACTT GCTCACCGTC TACCTGGTGG TGGCGTTGGC CTCGGTGTCT  2100
TCGCTCTTCC TCTTCTCGGT GCTCCTGTTC GTGGCGGTGC GGCTGTGCAG GAGGAGCAGG  2160
GCGGCCTCGG TGGGTCGCTG CTCGGTGCCC GAGGGCCCCT TTCCAGGGCA GATGGTGGAC  2220
GTGAGCGGCA CCGGGACCCT GTCCCAGAGC TACCAGTACG AGGTGTGTCT GACTGGAGGC  2280
TCCGGGACAA ATGAGTTCAA GTTCCTGAAG CCAATTATCC CCAACTTCGT TGCTCAGGGT  2340
GCAGAGAGGG TTAGCGAGGC AAATCCCAGT TTCAGGAAGA GCTTTGAATT CACTTAA
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Seq ID NO: 288 Protein sequence
Protein Accession #: AAD43756.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEAGEGKERV PKQRQVLIFF VLLGIAQASC QPRHYSVAEE TESGSFVANL LKDLGLEIGE    60
LAVRGARVVS KGKKMHLQFD RQTGDLLLNE KLDREELCGP TEPCVLPFQV LLENPLQFFQ   120
AELRIRDVND HSPVFLDKEI LLKIPESITP GTTFLIERAQ DLDVGTNSLQ NYTISPNFHF   180
HLNLQDSLDG IILPQLVLNR ALDREEQPEI RLTLTALDGG SPPRSGTALV RIEVVDINDN   240
VPEFAKLLYE VQIPEDSPVG SQVAIVSARD LDIGTNGEIS YAFSQASEDI RKTFRLSAKS   300
GELLLRQKLD FESIQTYTVN IQATDGGGLS GTCVVFVQVM DLNDNPPELT MSTLINQIPE   360
NLQDTLIAVF SVSDPDSGDN GRMVCSIQDD LPFFLKPSVE NFYTLVISTA LDRETRSEYN   420
ITITVTDFGT PRLKTEHNIT VLVSDVNDNA PAFTQTSYTL FVRENNSPAL HIGSVSATDR   480
DSGTNAQVTY SLLPPQDPHL PLASLVSINA DNGHLFALQS LDYEALQAFE FRVGAADRGS   540
PALSSEALVR VLVLDANDNS PFVLYPLQNG SAPCTELVPR AAEPGYLVTK VVAVDGDSGQ   600
NAWLSYQLLK ATEPGLFGVW AHNGEVRTAR LLRERDAAKQ RLVVLVKDNG EPPRSATATL   660
HVLLVDGFSQ PYLLLPEAAP AQAQADLLTV YLVVALASVS SLFLFSVLLF VAVRLCRRSR   720
AASVGRCSVP EGPFPGQMVD VSGTGTLSQS YQYEVCLTGG SGTNEFKFLK PIIPNFVAQG   780
AERVSEANPS PRKSPEFT
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Seq ID NO: 289 DNA sequence
Nucleic Acid Accession #: NM_018674.1
Coding sequence: 390..2009

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1          11         21         31         41         51
|          |          |          |          |          |
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CGGAGCACAT GCTGAGCGGA GCGGCTGGGG CTGCGCGGCG TGGCGGAGCA GCGCTCGCTC    60
CCTCGCTCAC TCGCTCGCTC GCAGGGACAC ACGCAGGGGC TGACAGCTGT GCTGGTGCTG   120
ATAAGGGAAG CCACAAGGAG ACGATCGAGG AGAGAGACAA GCGGCAGCAG AGGCAGCAGC   180
GGCAGAGGCA GCACCAGGGC TGCGGAGCTG CTGGGAGTGG GAGTGACTCC CCCACCTCGG   240
GCCCCCACCC TGTCCCTGTC CTCTTCCCGC TTGCCCTGAG TTTAGAAGAG CAGCCGCTGC   300
CACCACTGCC ACTCGGGAGG GCACCAGGGC TGCTGGCTAG GGAGGGACAG GGCAGGGAGG   360
CTCTGGCCAG TCCCAGCAGC CGGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAAT   420
TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTCG   480
GGGCTGTTGC CCCTGGAGCA GCCCCCCGAG ACCTGGCCAC CTTTGCCAGC ACCAGCACCC   540
TGCATGGACT GGGCCGGGCC TGTGGCCCAG GCCCCCACGG ACTGCGCAGA ACCCTGTGGG   600
CACTGGCCCT ACTCACCTCG CTGGCTGCCT TCCTGTACCA GGCGGCTGGC CTGGCCCGGG   660
GCTACCTGAC CCGGCCTCAC CTGGTGGCAA TGGACCCCGC TGCCCCAGCC CCAGTGGCGG   720
GCTTCCCGGC TGTCACCCTC TGCAATATCA ACCGCTTCCG GCATTCGGCA CTCAGCGATG   780
CCGACATCTT CCACCTGGCC AATCTGACAG GGCTGCCCCC CAAAGACCGG GATGGGCACC   840
GTGCGGCTGG CCTGCGCTAC CCAGAGCCTG ACATGGTAGA CATCCTCAAC CGCACTGGCC   900
ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACTGC TCCGCCAGCA   960
ACTTCTCTGT GGTCTATACT CGCTATGGGA AGTGTTACAC CTTCAACGCG GACCCGCGGA  1020
GCTCGCTGCC CAGCCGGGCA GGGGGCATGG GCAGTGGCCT GGAGATCATG CTGGACATCC  1080
AGCAGGAGGA GTACCTGCCC ATCTGGAGGG AGACAAATGA GACGTCGTTT GAGGCAGGTA  1140
TTCGGGTGCA GATCCACAGC CAGGAGGAGC CGCCCTACAT CCACCAGCTG GGGTTCGGGG  1200
TGTCCCCAGG CTTCCAGACC TTTGTGTCCT GCCAGGAACA GCGGCTGACC TACCTGCCCC  1260
AGCCCTGGGG CAACTGCCGC GCAGAGAGTG AGCTCAGGGA GCCTGAGCTT CAGGGCTACT  1320
CGGCCTACAG TGTGTCTGCC TGCCGGCTGC GCTGTGAAAA GGAGGCCGTG CTTCAGCGCT  1380
GCCACTGCCG GATGGTGCAC ATGCCAGGCA ATGAGACCAT CTGCCCACCA AATATCTACA  1440
TCGAGTGTGC AGACCACACA CTGGACTCCC TGGGTGGGGG CCCTGAGGGC CCGTGCTTCT  1500
GCCCCACCCC CTGCAACCTG ACACGCTATG GGAAAGAGAT CTCCATGGTC AGGATCCCCA  1560
ACAGGGGCTC AGCCCGGTAC CTGGCGAGGA AGTACAACCG CAACGAGACC TACATACGGG  1620
AGAACTTCCT GGTCCTAGAT GTCTTCTTTG AGGCCCTGAC CTCTGAAGCC ATGGAGCAGC  1680
GAGCAGCCTA TGGCCTGTCA GCCCTGCTGG GAGACCTCGG GGGACAGATG GGCCTGTTCA  1740
TTGGGGCCAG CATCCTCACG TTGCTGGAGA TCCTCGACTA CATCTATGAG GTGTCCTGGG  1800
ATCGACTGAA GCGGGTATGG AGGCGTCCCA AGACCCCCCT GCGGACCTCC ACTGGGGGCA  1860
TCTCCACTTT GGGGCTTCAG GAGCTGAAGG AACAGAGTCC CTGCCCGAGC CTGGGCCGAG  1920
CGGAGGGTGG GGGGGTCAGC AGTCTGCTCC CCAATCACCA CCACCCCCAC GGTCCCCCAG  1980
GAGGTCTCTT TGAAGATTTT GCTTGCTAGG ACGGTGCTGT GACTGAAAGG ACCCAGGAGT  2040
CTGGGACCCC TCCTGGGATC CCCAGCACAT TCTCCTGCTC CTGGGAGAGG CCTGGGGGCG  2100
GTGCTCACTG GGAGGGCCAG GACTCAGTTC CTGCTCTCAT CCTCCCCTGC CCTGATGTCA  2160
GCTGCTTTGC ACAAAGGTCC TTCTTGTCCA CACCCCTTAT CCCCAGGCTG GTGCCCCGGG  2220
AGGGCTGGAG ACCAGGCCAT GGGCCCTCAC GGAGAGGAAG GGAAGGAAGG AGAGGGAGGG  2280
GGAGGATAGA GCCCATCCCA GCCGGGGAGG GGGAGCCCTC TGTACATTTG TAAATATTTA  2340
GGGAAAGCCG GGTGGGGGGA GGGGATACAG ATGTAGAAGG TGGGTAGGGC TACAGGGGTG  2400
GGTGATTTAG GGACAGCCAG GGTCCCAGCC CCAATGTCAG CAGGATAGGG AGAGCCCCAG  2460
GACTCAGGAG TGCTGGGCTG GTCCTACTTC CTGCCCCTCT CCAGGCCCAG CTCCCCTCTT  2520
GGCAGGGGGA GAGGATGGCC CAGCAGGCCT GGCCCAGCTC CCAGTTCCCC CTGCACCAGC  2580
CCCACCCCTA GAGTCCCTTC TATAGGGAGG GGGCAGGAGA CCTTCCAGAC TTCGGCTGAG  2640
CTTGGAGGGT GGGAAGGGAG CCTTCTCAGT CCTCTCTCCC TCCAGTCTGA TTTTATAAAG  2700
TGCTGACGAG
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Seq ID NO: 290 Protein sequence
Protein Accession #: NP_061144.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPIEIVCKIK FAEEDAKPKE KEAGDEQSLL GAVAPGAAPR DLATFASTST LHGLGRACGP    60
GPHGLRRTLW ALALLTSLAA FLYQAAGLAR GYLTRPHLVA MDPAAPAPVA GFPAVTLCNI   120
NRFRHSALSD ADIFHLANLT GLPPKDRDGH RAAGLRYPEP DMVDILNRTG HQLADMLKSC   180
NFSGHHCSAS NFSVVYTRYG KCYTFNADPR SSLPSRAGGM GSGLEIMLDI QQEEYLPIWR   240
ETNETSFEAG IRVQIHSQEE PPYIHQLGFG VSPGFQTFVS CQEQRLTYLP QPWGNCRAES   300
ELREPELQGY SAYSVSACRL RCEKEAVLQR CHCRMVHMPG NETICPPNIY IECADHTLDS   360
LGGGPECPCF CPTPCNLTRY GKEISMVRIP NRGSARYLAR KYNRNETYIR ENFLVLDVFF   420
EALTSEAMEQ RAAYGLSALL GDLGGQMGLF IGASILTLLE ILDYIYEVSW DRLKRVWRRP   480
KTPLRTSTGG ISTLGLQELK EQSPCPSLGR AEGGGVSSLL PNHHHPHGPP GGLFEDFAC
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Seq ID NO: 291 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 62..895

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1          11         21         31         41         51
|          |          |          |          |          |
CACTGCTCTG AGAATTTGTG AGCAGCCCCT AACAGGCTGT TACTTCACTA CAACTGACGA    60
TATGATCATC TTAATTTACT TATTTCTCTT GCTATGGGAA GACACTCAAG GATGGGGATT   120
CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG   180
AGAAGCACGG TCTGGCAAAT ACAAGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT   240
TGAAGGCGGC CATCTCGCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTTCA   300
TGTCTGTGCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATTG TGAAGCCAGG   360
GCCCAACTGT GGATTTGGAA AAACTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG   420
TGAAAGATGG GATGCCTATT GCTACAACCC ACACGCAAAG GAGTGTGGTG GCGTCTTTAC   480
AGATCCAAAG CAAATTTTTA AATCTCCAGG CTTCCCAAAT GAGTACGAAG ATAACCAAAT   540
CTGCTACTGG CACATTAGAC TCAAGTATGG TCAGCGTATT CACCTGAGTT TTTTAGATTT   600
TGACCTTGAA GATGACCCAG GTTGCTTGGC TCATTATGTT GAAATATATG ACAGTTACGA   660
TGATGTCCAT GGCTTTGTGG GAAGATACTG TGGAGATGAG CTTCCAGATG ACATCATCAG   720
TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT   780
CCAAATCAAA TATGTTGCAA TGGATCCTGT ATCCAAATCC AGTCAAGGAA AAAATACAAG   840
TACTACTTCT ACTGGAAATA AAAACTTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAAA   900
AAAAAAAGGA TGATCAAAAC ACACAGTGTT TATGTTGGAA TCTTTTGGAA CTCCTTTGAT   960
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CTCACTGTTA TTATTAACAT TTATTTATTA TTTTTCTAAA TGTGAAAGCA ATACATAATT  1020
TAGGGAAAAT TGGAAAATAT AGGAAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC  1080
ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTTT TTCTTTCAGT CATTTTTCTA  1140
TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTGCAT TTGAAATTTT GGAATCCTGC  1200
TCTATGTACA GTTTTGTATT ATACTTTTTA AATCTTGAAC TTTATAAACA TTTTCTGAAA  1260
TCATTGATTA TTCTACAAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA  1320
TGTTTTATGC ATTATTTAAG CCTGTCTCTA TTGTTGGAAT TTCAGGTCAT TTTCATAAAT  1380
ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAAAA AA
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Seq ID NO: 292 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MIILIYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSGKYKLT YAEAKAVCEF    60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFGKTGI IDYGIRLNRS   120
ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF   180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF   240
QIKYVAMDPV SKSSQGKNTS TTSTGNKNFL AGRFSHL
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Seq ID NO: 293 DNA sequence
Nucleic Acid Accession #: NM_007115.1
Coding sequence: 69..902

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1          11         21         31         41         51
|          |          |          |          |          |
GAATTCGCAC TGCTCTGAGA ATTTGTGAGC AGCCCCTAAC AGGCTGTTAC TTCACTACAA    60
CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT   120
GGGGATTCAA GGATGGAATT TTTCATAACT CCATATGGCT TGAACGAGCA GCCGGTGTGT   180
ACCACAGAGA AGCACGGTCT GGCAAATACA AGCTCACCTA CGCAGAAGCT AAGGCGGTGT   240
GTGAATTTGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG   300
GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA   360
AGCCAGGGCC CAACTGATGA TTTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGTCTCA   420
ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAAGGAG TGTGGTGGCG   480
TCTTTACAGA TCCAAAGCGA ATTTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA   540
ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTCAC CTGAGTTTTT   600
TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA   660
GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA   720
TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG   780
GAGGTTTCCA AATCAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA   840
ATACAAGTAC TACTTCTACT GGAAATAAAA ACTTTTTAGC TGGAAGATTT AGCCACTTAT   900
AAAAAAAAAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAATCTTT TGGAACTCCT   960
TTGATCTCAC TGTTATTATT AACATTTATT TATTATTTTT CTAAATGTGA AAGAAATACA  1020
TAATTTAGGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAAATGAA ACCTCTCATA  1080
ATCCCACTGC ATAGAAATAA CAAGCGTTAA CATTTTCATA TTTTTTTCTT TCAGTCATTT  1140
TTGTATTTGT GGTATATGTA TATATGTACC TATATGTATT TGCATTTGAA ATTTTGGAAT  1200
CCTGCTCTAT GTACAGTTTT GTATTATACT TTTTAAATCT TGAACTTTAT GAACATTTTC  1260
TGAAATCATT GATTATTCTA CAAAAACATG ATTTTAAACA GCTGTAAAAT ATTCTATGAT  1320
ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTTCAG GTCATTTTCA  1380
TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC
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Seq ID NO: 294 Protein sequence
Protein Accession #: NP_009046.1

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1          11         21         31         41         51
|          |          |          |          |          |
MIILIYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSGKYKLT YAEAKAVCEF    60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNXXFGKTGI IDYGIRLNRS   120
ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF   180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF   240
QIKYVAMDPV SKSSQGKNTS TTSTGNKNFL AGRFSHL
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Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: NM_001218.2
Coding sequence: 116..1180

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1          11         21         31         41         51
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GTACTCGCCA CGGCACCCAG GCTGCGCGCA CGCGGTCCCG GTGTGCAGCT GGAGAGCGAG    60
CGGCCACCGG GAGCCCCCGG CACAGCCCGC GCCCGCCCCG CAGGAGCCCG CGAAGATGCC   120
CCGGCGCAGC CTGCACGCGG CGGCCGTGCT CCTGCTGGTG ATCTTAAAGG AACAGCCTTC   180
CAGCCCGGCC CCAGTGAACG GTTCCAAGTG GACTTATTTT GGTCCTGATG GGGAGAATAG   240
CTGGTCCAAG AAGTACCCGT CGTGTGGGGG CCTGCTGCAG TCCCCCATAG ACCTGCACAG   300
TGACATCCTC CAGTATGACG CCAGCCTCAC GCCCCTCGAG TTCCAAGGCT ACAATCTGTC   360
TGCCAACAAG CAGTTTCTCC TGACCAACAA TGGCCATTCA GTGAAGCTGA ACCTGCCCTC   420
GGACATGCAC ATCCAGGGCC TCCAGTCTCG CTACAGTGCC ACGCAGCTGC ACCTGCACTG   480
GGGGAACCCG AATGACCCGC ACGGCTCTGA GCACACCGTC AGCGGACAGC ACTTCGCCGC   540
CGAGCTGCAC ATTGTCCATT ATAACTCAGA CCTTTATCCT GACGCCAGCA CTGCCAGCAA   600
CAAGTCAGAA GGCCTCGCTG TCCTGGCTGT TCTCATTGAG ATGGGCTCCT TCAATCCGTC   660
CTATGACAAG ATCTTCAGTC ACCTTCAACA TGTAAAGTAC AAAGGCCAGG AAGCATTCGT   720
CCCGGGATTC AACATTGAAG AGCTGCTTCC GGAGAGGACC GCTGAATATT ACCGCTACCG   780
GGGGTCCCTG ACCACACCCC CTTGCAACCC CACTGTGCTC TGGACAGTTT TCCGAAACCC   840
CGTGCAAATT TCCCAGGAGC AGCTGCTGGC TTTGGAGACA GCCCTGTACT GCACACACAT   900
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GGACGACCCT TCCCCCAGAG AAATGATCAA CAACTTCCGG CAGGTCCAGA AGTTCGATGA   960
GAGGCTGGTA TACACCTCCT TCTCCCAAGT GCAAGTCTGT ACTGCGGCAG GACTGAGTCT  1020
GGGCATCATC CTCTCACTGG CCCTGGCTGG CATTCTTGGC ATCTGTATTG TGGTGGTGGT  1080
GTCCATTTGG CTTTTCAGAA GGAAGAGTAT CAAAAAAGGT GATAACAAGG GAGTCATTTA  1140
CAAGCCAGCC ACCAAGATGG AGACTGAGGC CCACGCTTGA GGTCCCCGGA GCTCCCGGGC  1200
ACATCCAGGA AGGACCTTGC TTTGGACCCT ACACACTTCG GCTCTCTGGA CACTTGCGAC  1260
ACCTCAAGGT GTTCTCTGTA GCTCAATCTG CAAACATGCC AGGCCTCAGG GATCCTCTGC  1320
TGGGTGCCTC CTTGCCTTGG GACCATGGCC ACCCCAGAGC CATCCGATCG ATCGATGGGA  1380
TGCACTCTCA GACCAAGCAG CAGGAATTCA AAGCTGCTTG CTGTAACTGT GTGAGATTGT  1440
GAAGTGGTCT GAATTCTGGA ATCACAAACC AAGCCATGCT GGTGGGCCAT TAATGGTTGG  1500
AAAACACTTT CATCCGGGGC TTTGCCAGAG CGTGCTTTCA AGTGTCCTGG AAAGTCTGCT  1560
GCTTCTCCAA GCTTTCAGAC AAGAATGTGC ACTCTCTGCT TAGGTTTTGC TTGGGAAACT  1620
CAACTTCTTT CCTCTGGAGA CGGGGCATCT CCCTCTGATT TCCTTCTGCT ATGACAAAAC  1680
CTTTAATCTG CACCTTACAA CTCGGGGACA AATGGGGACA GGAAGGATCA AGTTGTAGAG  1740
AGAAAAAAGA AAACAAGAGA TATACATTGT GATATATTAG GGACACTTTC ACAGTCCTGT  1800
CCTCTGGATC ACAGACACTG CACAGACCTT AGGGAATGGC AGGTTCAAGT TCCACTTCTT  1860
GGTGGGGATG AGAAGGGAGA GAGAGCTAGA GGGACAAAGA GAATGAGAAG ACATGGATGA  1920
TCTGGGAGAG TCTCACTTTG GAATCAGAAT TGGAATCACA TTCTGTTTAT CAAGCCATAA  1980
TGTAAGGACA GAATAATACA ATATTAAGTC CAAATCCAAC CTCCTGTCAG TGGAGCAGTT  2040
ATGTTTTATA CTCTACAGAT TTTACAAATA ATGAGGCTGT TCCTTGAAAA TGTGTTGTTG  2100
CTGTGTCCTG GAGGAGACAT GAGTTCCGAG ATGACCCAAT CTGCCTTTGA ATCTGGAGGA  2160
AATAGGCAGA AACAAAATGA CTGTAGAACT TATTCTCTGT AGGCCAAATT TCATTTCAGC  2220
CACTTCTGCA GGATCCCTAC TGCCAACCTG GAATGGAGAC TTTTATCTAC TTCTCTCTCT  2280
CTGAAGATGT CAAATCGTGG TTTAGATCAA ATATATTTCA AGCTATAAAA GCAGGAGGTT  2340
ATCTGTGCAG GGGGCTGGCA TCATGTATTT AGGGGCAAGT AATAATGGAA TGCTACTAAG  2400
ATACTCCATA TTCTTCCCCG AATCACACAG ACAGTTTCTG ACAGGCGCAA CTCCTCCATT  2460
TTCCTCCCGC AGGTGAGAAC CCTGTGGAGA TGAGTCAGTG CCATGACTGA GAAGGAACCG  2520
ACCCCTAGTT GAGAGCACCT TGCAGTTCCC CGAGAACTTT CTGATTCACA GTCTCATTTT  2580
GACAGCATGA AATGTCCTCT TGAAGCATAG CTTTTTAAAT ATCTTTTTCC TTCTACTCCT  2640
CCCTCTGACT CTAAGAATTC TCTCTTCTGG AATCGCTTGA ACCCAGGAGG CGGAGGTTGC  2700
AGTAAGCCAA GGTCATGCCA CTGCACTCTA GCCTGGGTGA CAGAGCGAGA CTCCATCTCA  2760
AAAAAAAAAA AAAAA
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Seq ID NO: 296 Protein sequence
Protein Accession #: NP_001209.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPRRSLHAAA VLLLVILKEQ PSSPAPVNGS KWTYFGPDGE NSWSKKYPSC GGLLQSPIDL    60
HSDILQYDAS LTPLEFQGYN LSANKQFLLT NNGHSVKLNL PSDMHIQGLQ SRYSATQLHL   120
HWGNPNDPHG SEHTVSGQHF AAELHIVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSFN   180
PSYDKIFSHL QHVKYKGQEA FVPGFNIEEL LPERTAEYYR YRGSLTTPPC NPTVLWTVFR   240
NPVQISQEQL LALETALYCT HMDDPSPREM INNFRQVQKF DERLVYTSFS QVQVCTAAGL   300
SLGIILSLAL AGILGICIVV VVSIWLFRRK SIKKGDNKGV IYKPATKMET EAHA
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Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: NM_006632.1
Coding sequence: 377..1582

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1          11         21         31         41         51
|          |          |          |          |          |
ACGCGTCCGC CCACGCGTCC GCCCACGCGT CCGGTCGGGG CCAGAGCGCA GGTGTACCTG    60
GCGGCCGTGC TGGAGCACCT GACCGCCGAG ATCCTGGAGC TGGCTGGCAA CCCGGCCCGC   120
GACAAGAAGA CCCGCATCAT CCTGCGCCAC CTGTAGCTGG CCATTCGCAA CGGCGAGGAG   180
CTTAACAAGC TGCTGGGCGA AGTCACCATC GCGCAGGGCG GTGTCCTGCC CAACATTCAG   240
GGCGTGCTTC TGCCCCAGAA GACCAAGAGC CACCACAACG CCAAGGGTGA AAACCATTCA   300
CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCCACAG CAAGGGAGAG   360
CAAGAACGCA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT   420
ATGTTCTGCT CGCTATGGAA TAGCCCTCGT CTTACATTTC TGCAATTTCA CAACGATAGC   480
ACAAAATGTC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACAA GCCCTCAATC   540
CCAGCTCAAT GATTCCTCTG AGGTGCTGCC TGTTGACTCA TTTGGTGGCC TAAGTAAAGC   600
CCCAAAGAGT CTTCCTGCAA AGTCCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAAA   660
GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTTACT   720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCATTAGT GAAACCCTTG GGTGGCCCTT   780
TGTCTTCTAT ATCTTTGGAG GTGTTGGCTG TGTCTGCTGC CTTCTCTGGT TTGTTGTGAT   840
TTATGATGAC CCCTTTTCCT ATCCATGGAT AAGCACCTCA GAAAAAGAAT ACATCATATC   900
CTCCTTGAAA CAACAGGTCG GGTCTTCTAA GCAGCCTCTT CCCATCAAAG CTATGCTCAG   960
ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGGT TAGTTAGCAC  1020
AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA  1080
TGGACTTCTA TCTGCCCTTC CTTTTATTGT TGCCTGGGTC ATAGGCATGG TGGGAGGCTA  1140
TCTGGCAGAT TTCCTTCTAA CCAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTGCCAC  1200
AATTTTAGGA AGTCTCCCCT CTTCAGCACT CATTGTGTCT CTGCCTTACC TCAATTCCGG  1260
CTATATCACA GCAACTGCCT TGCTGACGCT CTCTTGCGGA TTAAGCACAT TGTGTCAGTC  1320
AGGGATTTAT ATCAATGTCT TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC  1380
ATCAAGAGGA TTTTCGAGCA TAGCACCTGT CATTGTACCC ACTGTCAGCG GATTTCTTCT  1440
TAGTCAGGAC CCTGAGTTTG GGTGGAGGAA TGTCTTCTTC TTGCTGTTTG CCGTTAACCT  1500
GTTAGGACTA CTCTTCTACC TCATATTTGG AGAAGCAGAT GTCCAAGAAT GGGCTAAAGA  1560
GAGAAAACTC ACTCGTTTAT GAAGTTATCC CACCTTGGAT GGAAAAGTCA TTAGGCACCG  1620
TATTGCATAA AATAGAAGGC TTCCGTGATG AAAATACCAG TGAAAAGATT TTTTTTCCCT  1680
GTGGCTCTTT TCAATTATGA GATCAGTTCA TTATTTTATT CAGACTTTTT TTTGAGAGAA  1740
ATGTAAGATG AATAAAAATT CAAATAAAAT GATAACTAAG AAAAAAAAAA AAAAA
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Seq ID NO: 298 Protein sequence
Protein Accession #: NP_006623.1

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1          11         21         31         41         51
|          |          |          |          |          |
MQVDETLIPR KGPSLCSARY GIALVLHFCN FTTIAQNVIM NITMVAMVNS TSPQSQLNDS    60
SEVLPVDSFG GLSKAPKSLP AKSSILGGQF AIWEKWGPPQ ERSRLCSIAL SGMLLGCFTA   120
ILIGGFISET LGWPFVFYIF GGVGCVCCLL WFVVIYDDPF SYPWISTSEK EYIISSLKQQ   180
VGSSKQPLPI KAMLRSLPIW SICLGCFSHQ WLVSTMVVYI PTYISSVYHV NIRDNGLLSA   240
LPFIVAWVIG MVGGYLADFL LTKKFRLITV RKIATILGSL PSSALIVSLP YLNSGYITAT   300
ALLTLSCGLS TLCQSGIYIN VLDIAPRYSS FLMGASRGFS SIAPVIVPTV SGFLLSQDPE   360
FGWRNVFFLL FAVNLLGLLF YLIFGEADVQ EWAKERKLTR L
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Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: NM_003058.1
Coding sequence: 145..1812

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1          11         21         31         41         51
|          |          |          |          |          |
GGCCCTGCCC TGAAGGCTGG TCACTTGCAG AGGTAAACTC CCCTCTTTGA CTTCTGGCCA    60
GGGTTTGTGC TGAGCTGGCT GCAGCCGCTC TCAGCCTCGC TCCGGGCACG TCGGGCAGCC   120
TCGGGCCCTC CTGCCTGCAG GATCATGCCC ACCACCGTGG ACGATGTCCT GGAGCATGGA   180
GGGGAGTTTC ACTTTTTCCA GAAGCAAATG TTTTTCCTCT TGGCTCTGCT CTCGGCTACC   240
TTCGCGCCCA TCTACGTGGG CATCGTCTTC CTGGGCTTCA CCCCTGACCA CCGCTGCCGG   300
AGCCCCGGAG TGGCCGAGCT GAGTCTGCGC TGCGGCTGGA GTCCTGCAGA GGAACTGAAC   360
TACACGGTGC CGGGCCCAGG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC   420
GAGGTGGACT GGAACCAGAG CACCTTTGAC TGCGTGGACC CCCTGGCCAG CCTGGACACC   480
AACAGGAGCC GCCTGCCACT GGGCCCCTGC CGGGACGGCT GGGTGTACGA GACGCCTGGC   540
TCGTCCATCG TCACCGAGTT TAACCTGGTA TGTGCCAACT CCTGGATGTT GGACCTATTC   600
CAGTCATCAG TGAATGTAGG ATTCTTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC   660
AGGTTTGGCC GTAAGCTCTG CCTCCTAACT ACAGTCCTCA TAAATGCTGC AGCTGGAGTT   720
CTCATGGCCA TTTCCCCAAC CTATACGTGG ATGTTAATTT TTCGCTTAAT CCAAGGACTG   780
GTCAGCAAAG CAGGCTGGTT AATAGGCTAC ATCCTGATTA CAGAATTTGT TGGGCGGAGA   840
TATCGGAGAA CAGTGGGGAT TTTTTACCAA GTTGCCTATA CAGTTGGGCT CCTGGTGCTA   900
GCTGGGGTGG CTTACCCACT TCCTCACTGG AGGTGGTTGC AGTTCACAGT TGCTCTGCCC   960
AACTTCTTCT TCTTGCTCTA TTACTGGTGC ATACCTGAGT CTCCCAGGTG GCTGATCTCC  1020
CAGAATAAGA ATGCTGAAGC CATGAGAATC ATTAAGCACA TCGCAAAGAA AAATGGAAAA  1080
TCTCTACCCG CCTCCCTTCA GCGCCTGAGA CTTGAAGAGG AAACTGGCAA GAAATTGAAC  1140
CCTTCATTTC TTGACTTGGT CAGAACTCCT CAGATAAGGA AACATACTAT GATATTGATG  1200
TACAACTGGT TCACGAGCTC TGTGCTCTAC CAGGGCCTCA TCATGCACAT GGGCCTTGCA  1260
GGTGACAATA TCTACCTGGA TTTCTTCTAC TCTGCCCTGG TTGAATTCCC AGCTGCCTTC  1320
ATGATCATCC TCACCATCGA CCGCATCGGA CGCCGTTACC CTTGGGCTGC ATCAAATATG  1380
GTTGCAGGGG CAGCCTGTCT GGCCTCAGTT TTTATACCTG GTGATCTACA ATGGCTAAAA  1440
ATTATTATCT CATGCTTGGG AAGAATGGGG ATCACAATGG CCTATGAGAT AGTCTGCCTG  1500
GTCAATGCTG AGCTGTACCC CACATTCATT AGGAATCTTG GCGTCCACAT CTGTTCCTCA  1560
ATGTGTGACA TTGGTGGCAT CATCACGCCA TTCCTGGTCT ACCGGCTCAC TAACATCTGG  1620
CTTGAGCTCC CGCTGATGGT TTTCGGCGTA CTTGGCTTGG TTGCTGGAGG TCTGGTGCTG  1680
TTGCTTCCAG AAACTAAAGG GAAAGCTTTG CCTGAGACCA TCGAGGAAGC CGAAAATATG  1740
CAAAGACCAA GAAAAAATAA AGAAAAGATG ATTTACCTCC AAGTTCAGAA ACTAGACATT  1800
CCATTGAACT AAGAAGAGAG ACCGTTGCTG CTGTCATGAC CTAGCTTTGA TGGCAGCAAG  1860
ACCAAAAGTA GAAATCCCTG CACTCATCAC AAAGCCCATA CAACTCAACC AAACTTACCC  1920
CTGAGCCCTA TCAACCTAGG TCTACAGCCA GTGGAGTCTA TTGTACACTG TGGAAAAATA  1980
CCCATGGGAC CAGATCCTGC CAAATTCTTC CAGCTCACTT TATTCTCAGC ATTCCTAGGA  2040
CATTGGACAT TGGTTTTCTG GAGGGTTTTT TTTCCGATCT TTGTATTTTT TTAAATTTGA  2100
TTCTTTTCTT TGCAATGCTA GCAACCAGAA TACATAGGGG AACTGTGGGC TAGGCAAANA  2160
AAATAGAAAA AGTGTGAAAA ACAGTAAAGT TGGGAGAGGA GCATCTATTT TCTTAAAGAA  2220
ATAAAACACC NAAAACAAAA AAAAAAAAAA AAAAAAA
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Seq ID NO: 300 Protein sequence
Protein Accession #: NP_003049.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPTTVDDVLE HGGEFHFFQK QMFFLLALLS ATFAPIYVGI VFLGFTPDHR CRSPGVAELS    60
LRCGWSPAEE LNYTVPGPGP AGEASPRQCR RYEVDWNQST FDCVDPLASL DTNRSRLPLG   120
PCRDGWVYET PGSSIVTEFN LVCANSWMLD LFQSSVNVGF FIGSMSIGYI ADRFGRKLCL   180
LTTVLINAAA GVLMAISPTY TWMLIFRLIQ GLVSKAGWLI GYILITEFVG RRYRRTVGIF   240
YQVAYTVGLL VLAGVAYALP HWRWLQFTVA LPNFFFLLYY WCIPESPRWL ISQNKNAEAM   300
RIIKHIAKKN GKSLPASLQR LRLEEETGKK LNPSFLDLVR TPQIRKHTMI LMYNWFTSSV   360
LYQGLIMHMG LAGDNIYLDF FYSALVEFPA AFMIILTIDR IGRRYPWAAS NMVAGAACLA   420
SVFIPGDLQW LKIIISCLGR MGITMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII   480
TPFLVYRLTN IWLELPLMVF GVLGLVAGGL VLLLPETKGK ALPETIEEAE NMQRPRKNKE   540
KMIYLQVQKL DIPLN
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Seq ID NO: 301 DNA sequence
Nucleic Acid Accession #: NM_012206.1
Coding sequence: 52..1131

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1          11         21         31         41         51
|          |          |          |          |          |
GTTACCCAGC ATTGTGAGTG ACAGAGCCTG GATCTGAACG CTGATCCCAT AATGCATCCT    60
CAAGTGGTCA TCTTAAGCCT CATCCTACAT CTGGCAGATT CTGTAGCTGG TTCTGTAAAG   120
GTTGGTGGAG AGGCAGGTCC ATCTGTCACA CTACCCTGCC ACTACAGTGG AGCTGTCACA   180
TCAATGTGCT GGAATAGAGG CTCATGTTCT CTATTCACAT GCCAAAATGG CATTGTCTGG   240
ACCAATGGAA CCCACGTCAC CTATCGGAAG GACACACGCT ATAAGCTATT GGGGGACCTT   300
TCAAGAAGGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGTCTGACAG TGGCGTATAT   360
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TGTTGCCGTG TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACCGT ATCATTGGAG   420
ATTGTGCCAC CCAAGGTCAC GACTACTCCA ATTGTCACAA CTGTTCCAAC CGTCACGACT   480
GTTCGAACGA GCACCACTGT TCCAACGACA ACGACTGTTC CAACGACAAC TGTTCCAACA   540
ACAATGAGCA TTCCAACGAC AACGACTGTT CCGACGACAA TGACTGTTTC AACGACAACG   600
AGCGTTCCAA CGACAACGAG CATTCCAACA ACAACAAGTG TTCCAGTGAC AACAACGGTC   660
TCTACCTTTG TTCCTCCAAT GCCTTTGCCC AGGCAGAACC ATGAACCAGT AGCCACTTCA   720
CCATCTTCAC CTCAGCCAGC AGAAACCCAC CCTACGACAC TGCAGGGAGC AATAAGGAGA   780
GAACCCACCA GCTCACCATT GTACTCTTAC ACAACAGATG GGAATGACAC CGTGACAGAG   840
TCTTCAGATG GCCTTTGGAA TAACAATCAA ACTCAACTGT TCCTAGAACA TAGTCTACTG   900
ACGGCCAATA CCACTAAAGG AATCTATGCT GGAGTCTGTA TTTCTGTCTT GGTGCTTCTT   960
GCTCTTTTGG GTGTCATCAT TGCCAAAAAG TATTTCTTCA AAAAGGAGGT TCAACAACTA  1020
AGTGTTTCAT TTAGCAGCCT TCAAATTAAA GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC  1080
CAAGCAGAAG ACAATATCTA CATTGAGAAT AGTCTTTATG CCACGGACTA AGACCCAGTG  1140
GTGCTCTTTG AGAGTTTACG CCCATGACTG CAGAAGACTG AACAGGTATC AGCACATCAG  1200
ATGTCTTTTA GACTCCAAGA CAATTTTTCT GTTTCAGTTT CATCTGGCAT TCCAACATGT  1260
CAGTGATACT GGGTAGAGTA ACTCTCCCAC TCCAAACTGT GTATAGTCAA CCTCATCATT  1320
AATGTAGTCC TAATTTGTTT TGCTAAAACT GGCTCAATCC TTCTGATCAT TGCAGAGTTT  1380
TCTCTCAAAC ATGAACACTT TAGAATTGTA TGTTCTCTTT AGACCCCATA AATCCTGTAT
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Seq ID NO: 302 Protein sequence
Protein Accession #: NP_036338.1

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1          11         21         31         41         51
|          |          |          |          |          |
MHPQVVILSL ILHLADSVAG SVKVGGEAGP SVTLPCHYSG AVTSMCWNRG SCSLFTCQNG    60
IVWTNGTHVT YRKDTRYKLL GDLSRRDVSL TIENTAVSDS GVYCCRVEHR GWFNDMKITV   120
SLEIVPPKVT TTPIVTTVPT VTTVRTSTTV PTTTTVPTTT VPTTMSIPTT TTVPTTMTVS   180
TTTSVPTTTS IPTTTSVPVT TTVSTFVPPM PLPRQNHEPV ATSPSSPQPA ETHPTTLQGA   240
IRREPTSSPL YSYTTDGNDT VTESSDGLWN NNQTQLFLEH SLLTANTTKG IYAGVCISVL   300
VLLALLGVII AKKYFFKKEV QQLSVSFSSL QIKALQNAVE KEVQAEDNIY IENSLYATD
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Seq ID NO: 303 DNA sequence
Nucleic Acid Accession #: NM_001044.1
Coding sequence: 129..1991

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1          11         21         31         41         51
|          |          |          |          |          |
ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGCGTGC    60
AAAGCCCAGG CCCGGGCGGC CAGACCAAGA GGGAAGAAGC ACAGAATTCC TCAACTCCCA   120
GTGTGCCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCCGTG GTGGCCCCGG   180
CTAAGGAGCC CAATGCCGTG GGCCCGAAGG AGGTGGAGCT CATCCTTGTC AAGGAGCAGA   240
ACGGAGTGCA GCTCACCAGC TCCACCCTCA CCAACCCGCG GCAGAGCCCC GTGGAGGCCC   300
AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTTCTCCT GTCCGTCATT GGCTTTGCTG   360
TGGACCTGGC CAACGTCTGG CGGTTCCCCT ACCTGTGCTA CAAAAATGGT GGCGGTGCCT   420
TCCTGGTCCC CTACCTGCTC TTCATGGTCA TTGCTGGGAT GCCACTTTTC TACATGGAGC   480
TGGCCCTCGG CCAGTTCAAC AGGGAAGGGG CCGCTGGTGT CTGGAAGATC TGCCCCATAC   540
TGAAAGGTGT GGGCTTCACG GTCATCCTCA TCTCACTGTA TGTCGGCTTC TTCTACAACG   600
TCATCATCGC CTGGGCGCTG CACTATCTCT TCTCCTCCTT CACCACGGAG CTCCCCTGGA   660
TCCACTGCAA CAACTCCTGG AACAGCCCCA ACTGCTCGGA TGCCCATCCT GGTGACTCCA   720
GTGGAGACAG CTCGGGCCTC AACGACACTT TTGGGACCAC ACCTGCTGCC GAGTACTTTG   780
AACGTGGCGT GCTGCACCTC CACCAGAGCC ATGGCATCGA CGACCTGGGG CCTCCGCGGT   840
GGCAGCTCAC AGCCTGCCTG GTGCTGGTCA TCGTGCTGCT CTACTTCAGC CTCTGGAAGG   900
GCGTGAAGAC CTCAGGGAAG GTGGTATGGA TCACAGCCAC CATGCCATAC GTGGTCCTCA   960
CTGCCCTGCT CCTGCGTGGG GTCACCCTCC CTGGAGCCAT AGACGGCATC AGAGCATACC  1020
TGAGCGTTGA CTTCTACCGG CTCTGCGAGG CGTCTGTTTG GATTGACGCG GCCACCCAGG  1080
TGTGCTTCTC CCTGGGCGTG GGGTTCGGGG TGCTGATCGC CTTCTCCAGC TACAACAAGT  1140
TCACCAACAA CTGCTACAGG GACGCGATTG TCACCACCTC CATCAACTCC CTGACGAGCT  1200
TCTCCTCCGG CTTCGTCGTC TTCTCCTTCC TGGGGTACAT GGCACAGAAG CACAGTGTGC  1260
CCATCGGGGA CGTGGCCAAG GACGGGCCAG GGCTGATCTT CATCATCTAC CCGGAAGCCA  1320
TCGCCACGCT CCCTCTGTCC TCAGCCTGGG CCGTGGTCTT CTTCATCATG CTGCTCACCC  1380
TGGGTATCGA CAGCGCCATG GGTGGTATGG AGTCAGTGAT CACCGGGCTC ATCGATGAGT  1440
TCCAGCTGCT GCACAGACAC CGTGAGCTCT TCACGCTCTT CATCGTCCTG GCGACCTTCC  1500
TCCTGTCCCT GTTCTGCGTC ACCAACGGTG GCATCTACGT CTTCACGCTC CTGGACCATT  1560
TTGCAGCCGG CACGTCCATC CTCTTTGGAG TGCTCATCGA AGCCATCGGA GTGGCCTGGT  1620
TCTATGGTGT TGGGCAGTTC AGCGACGACA TCCAGCAGAT GACCGGGCAG CGGCCCAGCC  1680
TGTACTGCCG GCTGTGCTGG AAGCTGGTCA GCCCCTGCTT TCTCCTGTTC GTGGTCGTGG  1740
TCAGCATTGT GACCTTCAGA CCCCCCCACT ACGGAGCCTA CATCTTCCCC GACTGGGCCA  1800
ACGCGCTGGG CTGGGTCATC GCCACATCCT CCATGGCCAT GGTGCCCATC TATGCGGCCT  1860
ACAAGTTCTG CAGCCTGCCT GGGTCCTTTC GAGAGAAACT GGCCTACGCC ATTGCACCCG  1920
AGAAGGACCG TGAGCTGGTG GACAGAGGGG AGGTGCGCCA GTTCACGCTC CGCCACTGGC  1980
TCAAGGTGTA GAGGGAGCAG AGACGAAGAC CCCAGGAAGT CATCCTGCAA TGGGAGAGAC  2040
ACGAACAAAC CAAGGAAATC TAAGTTTCGA GAGAAAGGAG GGCAACTTCT ACTCTTCAAC  2100
CTCTACTGAA AACACAAACA ACAAAGCAGA AGACTCCTCT CTTCTGACTG TTTACACCTT  2160
TCCGTGCCGG GAGCGCACCT CGCCGTGTCT TGTGTTGCTG TAATAACGAC GTAGATCTGT  2220
GCAGCGAGGT CCACCCCGTT GTTGTCCCTG CAGGGCAGAA AAACGTCTAA CTTCATGCTG  2280
TCTGTGTGAG GCTCCCTCCC TCCCTGCTCC CTGCTCCCGG CTCTGAGGCT GCCCCAGGGG  2340
CACTGTGTTC TCAGGCGGGG ATCACGATCC TTGTAGACGC ACCTGCTGAG AATCCCCGTG  2400
CTCACAGTAG CTTCCTAGAC CATTTACTTT GCCCATATTA AAAAGCCAAG TGTCCTGCTT  2460
GGTTTAGCTG TGCAGAAGGT GAAATGGAGG AAACCACAAA TTCATGCAAA GTCCTTTCCC  2520
GATGCGTGGC TCCCAGCAGA GGCCGTAAAT TGAGCGTTCA GTTGACACAT TGCACACACA  2580
GTCTGTTCAG AGGCATTGGA GGATGGGGGT CCTGGTATGT CTCACCAGGA AATTCTGTTT  2640
ATGTTCTTGC AGCAGAGAGA AATAAAACTC CTTGAAACCA GCTCAGGCTA CTGCCACTCA  2700
GGCAGCCTGT GGGTCCTTGT GGTGTAGGGA ACGGCCTGAG AGGAGCGTGT CCTATCCCCG  2760
GACGCATGCA GGGCCCCCAC AGGAGCGTGT CCTATCCCCG GACGCATGCA GGGCCCCCAC  2820
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AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCCAG  2880
AACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCCAG GACGCATGCA GGGCCCCCAC  2940
TGGAGCGTGT ACTACCCCAG GACGCATGCA GGGCCCCCAC AGGAGCGTGT CCTATCCCCG  3000
GACCGGACGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC CCCAGGACGC ATGCAGGGCC  3060
CCCACAGGAG CGTGTACTAC CCCAGGATGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC  3120
CCCAGGACGC ATGCAGGGCC CCCATGCAGG CAGCCTGCAG ACCAACACTC TGCCTGGCCT  3180
TGAGCCGTGA CCTCCAGGAA GGGACCCCAC TGGAATTTTA TTTCTCTCAG GTGCGTGCCA  3240
CATCAATAAC AACAGTTTTT ATGTTTGCGA ATGGCTTTTT AAAATCATAT TTACCTGTGA  3300
ATCAAAACAA ATTCAAGAAT GCAGTATCCG CGAGCCTGCT TGCTGATATT GCAGTTTTTG  3360
TTTACAAGAA TAATTAGCAA TACTGAGTGA AGGATGTTGG CCAAAAGCTG CTTTCCATGG  3420
CACACTGCCC TCTGCCACTG ACAGGAAAGT GGATGCCATA GTTTGAATTC ATGCCTCAAG  3480
TCGGTGGGCC TGCCTACGTG CTGCCCCAGG GCAGGGGCCG TGCAGGGCCA GTCATGGCTG  3540
TCCCCTGCAA GTGGACGTGG GCTCCAGGGA CTGGAGTGTA ATGCTCGGTG GGAGCCGTCA  3600
GCCTGTGAAC TGCCAGGCAG CTGCAGTTAG CACAGAGGAT GGCTTCCCCA TTGCCTTCTG  3660
GGGAGGGACA CAGAGGACGG CTTCCCCATC GCCTTCTGGC CGCTGCAGTC AGCACAGAGA  3720
GCGGCTTCCC CATTGCCTTC TGGGGAGGGA CACAGAGGAC AGTTTCCCCA TCGCCTTCTG  3780
GTTGTTGAAG ACAGCACAGA GAGCGGCTTC CCCATCGCCT TCTGGGGAGG GGCTCCGTGT  3840
AGCAACCCAG GTGTTGTCCG TGTCTGTTGA CCAATCTCTA TTCAGCATCG TGTGGGTCCC  3900
TAAGCACAAT AAAAGACATC CACAATGGAA AAAAAAAAAG GAATTC
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Seq ID NO: 304 Protein sequence
Protein Accession #: NP_001035.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSKSKCSVGL MSSVVAPAKE PNAVGPKEVE LILVKEQNGV QLTSSTLTNP RQSPVEAQDR    60
ETWGKKIDFL LSVIGFAVDL ANVWRFPYLC YKNGGGAFLV PYLLFMVIAG MPLFYMELAL   120
GQFNREGAAG VWKICPILKG VGFTVILISL YVGFFYNVII AWALHYLFSS FTTELPWIHC   180
NNSWNSPNCS DAHPGDSSGD SSGLNDTFGT TPAAEYFERG VLHLHQSHGI DDLGPPRWQL   240
TACLVLVIVL LYFSLWKGVK TSGKVVWITA TMPYVVLTAL LLRGVTLPGA IDGIRAYLSV   300
DFYRLCEASV WIDAATQVCF SLGVGFGVLI AFSSYNKFTN NCYRDAIVTT SINSLTSFSS   360
GFVVFSFLGY MAQKHSVPIG DVAKDGPGLI FIIYPEAIAT LPLSSAWAVV FFIMLLTLGI   420
DSAMGGMESV ITGLIDEFQL LHRHRELFTL FIVLATFLLS LFCVTNGGIY VFTLLDHFAA   480
GTSILFGVLI EAIGVAWFYG VGQFSDDIQQ MTGQRPSLYW RLCWKLVSPC FLLFVVVVSI   540
VTFRPPHYGA YIFPDWANAL GWVIATSSMA MVPIYAAYKF CSLPGSFREK LAYAIAPEKD   600
RELVDRGEVR QFTLRHWLKV
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Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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1          11         21         31         41         51
|          |          |          |          |          |
GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC    60
AGCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG   120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT   180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC   240
AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG   300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC   360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCCAG   420
AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC   480
CCGCCCTGGC CCCGGGTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC   540
CGCCCCCAGC TCGCCCCCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG   600
CTCCCGCCGC TCCCAGAACT GCGCCTGCGC AACAATGGCC ACAGTGTGCA ACTGACCCTG   660
CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT   720
CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC   780
CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTTG CCAGAGTTGA CGAGGCCTTG   840
GGGCGCCCGG GAGGCCTGGC CGTGTTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC   900
AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT   960
CAGGTCCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA  1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC  1080
CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCTCT CTGACACCCT GTGGGGACCT  1140
GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT  1200
GAGGCCTCCT TCCCTGCTGG AGTGGACAGC AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG  1260
AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC  1320
ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT  1380
GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA  1440
TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCCTGT CCTGCTCATT  1500
ATGCCACTTC CTTTTAACTG CCAAGAAATT TTTTAAAATA AATATTTATA AT
```

Seq ID NO: 306 Protein sequence
Protein Accession #: NP_001207.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAPLCPSPWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL    60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG   120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL   180
ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT   240
VEGHRFPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPEENSAYE QLLSRLEEIA   300
EEGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS   360
DTLWGPGDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF   420
GLLFAVTSVA FLVQMRRQHR RGTKGGVSYR PAEVAETGA
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Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_003039.1
Coding sequence: 76..1581

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1          11         21         31         41         51
|          |          |          |          |          |
CTTCTCTCTC CATTCAGTGC ACGCGTTACT TTGGCTAAAA GGAGGTGAGC GGCACTCTGC    60
CCTTCCAGAG CAAGCATGCA GCAACAGGAT CACAGCATGA AGGAAGGGAG GCTGACGCTT   120
GTGCTTGCCC TGGCAACCCT GATAGCTGCC TTTGGGTCAT CCTTCCAGTA TGGGTACAAC   180
GTGGCTGCTG TCAACTCCCC AGCACTGCTC ATGCAACAAT TTTACAATGA GACTTACTAT   240
GGTAGGACCG GTGAATTCAT GGAAGACTTC CCCTTGACGT TGCTGTGGTC TGTAACCGTG   300
TCCATGTTTC CATTTGGAGG GTTTATCGGA TCCCTCCTGG TCGGCCCCTT GGTGAATAAA   360
TTTGGCAGAA AAGGGGCCTT GCTGTTCAAC AACATATTTT CTATCGTGCC TGCGATCTTA   420
ATGGGATGCA GCAGAGTCGC CACATCATTT GAGCTTATCA TTATTTCCAG ACTTTTGGTG   480
GGAATATGTG CAGGTGTATC TTCCAACGTG GTCCCCATGT ACTTAGGGGA GCTGGCCCCT   540
AAAAACCTGC GGGGGGCTCT CGGGGTGGTG CCCCAGCTCT TCATCACTGT TGGCATCCTT   600
GTGGCCCAGA TCTTTGGTCT TCGGAATCTC CTTGCAAACG TAGATGGCTG GCCGATCCTG   660
CTGGGGCTGA CCGGGGTCCC CGCGGCGCTG CAGCTCCTTC TGCTGCCCTT CTTCCCCGAG   720
AGCCCCAGGT ACCTGCTGAT TCAGAAGAAA GACGAAGCGG CCGCCAAGAA AGCCCTACAG   780
ACGCTGCGCG GCTGGGACTC TGTGGACAGG GAGGTGGCCG AGATCCGGCA GGAGGATGAG   840
GCAGAGAAGG CCGCGGGCTT CATCTCCGTG CTGAAGCTGT TCCGGATGCG CTCGCTGCGC   900
TGGCAGCTGC TGTCCATCAT CGTCCTCATG GGCGGCCAGC AGCTCTCGGC CGTCAACGCT   960
ATCTACTACT ACGCGGACCA GATCTACCTG AGCGCCGGCG TGCCGGAGGA GCACGTGCAG  1020
TACGTGACGG CCGGCACCGG GGCCGTGAAC GTGGTCATGA CCTTCTGCGC CGTGTTCGTG  1080
GTGGAGCTCC TGGGTCCGAG GCTGCTGCTG CTGCTGGGCT TCTCCATCTG CCTCATAGCC  1140
TGCTGCGTGC TCACTGCAGC TCTGGCACTG CAGGACACAG TGTCCTGGAT GCCATACATC  1200
AGCATCGTCT GTGTCATCTC CTACGTCATA GGACATGCCC TCGGGCCCAG TCCCATACCC  1260
GCGCTGCTCA TCACTGAGAT CTTCCTGCAG TCCTCTCGGC CATCTGCCTT CATGGTGGGG  1320
GGCAGTGTGC ACTGGCTCTC CAACTTCACC GTGGGCTTGA TCTTCCCGTT CATCCAGGAG  1380
GGCCTCGGCC CGTACAGCTT CATTGTCTTC GCCGTGATCT GCCTCCTCAC CACCATCTAC  1440
ATCTTCTTGA TTGTCCCGGA GACCAAGGCC AAGACGTTCA TAGAGATCAA CCAGATTTTC  1500
ACCAAGATGA ATAAGGTGTC TGAAGTGTAC CCGGAAAAGG AGGAACTGAA AGAGCTTCCA  1560
CCTGTCACTT CGGAACAGTG ACTCTGGAGA GGAAGCCAGT GGAGCTGGTC TGCCAGGGGC  1620
TTCCCACTTT GGCTTATTTT TCTGACTTCT AGCTGTCTGT GAATATCCAG AAATAAAACA  1680
ACTCTGATGT GGAATGCAGT CCTCATCTCC AGCCTCCCCA CCCCAGTGGG AACTGTGCAA  1740
AGGGCTGCCT TGCTGTTCTT GAAGCTGGGC TGTCTCTCTC CATGTTGGCC TGTCACCAGA  1800
CCCGAGTCAA TTAAACAGCT GGTCCTCCAC TTTGCTGGTT CAGCCTTCGT GTGGCTCCTG  1860
GTAACGTGGC TCCACCTTGA TGGGTCAACC TTTGTGTGGC TCCTGGTAAC ATAACAACAA  1920
CAGTTACTAT AGTGGTGAGA TGGAAGGAAT CAAATTTTGC CAGAGAAACT AACTCGGTGG  1980
CCCCAACAGG TCTTCCGGGG CCATGGGCAT TTGTTTAGAG CCAAATTCAT CCTCTTACCA  2040
GATCCTTTTC CAGAAATACC TGTCTAGGAA GGTGTGATGT CAGAAACAAT GACATCCAGA  2100
AAGCTGAGGA ACAGGTTCCT GTGGAGACAC TGAGTCAGAA TTCTTCATCC AAATTATTTT  2160
GTTAGTGGAA AATGGAATTG CTTCTGTGTA GTCAATAAAA TGAACCTGAT CACTTTTC
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Seq ID NO: 308 Protein sequence
Protein Accession #: NP_003030.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEQQDQSMKE GRLILVLALA TLIAAFGSSF QYGYNVAAVN SPALLMQQFY NETYYGRTGE    60
FMEDFPLTLL WSVTVSMFPF GGFIGSLLVG PLVNKFGRKG ALLFNNIFSI VPAILMGCSR   120
VATSFELIII SRLLVGICAG VSSNVVPMYL GELAPKNLRG ALGVVPQLFI TVGILVAQIF   180
GLRNLLANVD GWPILLGLTG VPAALQLLLL PFFPESPRYL LIQKKDEAAA KKALQTLRGW   240
DSVDREVAEI RQEDEAEKAA GFISVLKLFR MRSLRWQLLS IIVLMGGQQL SGVNAIYYYA   300
DQIYLSAGVP EEHVQVVTAG TGAVNVVMTF CAVFVVELLG RRLLLLLGFS ICLIACCVLT   360
AALALQDTVS WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRPS AFMVGGSVHW   420
LSNFTVGLIF PFIQEGLGPY SFIVFAVICL LTIIYIFLIV PETKAKTFIE INQIFTKMNK   480
VSEVYPEKEE LKELPPVTSE Q
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Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: NM_001252.1
Coding sequence: 138..719

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1          11         21         31         41         51
|          |          |          |          |          |
GGCTGGTCCC CTGACAGGTT GAAGCAAGTA GACGCCCAGG AGCCCCGGGA GGGGGCTGCA    60
GTTTCCTTCC TTCCTTCTCG GCAGCGCTCC GCGCCCCCAT CGCCCCTCCT GCGCTAGCGG   120
AGGTGATCGC CGCGGCGATG CCGGAGGAGG GTTCGGGGCTG CTCGGTGCGG CGCAGGCCCT   180
ATGGGTGCGT CCTGCGGGCT GCTTTGGTCC CATTGGTCGC GGGCTTGGTG ATCTGCCTCG   240
TGGTGTGCAT CCAGCGCTTC GCACAGGCTC AGCAGCAGCT GCCGCTCGAG TCACTTGGGT   300
GGGACGTAGC TGAGCTGCAG CTGAATCACA CAGGACCTCA GCAGGACCCC AGGCTATACT   360
GGCAGGGGGG CCCAGCACTG GGCCGCTCCT TCCTGCATGG ACCAGAGCTG GACAAGGGGC   420
AGCTACGTAT CCATCGTGAT GGCATCTACA TGGTACACAT CCAGGTGACG CTGGCCATCT   480
GCTCCTCCAC GACGGCCTCC AGGCACCACC CCACCACCCT GGCCGTGGGA ATCTGCTCTC   540
CCGCCTCCCG TAGCATCAGC CTGCTGCGTC TCAGCTTCCA CCAAGGTTGT ACCATTGCCT   600
CCCAGCGCCT GACGCCCCTG GCCCGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC   660
TTTTGCCTTC CCGAAACACT GATGAGACCT TCTTTGGAGT GCAGTGGGTG CGCCCCTGAC   720
CACTGCTGCT GATTAGGGTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAAA   780
AGTGTACACA CAGGGGCCAC CCGGGGTTGG GGTGGGAGTG TGGTGGGGGG TAGTGGTGGC   840
AGGACAAGAG AAGGCATTGA GCTTTTTCTT TCATTTTCCT ATTAAAAA
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Seq ID NO: 310 Protein sequence
Protein Accession #: NP_001243.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPEEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVAEL    60
QLNHTGPQQD PRLYWQGGPA LGRSFLHGPE LDKGQLRIHR DGIYMVHIQV TLAICSSTTA   120
SRHHPTTLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLLPSRN   180
TDETFFGVQW VRP

Seq ID NO: 311 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3978

1          11         21         31         41         51
|          |          |          |          |          |
ATGGTGGGTG AAGGACCCTA CCTTATCTCA GATCTGGACC AGCGAGGCCG GCGGAGATCC    60
TTTGCAGAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGCGACC CTGTGCAAGG   120
TTAGCACCCA ACCCGGTGGA TGATGCCGGG CTACTCTCCT TCGCCACATT TTCCTGGCTC   180
ACGCCGGTGA TGGTGAAAGG CTACCGGCAA AGGCTGACCG TAGACACCCT GCCCCCATTG   240
TCGACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCCTTTG GGATGAAGAG   300
GTAGCAAGGG TGGGTCCTGA GAAGCCCTCT CTGAGCCACG TGGTGTGGAA ATTCCAGAGG   360
ACACGCGTGT TGATGGACAT CGTGGCCAAC ATCCTGTGCA TCATCATGGC AGCCATAGGG   420
CCGACAGTTC TCATTCACCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG   480
GTTGGCATTG GACTGTGCAT AGCCCTTTTT GCCACCGAGT TTACCAAAGT CTTCTTTTGG   540
GCCCTTGCCT GGGCCATCAA CTACCGCACG GCCATCCGGT TGAAGGTGGC GCTCTCCACC   600
TTGGTTTTTG AAAACCTAGT GTCCTTCAAG ACATTGACCC ACATCTCTGT TGGCGAGGTG   660
CTCAATATAC TGTCAAGTGA TAGCTATTCT TTGTTTGAAG CTGCCTTGTT TTGTCCTTTG   720
CCAGCCACCA TCCCGATCCT AATGGTCTTT TGTGCGGCGT ACGCCTTTTT CATTCTGGGG   780
CCCACAGCTC TCATCGGGAT ATCAGTGTAT GTCATATTCA TACCCGTCCA GATGTTTATG   840
GCCAAGCTCA ATTCAGCTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTCAG   900
ACAATGAATG AGTTTCTGAC CTGCATCAGG CTGATCAAAA TGTATGCCTG GGAGAAATCT   960
TTTACCAACA CTATCCAAGA TATAAGAAGG AGGGAAAGAA AATTACTGGA AAAAGCTGGA  1020
TTTGTCCAAA GTGGAAACTC TGCCCTGGCC CCCATCGTGT CCACCATAGC CATCGTGCTG  1080
ACATTATCCT GCCACATCCT CCTGAGACGC AAACTCACCG CACCCGTGGC ATTTAGTGTG  1140
ATTGCCATGT TTAATGTAAT GAAGTTTTCC ATTGCAATCT TGCCCTTCTC CATCAAAGCA  1200
ATGGCTGAAG CGAATGTCTC TCTAAGGAGA ATGAAGAAAA TTCTCATAGA TAAAAGCCCC  1260
CCATCTTACA TCACCCAACC AGAAGACCCA GATACTGTCT TGCTTTTAGC AAATGCCACC  1320
TTGACATGGG AGCATGAAGC CAGCAGGAAA AGTACCCCAA AGAAATTGCA GAACCAGAAA  1380
AGGCATTTAT GCAAGAAACA GAGGTCAGAG GCATACAGTG AGAGGAGTCC ACCAGCCAAG  1440
GGAGCCACTG GCCCAGAGGA GCAAAGTGAC AGCCTCAAAT CGGTTCTGCA CAGCATAAGC  1500
TTTGTGGTGA GAAAGTTATG TCGTTATCCC GAAGCCCAGC TCCTGGCTTG GAGGTGGCCA  1560
GCAGTGTTTG TTGGGAGAAT CATCAGAGGA TACAGGCCTC ATGGATTTTC TGCTAAAGAC  1620
AAGGATGAAT CTAGAAGGCT TCTTACTTGG CCCCAAGAAG TGGATAGGAC TCAAAGGGCA  1680
GCCAAATACC TGGGGAAGAT CTTGGGAATA TGTGGGAATG TGGGAAGTGG AAAGAGCTCC  1740
CTCCTTGCAG CTCTCCTAGG ACAGATGCAG CTGCAGAAAG GGGTGGTGGC AGTCAATGGA  1800
ACTTTGGCCT ACGTTTCACA GCAGGCATGG ATCTTTCATG GAAATGTGAG AGAAAACATA  1860
CTCTTTGGAG AAAAGTATGA TCACCAAAGG TATCAGCACA CAGTCCGCGT CTGTGGCCTC  1920
CAGAAGGACC TGAGCAACCT CCCCTATGGA GACCTGACTG AGATTGGGGA GCGGGGCCTC  1980
AACCTCTCTG GGGGCAGAG GCAGAGGATT AGCCTGGCCC GCGCTGTCTA CTCCGACCGT  2040
CAGCTCTACC TGCTGGACGA CCCCCTGTCG GCCGTGGACG CCCACGTGGG GAAGCACGTC  2100
TTTGAGGAGT GCATTAAGAA GACGCTCAGG GGAAAGACAG TCGTCCTGGT GACCCACCAG  2160
CTACAGTTCT TAGAGTCTTG TGATGAAGTT ATTTTATTAG AAGATGGAGA GATTTGTGAA  2220
AAGGGAACCC ACAAGGAGTT AATGGAGGAG AGAGGGCGCT ATGCAAAACT GATTCACAAC  2280
CTGCGAGGAT TGCAGTTCAA GGATCCTGAA CACCTTTACA ATGCAGCAAT GGTGGAAGCC  2340
TTCAAGGAGA GCCCTGCTGA GAGAGAGGAA GATGCTGGTA TAATCGGGTA CCTCCTTTCT  2400
CTCTTCACTG TGTTCCTCTT CCTCCTGATG ATTGGCAGCG CTGCCTTCAG CAACTGGTGG  2460
CTGGGTCTCT GGTTGGACAA GGGCTCACGG ATGACCTGTG GGCCCCAGGG CAACAGGACC  2520
ATGTGTGAGG TCGGCGCGGT GCTGGCAGAC ATCGGTCAGC ATGTGTACCA GTGGGTGTAC  2580
ACTGCAAGCA TGGTGTTCAT GCTGGTGTTT GGCGTCACCA AAGGCTTCGT CTTCACCAAG  2640
ACCACACTGA TGGCATCCTC CTCTCTGCAT GACACGGTGT TTGATAAGAT CTTAAAGAGC  2700
CCAATGAGTT TCTTTGACAC GACTCCCACT GGCAGGCTAA TGAACCGTTT TTCCAAGGAT  2760
ATGGACGAGC TGGATGTGAG GCTGCCGTTT CACGCAGAGA ACTTTCTGCA GCAGTTTTTT  2820
ATGGTGGTGT TTATTCTCGT GATCTTGGCT GCTGTGTTTC CTGCTGTCCT TTTAGTCGTG  2880
GCCAGCCTTG CTGTAGGCTT CTTCATTCTG TTACGCATTT TCCACAGAGG AGTCCAGGAG  2940
CTCAAGAAGG TGGAGAATGT CAGCCGGTCA CCCTGGTTCA CCCACATCAC CTCCTCCATG  3000
CAGGGCCTGG GCATCATTCA CGCCTATGGC AAGAAGGAGA GCTGCATCAC CTATACTTCA  3060
TCCAAAGGCC TGTCATTGTC ATACATCATC CAGCTGAGCG GACTGCTCCA AGTGTGTGTG  3120
CGAACGGGAA CAGAGACGCA AGCCAAATTC ACCTCCGTGG AGCTGCTCAG GGAATACATT  3180
TCGACCTGTG TTCCTGAATG CACTCATCCC CTCAAAGTGG GGACCTGTCC CAAGGACTGG  3240
CCCAGCTGTG GGGAGATCAC CTTCAGAGAC TATCAGATGA GATACAGAGA CAACACCCCC  3300
CTTGTTCTCG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCGG GATTGTTGGA  3360
AGAACAGGTT CCGGAAAGTC ATCGTTAGGA ATGGCTTTGT TTCGTCTGGT GGAGCCAGCC  3420
AGTGGCACAA TCTTTATTGA TGAGGTGGAT ATCTGCATTC TCAGCTTGGA AGACCTCAGA  3480
ACCAAGCTGA CTGTGATCCC ACAGGATCCT GTCCTGTTTG TAGGTACAGT AAGGTACAAC  3540
TTGGATCCCT TTGAGAGTCA CACCGATGAG ATGCTCTGGC AGGTTCTGGA GAGAACATTC  3600
ATGAGAGACA CAATAATGAA ACTCCCAGAA AAATTACAGG CAGAAGTCAC AGAAAATGGA  3660
GAAAACTTCT CAGTAGGGGA ACGTCAGCTG CTTTGTGTGG CCCGAGCTCT TCTCCGTAAT  3720
TCAAAGATCA TTCTCCTTGA TGAAGCCACC GCCTCTATGG ACTCCAAGAC TGACACCCTG  3780
GTTCAGAACA CCATCAAAGA TGCCTTCAAG GGCTGCACTG TGCTGACCAT CGCCCACCGC  3840
CTCAACACAG TTCTCAACTG CGATCACGTC CTGGTTATGG AAAATGGGAA GGTGATTGAG  3900
TTTGACAAGC CTGAAGTCCT TGCAGAGAAG CCAGATTCTG CATTTGCGAT GTTACTAGCA  3960
GCAGAAGTCA GATTGTAG

Seq ID NO: 312 Protein sequence
Protein Accession #: Eos sequence
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1          11         21         31         41         51
|          |          |          |          |          |
MVGEGPYLIS DLDQRGRRRS FAERYDPSLK TMIPVRPCAR LAPNPVDDAG LLSPATFSWL    60
TPVMVKGYRQ RLTVDTLPPL STYDSSDTNA KRFRVLWDEE VARVGPEKAS LSHVVWKFQR   120
TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVW VGIGLCIALF ATEFTKVFFW   180
ALAWAINYRT AIRLKVALST LVFENLVSFK TLTHISVGEV LNILSSDSYS LFEAALFCPL   240
PATIPILMVF CAAYAFFILG PTALIGISVY VIFIPVQMFM AKLNSAFRRS AILVTDKRVQ   300
TMNEFLTCIR LIKMYAWEKS FTNTIQDIRR RERKLLEKAG FVQSGNSALA PIVSTIAIVL   360
TLSCHILLRR KLTAPVAFSV IAMFNVMKFS IAILPFSIKA MAEANVSLRR MKKILIDKSP   420
PSYITQPEDP DTVLLLANAT LTWEHEASRK STPKKLQNQK RHLCKKQRSE AYSERSPPAK   480
CATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSAKD   540
KDESRRLLTW PQEVDRTQRA AKYLGKILGI CGNVGSGKSS LLAALLGQMQ LQKGVVAVNG   600
TLAYVSQQAW IFHGNVRENI LFGEKYDHQR YQHTVRVCGL QKDLSNLPYG DLTEIGERGL   660
NLSGGQRQRI SLARAVYSDR QLYLLDDPLS AVDAHVGKHV FEECIKKTLR GKTVVLVTHQ   720
LQFLESCDEV ILLEDGEICE KGTHKELMEE RGRYAKLIHN LRGLQFKDPE HLYNAAMVEA   780
FKESPAEREE DAGIIGYLLS LFTVFLFLLM IGSAAFSNWW LGLWLDKGSR MTCGPQGNRT   840
MCEVGAVLAD IGQHVYQWVY TASMVFMLVF GVTKGFVFTK TTLMASSSLH DTVFDKILKS   900
PMSFFDTTPT GRLMNRFSKD MDELDVRLPF HAENFLQQFF MVVFILVILA AVFPAVLLVV   960
ASLAVGFFIL LRIFHRGVQE LKKVENVSRS PWFTHITSSM QGLGIIHAYG KKESCITYTS  1020
SKGLSLSYII QLSGLLQVCV RTGTETQAKF TSVELLREYI STCVPECTHP LKVGTCPKDW  1080
PSCGEITFRD YQMRYRDNTP LVLDSLNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA  1140
SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLFVGTVRYN LDPFESHTDE MLWQVLERTF  1200
MRDTIMKLPE KLQAEVTENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMDSKTDTL  1260
VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENGKVIE FDKPEVLAEK PDSAFAMLLA  1320
AEVRL
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Seq ID NO: 313 DNA sequence
Nucleic Acid Accession #: Z31560
Coding sequence: 1-966

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1          11         21         31         41         51
|          |          |          |          |          |
CACAGCGCCC GCATGTACAA CATGATGGAG ACGGAGCTGA AGCCGCCGGG CCCGCAGCAA    60
ACTTCGGGGG GCGGCGGCGG CAACTCCACC GCGGCGGCGG CCGGCGGCAA CCAGAAAAAC   120
AGCCCGGACC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGGTCCCG CGGGCAGCGG   180
CGCAAGATGG CCCAGGACAA CCCCAAGATG CACAACTCGG AGATCAGCAA GCGCCTGGGC   240
GCCGAGTGGA AACTTTTGTC GGAGACGGAG AAGCGGCCGT TCATCGACGA GGCTAAGCGG   300
CTGCGAGCGC TGCACATGAA GGAGCACCCG GATTATAAAT ACCGGCCCCG GCGGAAAACC   360
AAGACGCTCA TGAAGAAGGA TAAGTACACG CTGCCCGGCG GGCTGCTGGC CCCCGGCGGC   420
AATAGCATGG CGAGCGGGGT CGGGGTGGGC GCCGGCCTGG GCGCGGGCGT GAACCAGCGC   480
ATGGACAGTT ACGCGCACAT GAACGGCTGG AGCAACGGCA GCTACAGCAT GATGCAGGAC   540
CAGCTGGGCT ACCCGCAGCA CCCGGGCCTC AATGCGCACG GCGCAGCGCA GATGCAGCCC   600
ATGCACCGCT ACGACGTGAG CGCCCTGCAG TACAACTCCA TGACCAGCTC GCAGACCTAC   660
ATGAACGGCT CGCCCACCTA CAGCATGTCC TACTCGCAGC AGGGCACCCC TGGCATGGCT   720
CTTGGCTCCA TGGGTTCGGT GGTCAAGTCC GAGGCCAGCT CCAGCCCCCC TGTGGTTACC   780
TCTTCCTCCC ACTCCAGGGC GCCCTGCCAG GCCGGGGACC TCCGGGACAT GATCAGCATG   840
TATCTCCCCG GCGCCGAGGT GCCGGAACCC GCCGCCCCCA GCAGACTTCA CATGTCCCAG   900
CACTACCAGA GCGGCCCGGT GCCCGGCACG GCCATTAACG GCACACTGCC CCTCTCACAC   960
ATGTGAGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAAGAAAA ACGAGGGAAA  1020
TGGGAGGGGT GCAAAAGAGG AGAGTAAGAA ACAGCATGGA GAAAACCCGG TACGCTCAAA  1080
AAAAA
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Seq ID NO: 314 Protein sequence
Protein Accession #: CAA83435

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1          11         21         31         41         51
|          |          |          |          |          |
HSARMYNMME TELKPPGPQQ TSGGGGGNST AAAAGGNQKN SPDRVKRPMN AFMVWSRGQR    60
RKMAQENPKM HNSEISKRLG AEWKLLSETE KRPFIDEAKR LRALHMKEHP DYKYRPRRKT   120
KTLMKKDKYT LPGGLLAPGG NSMASGVGVG AGLGAGVNQR MDSYAHMNGW SNGSYSMMQD   180
QLGYPQHPGL NAHGAAQMQP MHRYDVSALQ YNSMTSSQTY MNGSPTYSMS YSQQGTPGMA   240
LGSMGSVVKS EASSSPPVVT SSSHSRAPCQ AGDLRDMISM YLPGAEVPEP AAPSRLHMSQ   300
HYQSGPVPGT AINGTLPLSH M
```

Seq ID NO: 315 DNA sequence
Nucleic Acid Accession #: U91618
Coding sequence: 29..541

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAAATCC AGCTTGTATG    60
CATGCTACTC CTGGCTTTCA GCTCCTGGAG TCTGTGCTCA GATTCAGAAG AGGAAATGAA   120
AGCATTAGAA GCAGATTTCT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT   180
TCCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCTT GTAAATAATT TGAACAGCCC   240
AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC   300
TGCTTTAGAT GGCTTTAGCT TGGAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG   360
TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA   420
TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAAACGGCA   480
GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAAA AGAGATTCTT ACTATTACTG   540
AGAGAATAAA TCATTTATTT ACATGTCATT GTGATTCATC ATCCCTTAAT TAAATATCAA   600
ATTATATTTG TGTGAAAATG TGACAAACAC ACTTATCTGT CTCTTCTACA ATTGTGGTTT   660
ATTGAATGTG TTTTTCTGCA CTAATAGAAA TTAGACTAAG TGTTTTCAAA TAAATCTAAA   720
TCTTCAAAAA AAAAAAAAAA AAATGGGGCC GCAATT
```

Seq ID NO: 316 Protein sequence
Protein Accession #: AAB50564

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1           11          21          31          41          51
|           |           |           |           |           |
MMAGMKIQLV CMLLLAFSSW SLCSDSEEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN    60
VCSLVNNLNS PAEETGEVHE EELVARRKLP TALDGFSLEA MLTIYQLHKI CHSRAFQHWE   120
LIQEDILDTG NDKNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY
```

Seq ID NO: 317 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109..2940

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1           11          21          31          41          51
|           |           |           |           |           |
ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA     60
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Protein Accession #: NP_006527.1

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FDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWTYTLN NTHHSLQALK VTVTSRASNS 600
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PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
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Seq ID NO: 319 DNA sequence
Nucleic Acid Accession #: NM_000228.1
Coding sequence: 82..3600

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Seq ID NO: 320 Protein sequence
Protein Accession #: NP_000219.1

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NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA   240
VSQLRLQGSC FCHGHADRCA PKPGASAGPS TAVQVHDVCV CQHNTAGPNC ERCAPFYNNR   300
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TTSPGTRYGR PHSGRLGPAA IGLLLLGLLL LLLAPLLLLT CDCGAGSTGG VTGGFIPVPD   660
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DGAISMNFLD SYFSQKAFAC AEEDDGQEAN DCLLIYDNEG ADATGSPVGS VGCCSFIADD   840
LDDSFLDSLG PKFKKLAEIS LGVDGEGKEV QPPSKDSGYG IESCGHPIEV QQTGFVKCQT   900
LSGSQGASAL SASGSVQPAV SIPDPLQHGN YLVTETYSAS GSLVQPSTAG FDPLLTQNVI   960
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Seq ID NO: 323 DNA sequence
Nucleic Acid Accession #: XM_058069.2
Coding sequence: 1..1413

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LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY   240
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF   300
FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP   360
EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK   420
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Seq ID NO: 325 DNA sequence
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Coding sequence: 64..2590

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ACCAAATTCA TTTGACTTTG GAGGCAAAAT GTGTTGAAGT GCCCTATGAA GTAGCAATTT 3300
TCTATAGGAA TATAGTTGGA AATAAATGTG TGTGTGTATA TTATTATTAA TCAATGCAAT 3360
ATTTAAAATG AAATGAGAAC AAAGAGGAAA ATGGTAAAAA CTTGAAATGA GGCTGGGGTA 3420
TAGTTTGTCC TACAATAGAA AAAAGAGAGA GCTTCCTAGG CCTGGGCTCT TAAATGCTGC 3480
ATTATAACTG AGTCTATGAG GAAATAGTTC CTGTCCAATT TGTGTAATTT GTTTAAAATT 3540
GTAAATAAAT TAAACTTTTC TGGTTTCTGT GGGAAGGAAA TAGGGAATCC AATGGAACAG 3600
TAGCTTTGCT TTGCAGTCTG TTTCAAGATT TCTGCATCCA CAAGTTAGTA GCAAACTGGG 3660
GAATACTCGC TGCAGCTGGG GTTCCCTGCT TTTTGGTAGC AAGGGTCCAG AGATGAGGTG 3720
TTTTTTTCGG GGAGCTAATA ACAAAAACAT TTTAAAACTT ACCTTTACTG AAGTTAAATC 3780
CTCTATTGCT GTTTCTATTC TCTCTTATAG TGACCAACAT CTTTTTAATT TAGATCCAAA 3840
TAACCATGTC CTCCTAGAGT TTAGAGGCTA GAGGGAGCTG AGGGGAGGAT CTTACTGAAA 3900
GCACCCTGGG GAGATTGATT GTCCTTAAAC CTAAGCCCCA CAAACTTGAC ACCTGATCAG 3960
GTCTGGGAGC TACAAAATTT CATTTTTCTC CTCACTGCCC TTCTTCTGAG TGGCATTGGC 4020
CTGAATCAAG GAAAGCCAGG CCTTGTGGGC CCCCTTCTTT CGGCTTTCTG CTAAAGCAAC 4080
ACCTCCAGCA GAGATTCCCT TAAGTGACTC CAGGTTTTCC ACCATCCTTC AGCGTGAATT 4140
AATTTTTAAT CAGTTTGCTT TCTCCAGAGA AATTTTAAAA TAATAGAAGA AATAGAAATT 4200
TTGAATGTAT AAAAGAAAAA GATCAAGTTG TCATTTTAGA ACAGAGGGAA CTTTGGGAGA 4260
AAGCAGCCCA AGTAGGTTAT TTGTACAGTC AGAGGGCAAC AGGAAGATGC AGGCCTTCAA 4320
GGGCAAGGAG AGGCCACAAG GAATATGGGT GGGAGTAAAA GCAACATCGT CTGCTTCATA 4380
CTTTTTCCTA GGCTTGGCAC TGCCTTTTCC TTTCTCAGGC CAATGGCAAC TGCCATTTGA 4440
GTCCGGTGAG GGATCAGCCA ACCTCTTCTC TATGGCTCAC CTTATTTGGA GTGAGAAATC 4500
AAGGAGACAG AGCTGACTGC ATGATGAGTC TGAAGGCATT TGCAGGATGA GCCTGAACTG 4560
GTTGTGCAGA ACAAACAAGG CATTCATGGG AATTGTTGTA TTCCTTCTGC AGCCCTCCTT 4620
CTGGGCACTA AGAAGGTCTA TGAATTAAAT GCCTATCTAA AATTCTGATT TATTCCTACA 4680
TTTTCTGTTT TCTAATTTGA CCCTAAAATC TATGTGTTTT AGACTTAGAC TTTTTATTGC 4740
CCCCCCCCCC TTTTTTTTTG AGACGGAGTC TCGCTCTGAC GCACAGGCTG GAGTGCAGTG 4800
GCTCCGATCT CTGCTCACTG AAAGCTCCGC CTCCCGGGTT CATGCCATTC TCCTGCCTCA 4860
GCCTCCTGAG TAGCTGGGAC TACAGGCGCC CACCACCACG CCCGGCTAAT TTTTTGTATT 4920
TTTAATAGAG ACGGGGTTTC ACTGTGTTAG CCAGGATGGT CTCGATCTCC TGACCTCGTG 4980
ATCCGCCTGC CTCGGCCTCC CAAAGTGCTG GGATTACAGG CATGACCCAC CGCTCCCGGC 5040
CTTGTTTTCC GTTTAAAGTC GTCTTCTTTT AATGTAATCA TTTTGAACAT GTGTGAAAGT 5100
TGATCATACG AATTGGATCA ATCTTGAAAT ACTCAACCAA AAGACAGTCG AGAAGCCAGG 5160
GGGAGAAAGA ACTCAGGGCA CAAAATATTG GTCTGAGAAT GGAATTCTCT GTAAGCCTAG 5220
TTGCTGAAAT TTCCTGCTGT AACCAGAAGC CAGTTTTATC TAACGGCTAC TGAAACACCC 5280
ACTGTGTTTT GCTCACTCCC TCACTCACCG ATCAAAACCT GCTACCTCCC CAAGACTTTA 5340
CTAGTGCCGA TAAACTTTCT CAAAGAGCAA CCAGTATCAC TTCCCTGTTT ATAAAACCTC 5400
TAACCATCTC TTTGTTCTTT GAACATGCTG AAAACCACCT GGTCTGCATG TATGCCCGAA 5460
TTTGTAATTC TTTTCTCTCA AATGAAAATT TAATTTTAGG GATTCATTTC TATATTTTCA 5520
CATATGTAGT ATTATTATTT CCTTATATGT GTAAGGTGAA ATTTATGGTA TTTGAGTGTG 5580
CAAGAAAATA TATTTTTAAA GCTTTCATTT TTCCCCCAGT GAATGATTTA GAATTTTTTA 5640
TGTAAATATA CAGAATGTTT TTTCTTACTT TTATAAGGAA GCAGCTGTCT AAAATGCAGT 5700
GGGGTTTGTT TTGCAATGTT TTAAACAGAG TTTTAGTATT GCTATTAAAA GAAGTTACTT 5760
TGCTTTTAAA CAAACTTGGC TGCTTAAAAT AAGCAAAAAT TGGATGCATA AAGTAATATT 5820
TACAGATGTG GGGAGATGTA ATAAAACAAT ATTAACTTGG TTTCTTGTTT TTGCTGTATT 5880
TAGAGATTAA ATAATTCTAA GATGATCACT TTGCAAAATT ATGCTTATGG CTGGCATGGA 5940
AATAGAAATA CTCAATTATG TCTTTGTTGT ATTAATGGGG AATATTTTGG ACAATGTTTC 6000
ATTATCAAAT TGTCGACATC ATTAATATAT ATTGTAATGT TGGGAAGAGA TCACTATTTT 6060
GAAGCACAGC TTTACAGATG AGTATCTATG ATACATATGT ATAATAAATT TTGATCGGGT 6120
ATTAAAAGTA TTAGAAGGTG GTTATAATTG CAGAGTATTC CATGAATAGT ACACTGACAC 6180
AGGGGTTTTA CTTTGAGGAC CAGTGTAGTC AAGGGAAAAC ATGAGTTAAA AAGAAAAGCA 6240
GGCAATATTG CAGTCTTGAT TCTGCCACTT ACAGGATAGA TAATGCCTGA ACTTTAATGA 6300
CAAGATGATC CAACCATAAA GGTGCTCTGT GCTTCACAGT GAATCTTTTC CCCATGCAGG 6360

AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACTT CTATTGTAAC 6480
CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTA ATAGTAAAAT 6540
ACCGGATACA TTTCACGTGT CCTTCAGTAT TGATTTGGTT GAATATTGGG TCATAATGGT 6600
TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660
TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTTCTCAT TAAAATCAAT 6720
GAACAATGCC AGCCTCATGG GGTTGTTGAA TGATTAAATT AGTTAATATA CCTAAAGTAC 6780
ATAGAACACT GCCTGCACAT AGTAAAAGAA TTATAAGTGT GAGGTAGTTG GTAAAATTAT 6840
GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTTT AGGGAAATAA AGTTTGTGCA 6900
TATATATAAT CCCGAAACAT G 6921

Seq ID NO: 328 Protein sequence
Protein Accession #: NP_001932.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS   60
ADLIRSSDPD FRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLLEHQKKVS  120
KTRHTRETVL RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAAQNYTVF YSISGRGVDK  180
EPLNLFYIER DTGNLFCTRP VDREEYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH  240
PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEPDTMHTRL KYSILQQTPR SPGLFSVHPS  300
TGVITTVSHY LDREVVDKYS LIMKVQDMDG QFFGLIGTST CIITVTDSND NAPTFRQNAY  360
EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKGNE NGHFKISTDK ETNEGVLSVV  420
KPLNYEENRQ VNLEIGVNNE APFARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQYVRI  480
KENLAVGSKI NGYKAYDPEN RNGNGLRYKK LHDPKGWITI DEISGSIITS KILDREVETP  540
KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPEILQE YVVICKPKMG YTDILAVDPD  600
EPVHGAPFYF SLPNTSPEIS RLWSLTKVND TAARLSYQKN AGFQEYTIPI TVKDRAGQAA  660
TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATKG  720
KRFPEDLAQQ NLIISNTEAP GDDRVCSANG FMTQTTNNSS QGFCGTMGSG MKNGGQETIE  780
MMKGGNQTLE SCRGAGHHHT LDSCRGGHTE VDNCRYTYSE WHSFTQPRLG EKLHRCNQNE  840
DRMPSQDYVL TYNYEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR
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Seq ID NO: 329 DNA sequence
Nucleic Acid Accession #: NM_016583.2
Coding sequence: 72..842

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC   60
TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCCAGA  120
CCATGGCCCA GTTTGGAGGC CTGCCCGTGC CCCTGGACCA GACCCTGCCC TTGAATGTGA  180
ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA  240
ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCCGCTC CTGGACATCC  300
TGAAGCCTGG AGGAGGTACT TCTGGTGGCC TCCTTGGGGG ACTGCTTGGA AAAGTGACGT  360
CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG  420
AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTCACCATC CCTCTCGGCA  480
TAAAGCTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC  540
TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC  600
TTGGTGACTG CACCCATTCC CCTGGAAGCC TGCAAATTTC TCTGCTTGAT GGACTTGGCC  660
CCCTCCCCAT TCAAGGTCTT CTGGACAGCC TCACAGGGAT CTTGAATAAA GTCCTGCCTG  720
AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA  780
CCCTGGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTC ATCAAGGTCT  840
AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGCTCA CAGATGGCTG  900
GCCCATGTGC TGGAAGATGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCCTCTCCTT  960
TCCCACCAGG CGTGTGTAAC ATCCCATGTG CCTCACCTAA TAAAATGGCT CTTCTTCTGC 1020
AAAAAAAAAA AAAAAAAAAA AAAAAAAAA
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Seq ID NO: 330 Protein sequence
Protein Accession #: NP_057667.1

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1          11         21         31         41         51
|          |          |          |          |          |
MFQTGGLIVF YGLLAQTMAQ FGGLPVPLDQ TLPLNVNPAL PLSPTGLAGS LTNALSNGLL   60
SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL  120
VQSPDGHRLY VTIPLGIKLQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC  180
THSPGSLQIS LLDGLGPLPI QGLLDSLTGI LNKVLPELVQ GNVCPLVNEV LRGLDITLVH  240
DIVNMLIHGL QFVIKV
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Seq ID NO: 331 DNA sequence
Nucleic Acid Accession #: NM_004363.1
Coding sequence: 115..2223

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1          11         21         31         41         51
|          |          |          |          |          |
CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT   60
TCCTGGAACT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG  120
TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCCTGGC AGAGGCTCCT GCTCACAGCC  180
TCACTTCTAA CCTTCTGGAA CCCGCCCACC ACTGCCAAGC TCACTATTGA ATCCACGCCG  240
TTCAATGTCG CAGAGGGGAA GGAGGTGCTT CTACTTGTCC ACAATCTGCC CCAGCATCTT  300
TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT  360
GTAATAGGAA CTCAACAAGC TACCCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC  420
CCCAATGCAT CCCTGCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCCTA  480
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CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCCG GGTATACCCG   540
GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT   600
GTGGCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT   660
CAGAGCCTCC CGGTCAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA   720
TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT   780
GCCAGGCGCA GTGATTCAGT CATCCTGAAT GTCCTCTATG GCCCGGATGC CCCCACCATT   840
TCCCCTCTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCCTG CCACGCAGCC   900
TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA   960
GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT  1020
AACTCAGACA CTGGCCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA  1080
CCCAAACCCT TCATCACCAG CAACAACTCC AACCCCGTGG AGGATGAGGA TGCTGTAGCC  1140
TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC  1200
CTCCCGGTCA GTCCCAGGCT GCAGCTGTCC AATGACAACA GGACCCTCAC TCTACTCAGT  1260
GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTTGAC  1320
CACAGCGACC CAGTCATCCT GAATGTCCTC TATGGCCCAG ACGACCCCAC CATTTCCCCC  1380
TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC  1440
CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACATCC AGCAACACAC ACAAGAGCTC  1500
TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA  1560
GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCACAG TCTCTGCGGA GCTGCCCAAG  1620
CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC  1680
TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA  1740
GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTCACA  1800
AGAAATGACG CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT  1860
GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTC CCCCCCAGAC  1920
TCGTCTTACC TTTCGGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCTC TAACCCATCC  1980
CCGCAGTATT CTTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC  2040
GCCAAAATCA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGTCTCTAA CTTGGCTACT  2100
GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT  2160
CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA  2220
TAGCAGCCCT GGTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTTGTTTT GCTTCTTCCT  2280
TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA  2340
AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAAACCCCA TCTCTACTAA  2400
AAATACAAAA ATGAGCTGGG CTTGGTGGCG CGCACCTGTA GTCCCAGTTA CTCGGGAGGC  2460
TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC  2520
ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCCATCTCA AAAAGAAAAG AAAAGAAGAC  2580
TCTGACCTGT ACTCTTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA  2640
AACTTTAATG AACTAACTGA CAGCTTCATG AAACTGTCCA CCAAGATCAA GCAGAGAAAA  2700
TAATTAATTT CATGGGACTA AATGAACTAA TGAGGATTGC TGATTCTTTA AATGTCTTGT  2760
TTCCCAGATT TCAGGAAACT TTTTTTCTTT TAAGCTATCC ACTCTTACAG CAATTTGATA  2820
AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC  2880
AGACTTGGGA AACTATTCAT GAATATTTAT ATTGTATGGT AATATAGTTA TTGCACAAGT  2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA
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Seq ID NO: 332 Protein sequence
Protein Accession #: NP_004354.1

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1          11         21         31         41         51
|          |          |          |          |          |
MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLPQ    60
HLFGYSWYKG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY   120
TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTCEPE TQDATYLWWV   180
NNQSLPVSPR LQLSNGNRTL TLFNVTRNDT ASYKCETQNP VSARRSDSVI LNVLYGPDAP   240
TISPLNTSYR SGENLNLSCH AASNPPAQYS WFVNGTFQQS TQELFIPNIT VNNSGSYTCQ   300
AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTTYLWWVNN   360
QSLPVSPRLQ LSNDNRTLTL LSVTRNDVGP YECGIQNELS VDHSDPVILN VLYGPDDPTI   420
SPSYTYYRPG VNLSLSCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN   480
NSASGHSRTT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWWVNGQS   540
LPVSPRLQLS NGNRTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDTPIISP   600
PDSSYLSGAN LNLSCHSASN PSPQYSWRIN GIPQQHTQVL FIAKITPNNN GTYACFVSNL   660
ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI
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Seq ID NO: 333 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

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1          11         21         31         41         51
|          |          |          |          |          |
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT    60
TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT   120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG   180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT   240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT   300
AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC   360
ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACAACAGCC CTCCAAACAA   420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA   480
CAATTGCTGT GGCGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC   540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA   600
AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG   660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG   720
ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG   780
AATTGAATAT TAAGAA
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Seq ID NO: 334 Protein sequence
Protein Accession #: NP_008883.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW    60
IGIFVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL   120
FLKQMLERYQ NNSPPNNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN   180
DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI   240
LCWTFWVLLG TMFYWSRIEY
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Seq ID NO: 335 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120..473

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1          11         21         31         41         51
|          |          |          |          |          |
CAATACAGCT AAGGAATTAT CCCTTGTAAA TACCACAGAC CCGCCCTGGA GCCAGGCCAA    60
GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA   120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG   180
AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCCAT   240
TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG   300
CGCAAGAGCC AGTCAAAGGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA   360
TCCGGTGCGC CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCCAGGAA   420
TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC   480
CGGTCCTTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC   540
TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCCTCCC ATTCAGGATG CCCACGGCTG   600
GAGCTGCCTC TCTCATCCAC TTTCCAATAA A
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Seq ID NO: 336 Protein sequence
Protein Accession #: NP_002629.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRASSFLIVV VFLIAGTLVL EAAVTGVPVK GQDTVKGRVP FNGQDPVKGQ VSVKGQDKVK    60
AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCCEGSCG MACFVPQ
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Seq ID NO: 337 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71..2560

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1          11         21         31         41         51
|          |          |          |          |          |
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT    60
CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG   120
CTGGCTGCAG TGCGCGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC   180
CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG   240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA   300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC   360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC   420
TGAAAATGGC AAGGGTCCCT TCCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG   480
AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT   540
CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTTGAAT AAGCCACTGG ACCGGGAGGA   600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA   660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA   720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAGGT   780
GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT   840
CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTTC ACCATTCACC GGAGCACAGG   900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC   960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA  1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT  1080
GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC  1140
CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT  1200
TACCATCACC ACCCACCCTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA  1260
TTTTCAGGCC AAAAACCAGC ACACCCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT  1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC  1380
ACCTGTGTTT GTCCCACCCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA  1440
GCCTCTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG  1500
CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTCACAGC  1560
TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT  1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC  1680
ACTGATTGAT GTCAATGACC ATGGCCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA  1740
CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC  1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA  1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT  1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT  1980
GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAGGGAG GTTTCATCCT  2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCCTCCTG CTGGTGCTGC TTTTGTTGGT  2100
GAGAAAGAAG CGGAAGATCA AGGAGCCCCT CCTACTCCCA GAAGATGACA CCCGTGACAA  2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA  2220
GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC  2280
CATCATCCCG ACACCCATGT ACCGTCCTCG GCCAGCCAAC CCAGATGAAA TCGGCAACTT  2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCACA GCCCCGCCCT ACGACACCCT  2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC  2460
CTCCGCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGGCTTCAA  2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCCTGCC TGCAGGGCTG  2580
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GGGACCAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG  2640
GACTTCGGAG CTTGTCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG  2700
ACGTTAGAGT GGTTGCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC  2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC  2820
TCTTACCTGC CGTAAAATGC TCAACCCTGT GTCCTGGGCC TGGGCCTGCT GTGACTGACC  2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT  2940
TTTTTTTAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT  3000
GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTTCCAGAC CCCAATGCCT CCCATTCGGA  3060
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT  3120
GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT  3180
TAAAGAAACT TTTCCCAGAA AAAAA
```

Seq ID NO: 338 Protein sequence
Protein Accession #: NP_001784.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG    60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG   120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK   180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT   240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA   300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP   360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL   420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR   480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID   540
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD   600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL   660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR   720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF   780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD
```

Seq ID NO: 339 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAGGCTCC AAAGACCCCG ACAGGCCCCG GCGGGTGGGA GGCGCGCGCC CCGGGGCGGG    60
CGGGGCTCCC CCTACCGGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG   120
AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG   180
CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT   240
GCGAGACAAC GAGATCCAGA GGACTCCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG   300
TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAATGG   360
ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGGTTGCG   420
AAGCAGTGCT CCGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT   480
CTCCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAAGTGTT GTAAAATTCG CTACTGCAAT   540
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG   600
AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGGCCTC   660
AGCCTGTCTT GA
```

Seq ID NO: 340 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MRLQRPRQAP AGGRRAPRGG RGSPYRPDPG RGARRLRRFQ KGGEGAPRAD PPWAPLGTMA    60
LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVW CHVCERENTF ECQNPRRCKW   120
TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEEPMPFFY LKCCKIRYCN   180
LEGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASIAAGL SLS
```

Seq ID NO: 341 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

```
1          11         21         31         41         51
|          |          |          |          |          |
GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG    60
TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGGCGGCC GAGGAGAAGG AAGAGGCGCG   120
GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG   180
CGTGACCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT   240
TATCGGCTCG GGCATCTTCG TGACGCCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCCGGG   300
GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA   360
CGCGGAGCTC GGCACCACCA TCTCCAAATC GGGCGGCGAC TACGCCTACA TGCTGGAGGT   420
CTACGGCTCG CTGCCCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCTTC   480
ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCGC TCTTCCCCAC   540
CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC   600
GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCCGC   660
CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA   720
TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACTGGATG TGGGGAACAT   780
TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAATTACT TGAATTTCGT   840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCCTG GCCATCATCA TCTCCCTGCC   900
CATCGTGACG CTGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCCACCGA   960
GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT  1020
```

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GTCCTGGATC ATCCCCGTCT TCGTGGGCCT GTCCTGCTTC GGCTCCGTCA ATGGGTCCCT  1080
GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT  1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTCGTGTTCA CGTGTGTGAT  1200
GACGCTGCTC TACGCCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT  1260
CAACTGGCTC TGCGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC  1320
TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG  1380
CCTCTTCCTG ATCGCCGTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC  1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA  1500
GTGGCTCCTC CAGCGCATCT TCTCCACGAC CGTCCTGTGT CAGAAGCTCA TGCAGGTGGT  1560
CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC
```

Seq ID NO: 342 Protein sequence
Protein Accession #: XP_035292.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV    60
GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAELGTTI SKSGGDYAYM   120
LEVYGSLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCVL   180
LLTAVNCYSV KAATRVQDAF AAAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV   240
GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL   300
STEQMLSSEA VAVDFGNYHL GVMSWIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP   360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCVAL AIIGMIWLRH   420
RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWWKN   480
KPKWLLQGIF STTVLCQKLM QVVPQET
```

Seq ID NO: 343 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

```
1          11         21         31         41         51
|          |          |          |          |          |
TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCGAAAAC CTTCCCCGCT    60
TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCCTATTGC CGGCTGCTGG GAGCCAGGAG   120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA   180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC   240
TGTCTCTGGT CTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA   300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT   360
TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA   420
CATGCCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTCAG GAGAAGAGGC   480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG   540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT   600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC   660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA   720
TTTTCACCCT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC   780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA   840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCCTG CAAACAAGAC GACCTCCTTT   900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCCTCC TCTCTTACCA GACCGCCCCC   960
GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG  1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC  1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC  1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA  1200
GCTCGGTTTC CTTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC
```

Seq ID NO: 344 Protein sequence
Protein Accession #: NP_005259.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVTA ERVWSDDHKD FDCNTRQPGC    60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP   120
GKKRGGLWWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP   180
SEKNIFTLFM VATAAICILL NLVELIYLVS KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ   240
DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL
```

Seq ID NO: 345 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

```
1          11         21         31         41         51
|          |          |          |          |          |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCCTCC TCACCCTCCT    60
CGCCCTGCTG GCGCTCACCT CCGCGGTCGC CAAAAAGAAA GATAAGGTGA AGAAGGGCGG   120
CCCGGGGAGC GAGTGCGCTG AGTGGGCCTG GGGGCCCTGC ACCCCCAGCA GCAAGGATTG   180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGCCCAGACC CAGCGCATCC GGTGCAGGGT   240
GCCCTGCAAC TGGAAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG   300
TGCGTGTGAT GGGGGCACAG GCACCAAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA   360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCCA AGACCAAAGC   420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA   480
GCCCCTGGTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC   540
CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC   600
ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT   660
TGAGCCTCCC CCAAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC   720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTTCCCCC CAATAAAAGC TCTTCTTTTT   780
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TAATAT

Seq ID NO: 346 Protein sequence
Protein Accession #: NP_002382.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GGPGSECAEW AWGPCTPSSK DCGVGFREGT    60
CGAQTQRIRC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLKKA RYNAQCQETI   120
RVTKPCTPKT KAKAKAKKGK GKD
```

Seq ID NO: 347 DNA sequence
Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC    60
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC   120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC   180
AAAAATGTGT GCTATGACCA CTTTTTCCCG GTGTCCCACA TCCGGCTGTG GGCCCTCCAG   240
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC   300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC   360
ATTAAAAAGC ACAAGGTTCG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC   420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCCT TTACAATGGG   480
TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCCAACCT TGTTGACTGC   540
TTTATTTCTA GGCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TGCGTCTGTG   600
ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTTAGG   660
AGATCAAAGA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG   720
CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA   780
AGCTAA
```

Seq ID NO: 348 Protein sequence
Protein Accession #: NP_006774.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDWGTLHTFI GGVNKHSTSI GKVWITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC    60
KNVCYDHFFP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDFKDIED   120
IKKHKVRIEG SLWWTYTSSI FFRIIFEAAF MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC   180
FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLLKVCFR RSKRAQTQKN HPNHALKESK   240
QNEMNELISD SGQNAITGFP S
```

Seq ID NO: 349 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

```
1          11         21         31         41         51
|          |          |          |          |          |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC    60
TCACCCTGGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC   120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA   180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC   240
CCACCCCCGA GGACAACCTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTG   300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG   360
TGGCGAACGA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCCTGTTT CTCTGCCTAC   420
AGGACACCAC CACCCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG   480
AGGACGATGA GATCATGCAG GGATTCATCA GGGCTTTCAG GCCCCTGCCC AGGCACCTAT   540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCCT   600
CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCCTGCCC   660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT   720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG   780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G
```

Seq ID NO: 350 Protein sequence
Protein Accession #: NP_002562.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR    60
WENNSCVEKK VLGEKTGNPK KFKINYTVAN EATLLDTDYD NFLFLCLQDT TTPIQSMMCQ   120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMEEPC RF
```

Seq ID NO: 351 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

```
1          11         21         31         41         51
|          |          |          |          |          |
ACTTGCGTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC    60
TCGCCGCCTG CTGCTGCTGT CCTCGCGTCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG   120
CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC   180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC   240
TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC   300
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TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC   360
GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG   420
TCTACAAAGC TCCGGAGGAG CCAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA   480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCCTCAAG   540
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAGT   600
CGTCCCAGAC TGTGGAGTCG AGTCGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC   660
TGGTTAAAGA AGACAAAGAT GCCCAGTTTT ACTGTGAGCT CAACTACCGG CTGCCCAGTG   720
GGAACCACAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCCG ACAGAAAAAG   780
TGTGGCTGGA AGTGGAGCCC GTCGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT   840
GTTTGGCTGA TGGCAACCCT CCACCACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA   900
GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCCT GGTGCTGGAG CCTGCCCGGA   960
AGGAACACAG TGGGCGCTAT GAATGTCAGG CCTGGAACTT GGACACCATG ATATCGCTGC  1020
TGAGTGAACC ACAGGAACTA CTGGTGAACT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG  1080
CCCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG  1140
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAAGG GGGCCTGTGC  1200
TTCAGTTGCA TGACCTGAAA CGGGAGGCAG GAGCCGGCTA TCGCTGCGTG GCGTCTGTGC  1260
CCAGCATACC CGGCCTGAAC CGCACACAGC TGGTCAAGCT GGCCATTTTT GGCCCCCCTT  1320
GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAAGAGAA TATGGTGTTG AATCTGTCTT  1380
GTGAAGCGTC AGGGCACCCC CGGCCCACCA TCTCCTGGAA CGTCAACGGC ACGGCAAGTG  1440
AACAAGACCA AGATCCACAG CGAGTCCTGA GCACCCTGAA TGTCCTCGTG ACCCCGGAGC  1500
TGTTGGAGAC AGGTGTTGAA TGCACGGCCT CCAACGACCT GGGCAAAAAC ACCAGCATCC  1560
TCTTCCTGGA GCTGGTCAAT TTAACCACCC TCACACCAGA CTCCAACACA ACCACTGGCC  1620
TCAGCACTTC CACTGCCAGT CCTCATACCA GAGCCAACAG CACCTCCACA GAGAGAAAGC  1680
TGCCGGAGCC GGAGAGCCGG GGCGTGGTCA TCGTGGCTGT GATTGTGTGC ATCCTGGTCC  1740
TGGCGGTGCT GGGCGCTGTC CTCTATTTCC TCTATAAGAA GGGCAAGCTG CCGTGCAGGC  1800
GCTCAGGGAA GCAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAACTT GTAGTTGAAG  1860
TTAAGTCAGA TAAGCTCCCA GAAGAGATGG GCCTCCTGCA GGGCAGCAGC GGTGACAAGA  1920
GGGCTCCGGG AGACCAGGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT  1980
CAGCTCCCTT CCCTGCCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG  2040
CCTCCAAAGG GACTAGAGAG AAGCCTCCTG CTCCCCTCAC CTGCACACCC CCTTTCAGAG  2100
GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTTT TCAGGGACCA  2160
GTCCACCACC ATCTCCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCCAGTCTC  2220
CCGAGCGGGT AGGAGAGTTT CTTGCAGAAC GTGTTTTTTC TTTACACACA TTATGGCTGT  2280
AAATACCTGG CTCCTGCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTTCCTGCCC  2340
CAAAGGCTGG CTTCCACCAT CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC  2400
GCCTGCTCAT GTTGAAGTGC GCTGTTCACA CCCGCTCCGG AGAGCACCCC AGCGGCATCC  2460
AGAAGCAGCT GCAGTGTTGC TGCCACCACC CTCCTGCTCG CCTCTTCAAA GTCTCCTGTG  2520
ACATTTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCATT CCTTAAAAGA TACGTGCCGG  2580
GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGCGGGCGGA  2640
TCACAAAGTC AGGACGAGAC CATCCTGGCT AACACGGTGA AACCCTGTCT CTACTAAAAA  2700
TACAAAAAAA AATTAGCTAG GCGTAGTGGT TGGCACCTAT AGTCCCAGCT ACTCGGAAGG  2760
CTGAAGCAGG AGAATGGTAT GAATCCAGGA GGTGGAGCTT GCAGTGAGCC GAGACCGTGC  2820
CACTGCACTC CAGCCTGGGC AACACAGCGA GACTCCGTCT CGAGGAAAAA AAAAGAAAAG  2880
ACGCGTACCT GCGGTGAGGA AGCTGGGCGC TGTTTTCGAG TTCAGGTGAA TTAGCCTCAA  2940
TCCCCGTGTT CACTTGCTCC CATAGCCCTC TTGATGGATC ACGTAAAACT GAAAGGCAGC  3000
GGGGAGCAGA CAAAGATGAG GTCTACACTG TCCTTCATGG GGATTAAAGC TATGGTTATA  3060
TTAGCACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAGGG CCCAAATGAG  3120
AGAATGGTAC TTAGGGATGG AAAACGGGGC CTGGCTAGAG CTTCGGGTGT GTGTGTCTGT  3180
CTGTGTGTAT GCATACATAT GTGTGTATAT ATGGTTTTGT CAGGTGTGTA AATTTGCAAA  3240
TTGTTTCCTT TATATATGTA TGTATATATA TATATGAAAA TATATATATA TATGAAAAAT  3300
AAAGCTTAAT TGTCCCAGAA AATCATACAT TGCTTTTTTA TTCTACATGG GTACCACAGG  3360
AACCTGGGGG CCTGTGAAAC TACAACCAAA AGGCACACAA AACCGTTTCC AGTTGGCAGC  3420
AGAGATCAGG GGTTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG  3480
CTACCCTACT TTTCAGCAGC AAAACGTCCC GTATGACGCA GCACGAAGGG CCTGGCAGGC  3540
TGTTAGCAGG AGCTATGTCC CTTCCTATCG TTTCCGTCCA CTT
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Seq ID NO: 352 Protein sequence
Protein Accession #: NP_006491.1

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1          11         21         31         41         51
|          |          |          |          |          |
GLPRLVCAFL LAACCCCPRV AGVPGEAEQP APELVEVEVG STALLKCGLS QSQGNLSHVD    60
WFSVHKEKRT LIFRVRQGQG QSEPGEYEQR LSLQDRGATL ALTQVTPQDE RIFLCQGKRP   120
RSQEYRIQLR VYKAPEEPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIPQ VIWYKNGRPL   180
KEEKNRVHIQ SSQTVESSGL YTLQSILKAQ LVKEDKDAQF YCELNYRLPS GNHMKESREV   240
TVPVFYPTEK VWLEVEPVGM LKEGDRVEIR CLADGNPPPH FSISKQNPST REAEEETTND   300
NGVLVLEPAR KEHSGRYECQ AWNLDTMISL LSEPQELLVN YVSDVRVSPA APERQEGSSL   360
TLTCEAESSQ DLEFQWLREE TDQVLERGPV LQLHDLKREA GGGYRCVASV PSIPGLNRTQ   420
LVKLAIFGPP WMAFKERKVW VKENMVLNLS CEASGHPRPT ISWNVNGTAS EQDQDPQRVL   480
STLNVLVTPE LLETGVECTA SNDLGKNTSI LFLELVNLTT LTPDSNTTTG LSTSTASPHT   540
RANSTSTERK LPEPESRGVV IVAVIVCILV LAVLGAVLYF LYKKGKLPCR RSGKQEITLP   600
PSRKTELVVE VKSDKLPEEM GLLQGSSGDK RAPGDQGEKY IDLRH
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Seq ID NO: 353 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

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GCTAGGCCGG GCGGATCCCG TCCTCCCCCG ATGTGAGCAG TTTTCCGAAA CCCCGTCAGG   120
CGAAGGCTGC CCAGAGAGGT GGAGTCGGTA GCGGGGCCGG GAACATGAGG CAGTCTCTCC   180
TATTCCTGAC CAGCGTGGTT CCTTTCGTGC TGGCGCCGCG ACCTCCGGAT GACCCGGGCT   240
TCGGCCCCCA CCAGAGACTC GAGAAGCTTG ATTCTTTGCT CTCAGACTAC GATATTCTCT   300
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CTTTATCTAA TATCCAGCAG CATTCGGTAA GAAAAAGAGA TCTACAGACT TCAACACATG   360
TAGAAACACT ACTAACTTTT TCAGCTTTGA AAAGGCATTT TAAATTATAC CTGACATCAA   420
GTACTGAACG TTTTTCACAA AATTTCAAGG TCGTGGTGGT GGATGGTAAA AACGAAAGCG   480
AGTACACTGC AAAATGGCAG GACTTCTTCA CTGGACACGT GGTTGGTGAG CCTGACTCTA   540
GGGTTCTAGC CCACATAAGA GATGATGATG TTATAATCAG AATCAACACA GATGGGGCCG   600
AATATAACAT AGAGCCACTT TGCAGATTTG TTAATGATAC CAAAGACAAA AGAATGTTAG   660
TTTATAAATC TGAAGATATC AAGAATGTTT CACGTTTGCA GTCTCCAAAA GTGTGTGGTT   720
ATTTAAAAGT GGATAATGAA GAGTTGCTCC CAAAAGGGTT AGTAGACAGA GAACCACCTG   780
AAGAGCTTGT TCATCGAGTG AAAAGAAGAG CTGACCCAGA TCCCATGAAG AACACGTGTA   840
AATTATTGGT GGTAGCAGAT CATCGCTTCT ACAGATACAT GGGCAGAGGG GAAGAGAGTA   900
CAACTACAAA TTACTTAATA GAGCTAATTG ACAGAGTTGA TGACATCTAT CGGAACACTT   960
CATGGGATAA TGCAGGTTTT AAAGGCTATG GAATACAGAT AGAGCAGATT CGCATTCTCA  1020
AGTCTCCACA AGAGGTAAAA CCTGGTGAAA AGCACTACAA CATGGCAAAA AGTTACCCAA  1080
ATGAAGAAAA GGATGCTTGG GATGTGAAGA TGTTGCTAGA GCAATTTAGC TTTGATATAG  1140
CTGAGGAAGC ATCTAAAGTT TGCTTGGCAC ACCTTTTCAC ATACCAAGAT TTTGATATGG  1200
GAACTCTTGG ATTAGCTTAT GTTGGCTCTC CCAGAGCAAA CAGCCATGGA GGTGTTTGTC  1260
CAAAGGCTTA TTATAGCCCA GTTGGGAAGA AAAATATCTA TTTGAATAGT GGTTTGACGA  1320
GCACAAAGAA TTATGGTAAA ACCATCCTTA CAAAGGAAGC TGACCTGGTT ACAACTCATG  1380
AATTGGGACA TAATTTTGGA GCAGAACATG ATCCGGATGG TCTAGCAGAA TGTGCCCCGA  1440
ATGAGGACCA GGGAGGGAAA TATGTCATGT ATCCCATAGC TGTGAGTGGC GATCACGAGA  1500
ACAATAAGAT GTTTTCAAAC TGCAGTAAAC AATCAATCTA TAAGACCATT GAAAGTAAGG  1560
CCCAGGAGTG TTTTCAAGAA CGCAGCAATA AAGTTTGTGG GAACTCGAGG GTGGATGAAG  1620
GAGAAGAGTG TGATCCTGGC ATCATGTATC TGAACAACGA CACCTGCTGC AACAGCGACT  1680
GCACGTTGAA GGAAGGTGTC CAGTGCAGTG ACAGGAACAG TCCTTGCTGT AAAAACTGTC  1740
AGTTTGAGAC TGCCCAGAAG AAGTGCCAGG AGGCGATTAA TGCTACTTGC AAAGGCGTGT  1800
CCTACTGCAC AGGTAATAGC AGTGAGTGCC CGCCTCCAGG AAATGCTGAA AATGACACTG  1860
TTTGCTTGGA TCTTGGCAAG TGTAAGGATG GGAAATGCAT CCCTTTCTGC GAGAGGGAAC  1920
AGCAGCTGGA GTCCTGTGCA TGTAATGAAA CTGACAACTC CTGCAAGGTG TGCTGCAGGG  1980
ACCTTTCTGG CCGCTGTGTG CCCTATGTCG ATGCTGAACA AAAGAACTTA TTTTTGAGGA  2040
AAGGAAAGCC CTGTACAGTA GGATTTTGTG ACATGAATGG CAAATGTGAG AAACGAGTAC  2100
AGGATGTAAT TGAACGATTT TGGGATTTCA TTGACCAGCT GAGCATCAAT ACTTTTGGAA  2160
AGTTTTTAGC AGACAACATC GTTGGGTCTG TCCTGGTTTT CTCCTTGATA TTTTGGATTC  2220
CTTTCAGCAT TCTTGTCCAT TGTGTGGATA AGAAATTGGA TAAACAGTAT GAATCTCTGT  2280
CTCTGTTTCA CCCCAGTAAC GTCGAAATGC TGAGCAGCAT GGATTCTGCA TCGGTTCGCA  2340
TTATCAAACC CTTTCCTGCG CCCCAGACTC CAGGCCGCCT GCAGCCTGCC CCTGTGATCC  2400
CTTCGGCGCC AGCAGCTCCA AAACTGGACC ACCAGAGAAT GGACACCATC CAGGAAGACC  2460
CCAGCACAGA CTCCCATATG GACGAGGATG GGTTTGAGAA GGACCCCTTC CCAAATAGCA  2520
GCACAGCTGC CAAGTCATTT GAGGATCTCA CGGACCATCC GGTCGCCAGA AGTGAAAAGG  2580
CTGCCTCCTT TAAACTGCAG CGTCAGAATC GTGTTAACAG CAAAGAAACA GAGTGCTAAT  2640
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TAAGGTGAAA GTGAATCTAC TTATTTTGAG GCTTTCAGGT TTTAGTTTTT AAAATATCTT  2880
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TGTAAATTAA TCTTTTATAT TGATAACAGC ACTGACTAGG GAAATGATCA GTTTTTTTTT  3000
ATACACTGTA ATGAACCGCT GAATATGAAG CATTTGGCAT TTATTTGTGA GAAAAGTGGA  3060
ATAGTTTTTT TTTTTTTTTT TTTTTTTTGC CTTCAACTAA AAACAAAGGA GATAAATTTA  3120
GTATACATTG TATCTAAATT GTGGGTCTAT TTCTAGTTAT TACCCAGAGT TTTTATGTAG  3180
CAGGGAAAAT ATATATCTAA ATTTAGAAAT CATTTGGGTT AATATGGCTC TTCATAATTC  3240
TAAGACTAAT GCTCAGAACC TAACCACTAC CTTACAGTGA GGGCTATACA TGGTAGCCAG  3300
TTGAATTTAT GGAATCTACC AACTGTTTAG GGCCCTGATT TGCTGGGCAG TTTTTCTGTA  3360
TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT AGAAAATTCA  3420
CTATTGGCTG GGAGTGGTGG CTCATGCCTG TAATCCCAGC ACTTGGAGAG GCTGAGGTTG  3480
CGCCACTACA CTCCAGCCTG GGTGACAGAG TGAGATCTGC CTC
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Seq ID NO: 354 Protein sequence
Protein Accession #: NP_003174.2

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1          11         21         31         41         51
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QTSTHVETLL TFSALKRHFK LYLTSSTERF SQNFKVVVVD GKNESEYTAK WQDFFTGHVV   120
GEPDSRVLAH IRDDDVIIRI NTDGAEYNIE PLWRFVNDTK DKRMLVYKSE DIKNVSRLQS   180
PKVCGYLKVD NEELLPKGLV DREPPEELVH RVKRRADPDP MKNTCKLLVV ADHRFYRYMG   240
RGEESTTTNY LIELIDRVDD IYRNTSWDNA GFKGYGIQIE QIRILKSPQE VKPGEKHYNM   300
AKSYPNEEKD AWDVKMLLEQ FSFDIAEEAS KVCLAHLFTY QDFDMGTLGL AYVGSPRANS   360
HGGVCPKAYY SPVGKKNIYL NSGLTSTKNY GKTILTKEAD LVTTHELGHN FGAEHDPDGL   420
AECAPNEDQG GKYVMYPIAV SGDHENNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN   480
SRVDEGEECD PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKKCQEAINA   540
TCKGVSYCTG NSSECPPPGN AENDTVCLDL GKCKDGKCIP FCEREQQLES CACNETDNSC   600
KVCCRDLSGR CVPYVDAEQK NLFLRKGKPC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS   660
INTFGKFLAD NIVGSVLVFS LIFWIPFSIL VHCVDKKLDK QYESLSLFHP SNVEMLSSMD   720
SASVRIIKPF PAPQTPGRLQ PAPVIPSAPA APKLDHQRMD TIQEDPSTDS HMDEDGFEKD   780
PFPNSSTAAK SFEDLTDHPV ARSEKAASFK LQRQNRVNSK ETEC
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Seq ID NO: 355 DNA sequence
Nucleic Acid Accession #: NM_021832.1
Coding sequence: 164..2248

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CTAGGCCGGG CGGATCCCGT CCTCCCCCGA TGTGAGCAGT TTTCCGAAAC CCCGTCAGGC   120
GAAGGCTGCC CAGAGAGGTG GAGTCGGTAG CGGGGCCGGG AACATGAGGC AGTCTCTCCT   180
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ATTCCTGACC AGCGTGGTTC CTTTCGTGCT GGCGCCGCGA CCTCCGGATG ACCCGGGCTT   240
CGGCCCCCAC CAGAGACTCG AGAAGCTTGA TTCTTTGCTC TCAGACTACG ATATTCTCTC   300
TTTATCTAAT ATCCAGCAGC ATTCGGTAAG AAAAAGAGAT CTACAGACTT CAACACATGT   360
AGAAACACTA CTAACTTTTT CAGCTTTGAA AAGGCATTTT AAATTATACC TGACATCAAG   420
TACTGAACGT TTTTCACAAA ATTTCAAGGT CGTGGTGGTG GATGGTAAAA ACGAAAGCGA   480
GTACACTGTA AAATGGCAGG ACTTCTTCAC TGGACACGTG GTTGGTGAGC CTGACTCTAG   540
GGTTCTAGCC CACATAAGAG ATGATGATGT TATAATCAGA ATCAACACAG ATGGGGCCGA   600
ATATAACATA GAGCCACTTT GGAGATTTGT TAATGATACC AAAGACAAAA GAATGTTAGT   660
TTATAAATCT GAAGATATCA AGAATGTTTC ACGTTTGCAG TCTCCAAAAG TGTGTGGTTA   720
TTTAAAAGTG GATAATGAAG AGTTGCTCCC AAAAGGGTTA GTAGACAGAG AACCACCTGA   780
AGAGCTTGTT CATCGAGTGA AAAGAAGAGC TGACCCAGAT CCCATGAAGA ACACGTGTAA   840
ATTATTGGTG GTAGCAGATC ATCGCTTCTA CAGATACATG GGCAGAGGGG AAGAGAGTAC   900
AACTACAAAT TACTTAATAG AGCTAATTGA CAGAGTTGAT GACATCTATC GGAACACTTC   960
ATGGGATAAT GCAGGTTTTA AAGGCTATGG AATACAGATA GAGCAGATTC GCATTCTCAA  1020
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TGAAGAAAAG GATGCTTGGG ATGTGAAGAT GTTGCTAGAG CAATTTAGCT TTGATATAGC  1140
TGAGGAAGCA TCTAAAGTTT GCTTGGCACA CCTTTTCACA TACCAAGATT TTGATATGGG  1200
AACTCTTGGA TTAGCTTATG TTGGCTCTCC CAGAGCAAAC AGCCATGGAG GTGTTTGTCC  1260
AAAGGCTTAT TATAGCCCAG TTGGGAAGAA AAATATCTAT TTGAATAGTG GTTTGACGAG  1320
CACAAAGAAT TATGGTAAAA CCATCCTTAC AAAGGAAGCT GACCTGGTTA CAACTCATGA  1380
ATTGGGACAT AATTTTGGAG CAGAACATGA TCCGGATGGT CTAGCAGAAT GTGCCCCGAA  1440
TGAGGACCAG GGAGGGAAAT ATGTCATGTA TCCCATAGCT GTGAGTGGCG ATCACGAGAA  1500
CAATAAGATG TTTTCAAACT GCAGTAAACA ATCAATCTAT AAGACCATTG AAAGTAAGGC  1560
CCAGGAGTGT TTTCAAGAAC GCAGCAATAA AGTTTGTGGG AACTCGAGGG TGGATGAAGG  1620
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CACGTTGAAG GAAGGTGTCC AGTGCAGTGA CAGGAACAGT CCTTGCTGTA AAAACTGTCA  1740
GTTTGAGACT GCCCAGAAGA AGTGCCAGGA GGCGATTAAT GCTACTTGCA AAGGCGTGTC  1800
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TTGCTTGGAT CTTGGCAAGT GTAAGGATGG GAAATGCATC CCTTTCTGCG AGAGGGAACA  1920
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CCTTTCCGGC CGCTGTGTGC CCTATGTCGA TGCTGAACAA AAGAACTTAT TTTTGAGGAA  2040
AGGAAAGCCC TGTACAGTAG GATTTTGTGA CATGAATGGC AAATGTGAGA AACGAGTACA  2100
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CGGTTCGCAT TATCAAACCC TTTCCTGCGC CCCAGACTCC AGGCCGCCTG CAGCCTGCCC  2340
CTGTGATCCC TTCGGCGCCA GCAGCTCCAA AACTGGACCA CCAGAGAATG GACACCATCC  2400
AGGAAGACCC CAGCACAGAC TCACATATGG ACGAGGATGG GTTTGAGAAG GACCCCTTCC  2460
CAAATAGCAG CACAGCTGCC AAGTCATTTG AGGATCTCAC GGACCATCCG GTCACCAGAA  2520
GTGAAAAGGC TGCCTCCTTT AAACTGCAGC GTCAGAATCG TGTTGACAGC AAAGAAACAG  2580
AGTGCTAATT TAGTTCTCAG CTCTTCTGAC TTAAGTGTGC AAAATATTTT TATAGATTTG  2640
ACCTACAATC AATCACAGCT TATATTTTGT GAAGACTGGG AAGTGACTTA GCAGATGCTG  2700
GTCATGTGTT TGAACTTCCT GCAGGTAAAC AGTTCTTGTG TGGTTTGGCC CTTCTCCTTT  2760
TGAAAAGGTA AGGTGAAGGT GAATCTAGCT TATTTTGAGG CTTTCAGGTT TTAGTTTTTA  2820
AAATATCTTT TGACCTGTGG TGCAAAAGCA GAAAATACAG CTGGATTGGG TTATGAGTAT  2880
TTACGTTTTT GTAAATTAAT CTTTTATATT GATAACAGGC ACTGACTAGG GAAATGATCA  2940
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GAAAAGTGGA ATAGTTTTTT TTTTTTTTTT TTTTTTTTGC CTTCAACTAA AAACAAAGGA  3060
GATAAATTTA GTATACATTG TATCTAAATT GTGGGTCTAT TTCTAGTTAT TACCCAGAGT  3120
TTTTATGTAG CAGGGAAAAT ATATATCTAA ATTTAGAAAT CATTTGGGTT AATATGGCTC  3180
TTCATAATTC TAAGACTAAT GCTCAGAACC TAACCACTAC CTTACAGTGA GGGCTATACA  3240
TGGTAGCCAG TTGAATTTAT GGAATCTACC AACTGTTTAG GGCCCTGATT TGCTGGGCAG  3300
TTTTTCTGTA TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT  3360
AGAAAATTCA CTATTGGCTG GGAGTGGTGG CTCATGCCTG TAATCCCAGC ACTTGGAGAG  3420
 3421 GCTGAGGTTG CGCCACTACA CTCCAGCCTG GGTGACAGAG TGAGATCTGC CTC
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Seq ID NO: 356 Protein sequence
Protein Accession #: NP_068604.1

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QTSTHVETLL TFSALKRHFK LYLTSSTERF SQNFKVVVVD GKNESEYTVK WQDFFTGHVV   120
GEPDSRVLAH IRDDDVIIRI NTDGAEYNIE PLWRFVNDTK DKRMLVYKSE DIKNVSRLQS   180
PKVCGYLKVD NEELLPKGLV DREPPEELVH RVKRRADPDP MKNTCKLLVV ADHRFYRYMG   240
RGEESTTTNY LIELIDRVDD IYRNTSWDNA GFKGYGIQIE QIRILKSPQE VKPGEKHYNM   300
AKSYPNEEKD AWDVKMLLEQ FSFDIAEEAS KVCLAHLFTY QDFDMGTLGL AYVGSPRANS   360
HGGVCPKAYY SPVGKKNIYL NSGLTSTKNY GKTILTKEAD LVTTHELGHN FGAEHDPDGL   420
AECAPNEDQG GKYVMYPIAV SGDHENNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN   480
SRVDEGEECD PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKKCQEAINA   540
TCKGVSYCTG NSSECPPPGN AEDDTVCLDL GKCKDGKCIP FCEREQQLES CACNETDNSC   600
KVCCRDLSGR CVPYVDAEQK NLFLRKGKPC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS   660
INTFGKFLAD NIVGSVLVFS LIFWIPFSIL VHCV
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Seq ID NO: 357 DNA sequence
Nucleic Acid Accession #: NM_004994.1
Coding sequence: 20..2143

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1          11         21         31         41         51
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GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA   120
CCTGAGAACC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA   180
CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT   240
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CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT   300
GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGGCAGATTC CAAACCTTTG AGGGCGACCT   360
CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG   420
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CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTCGCGGA   540
GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC   600
TGGCCCCGGC ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA   660
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CATCTTCGAG GGCCGCTCCT ACTCTGCCTG CACCACCGAC GGTCGCTCCG ACGGCTTGCC   780
CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA   840
GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCATCTT   900
CCAAGGCCAA TCCTACTCCG CCTGCACCAC GGACGGTCGC TCCGACGGCT ACCGCTGGTG   960
CGCCACCACC GCCAACTACG ACCGGGACAA GCTCTTCGGC TTCTGCCCGA CCCGAGCTGA  1020
CTCGACGGTG ATGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCCT TCACTTTCCT  1080
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TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG  1200
TTTGTTCCTC GTGGCGGCGC ATGAGTTCGG CCACGCGCTG GGCTTAGATC ATTCCTCAGT  1260
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CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCCTCC  1380
AACCACCACC ACACCGCAGC CCACGGCTCC CCCGACGGTC TGCCCCACCG GACCCCCCAC  1440
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TGCCTGCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGGAACCAGC TGTATTTGTT  1620
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CCTTATCGCC GACAAGTGGC CCCCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC  1740
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GGTGCTGGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC  1860
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CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACCAGG TGGACCAAGT  2100
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GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA  2220
CAAACTGGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC  2280
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Seq ID NO: 358 Protein sequence
Protein Accession #: NP_004985.1

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RGESKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLKWHHHN   120
ITYWIQNYSE DLPRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP   180
FDGKDGLLAH AFPPGPGIQG DAHFDDDELW SLGKGVVVPT RFGNADGAAC HFPFIFEGRS   240
YSACTTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS   300
ACTTDGRSDG YRWCATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST   360
CTSEGRGDGR LWCATTSNFD SDKKWGFCPD QGYSLFLVAA HEFGHALGLD HSSVPEALMY   420
PMYRFTEGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER   480
PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFKDGKYW   540
RFSEGRGSRP QGPFLIADKW PALPRKLDSV FEEPLSKKLF FFSGRQVWVY TGASVLGPRR   600
LDKLGLGADV AQVTGALRSG RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD   660
THDVFQYREK AYFCQDRFYW RVSSRSELNQ VDQVGYVTYD ILQCPED
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Seq ID NO: 359 DNA sequence
Nucleic Acid Accession #: NM_000213.1
Coding sequence: 127..5385

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CCCCGAGGTA GGTCCAGGAC GGGCGCACAG CAGCAGCCGA GGCTGGCCGG GAGAGGGAGG   120
AAGAGGATGG CAGGGCCACG CCCCAGCCCA TGGGCCAGGC TGCTCCTGGC AGCCTTGATC   180
AGCGTCAGCC TCTCTGGGAC CTTGGCAAAC CGCTGCAAGA AGGCCCCAGT GAAGAGCTGC   240
ACGGAGTGTG TCCGTGTGGA TAAGGACTGC GCCTACTGCA CAGACGAGAT GTTCAGGGAC   300
CGGCGCTGCA ACACCCAGGC GGAGCTGCTG GCCGCGGGCT GCCAGCGGGA GAGCATCGTG   360
GTCATGGAGA GCAGCTTCCA AATCACAGAG GAGACCCAGA TTGACACCAC CCTGCGGCGC   420
AGCCAGATGT CCCCCCAAGG CCTGCGGGTC CGTCTGCGGC CCGGTGAGGA GCGGCATTTT   480
GAGCTGGAGG TGTTTGAGCC ACTGGAGAGC CCCGTGGACC TGTACATCCT CATGGACTTC   540
TCCAACTCCA TGTCCGATGA TCTGGACAAC CTCAAGAAGA TGGGGCAGAA CCTGGCTCGG   600
GTCCTGAGCC AGCTCACCAG CGACTACACT ATTGGATTTG GCAAGTTTGT GGACAAAGTC   660
AGCGTCCCGC AGACGGACAT GAGGCCTGAG AAGCTGAAGG AGCCCTGGCC CAACAGTGAC   720
CCCCCCTTCT CCTTCAAGAA CGTCATCAGC CTGACAGAAG ATGTGGATGA GTTCCGGAAT   780
AAACTGCAGG GAGAGCGGAT CTCAGGCAAC CTGGATGCTC CTGAGGGCGG CTTCGATGCC   840
ATCCTGCAGA CAGCTGTGTG CACGAGGGAC ATTGGCTGGC GCCCGGACAG CACCCACCTG   900
CTGGTCTTCT CCACCGAGTC AGCCTTCCAC TATGAGGCTG ATGGCGCCAA CGTGCTGGCT   960
GGCATCATGA GCCGCAACGA TGAACGGTGC CACCTGGACA CCACGGGCAC CTACACCCAG  1020
TACAGGACAC AGGACTACCC GTCGGTGCCC ACCCTGGTGC GCCTGCTCGC CAAGCACAAC  1080
ATCATCCCCA TCTTTGCTGT CACCAACTAC TCCTATAGCT ACTACGAGAA GCTTCACACC  1140
TATTTCCCTG TCTCCTCACT GGGGGTGCTG CAGGAGGACT CGTCCAACAT CGTGGAGCTG  1200
CTGGAGGAGG CCTTCAATCG GATCCGCTCC AACCTGGACA TCCGGGCCCT AGACAGCCCC  1260
CGAGGCCTTC GGACAGAGGT CACCTCCAAG ATGTTCCAGA AGACGAGGAC TGGGTCCTTT  1320
CACATCCGGC GGGGGGAAGT GGGTATATAC CAGGTGCAGC TGCGGGCCCT TGAGCACGTG  1380
GATGGGACGC ACGTGTGCCA GCTGCCGGAG GACCAGAAGG GCAACATCCA TCTGAAACCT  1440
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TCCTTCTCCG ACGGCCTCAA GATGGACGCG GGCATCATCT GTGATGTGTG CACCTGCGAG  1500
CTGCAAAAAG AGGTGCGGTC AGCTCGCTGC AGCTTCAACG GAGACTTCGT GTGCGGACAG  1560
TGTGTGTGCA GCGAGGGCTG GAGTGGCCAG ACCTGCAACT GCTCCACCGG CTCTCTGAGT  1620
GACATTCAGC CCTGCCTGCG GGAGGGCGAG GACAAGCCGT GCTCCGGCCG TGGGGAGTGC  1680
CAGTGCGGGC ACTGTGTGTG CTACGGCGAA GGCCGCTACG AGGGTCAGTT CTGCGAGTAT  1740
GACAACTTCC AGTGTCCCCG CACTTCCGGG TTCCTCTGCA ATGACCGAGG ACGCTGCTCC  1800
ATGGGCCAGT GTGTGTGTGA GCCTGGTTGG ACAGGCCCAA GCTGTGACTG TCCCCTCAGC  1860
AATGCCACCT GCATCGACAG CAATGGGGGC ATCTGTAATG GACGTGGCCA CTGTGAGTGT  1920
GGCCGCTGCC ACTGCCACCA GCAGTCGCTC TACACGGACA CCATCTGCGA GATCAACTAC  1980
TCGGCGATCC ACCCGGGCCT CTGCGAGGAC CTACGCTCCT GCGTGCAGTG CCAGGCGTGG  2040
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GACGAGCTTA AGAGAGCCGA GGAGGTGGTG GTGCGCTGCT CCTTCCGGGA CGAGGATGAC  2160
GACTGCACCT ACAGCTACAC CATGGAAGGT GACGGCGCCC CTGGGCCCAA CAGCACTGTC  2220
CTGGTGCACA AGAAGAAGGA CTGCCCTCCG GGCTCCTTCT GGTGGCTCAT CCCCCTGCTC  2280
CTCCTCCTCC TGCCGCTCCT GGCCCTGCTA CTGCTGCTAT GCTGGAAGTA CTGTGCCTGC  2340
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GAAGACCACT ACATGCTGCG GGAGAACCTG ATGGCCTCTG ACCACTTGGA CACGCCCATG  2460
CTGCGCAGCG GGAACCTCAA GGGCCGTGAC GTGGTCCGCT GGAAGGTCAC CAACAACATG  2520
CAGCGGCCTG GCTTTGCCAC TCATGCCGCC AGCATCAACC CCACAGAGCT GGTGCCCTAC  2580
GGGCTGTCCT TGCGCCTGGC CCGCCTTTGC ACCGAGAACC TGCTGAAGCC TGACACTCGG  2640
GAGTGCGCCC AGCTGCGCCA GGAGGTGGAG GAGAACCTGA ACGAGGTCTA CAGGCAGATC  2700
TCCGGTGTAC ACAAGCTCCA GCAGACCAAG TTCCGGCAGC AGCCCAATGC CGGGAAAAAG  2760
CAAGACCACA CCATTGTGGA CACAGTGCTG ATGGCGCCCC GCTCGGCCAA GCCGGCCCTG  2820
CTGAAGCTTA CAGAGAAGCA GGTGGAACAG AGGCCCTTCC ACGACCTCAA GGTGGCCCCC  2880
GGCTACTACA CCCTCACTGC AGACCAGGAC GCCCGGGGCA TGGTGGAGTT CCAGGAGGGC  2940
GTGGAGCTGG TGGACGTACG GGTGCCCCTC TTTATCCGGC CTGAGGATGA CGACGAGAAG  3000
CAGCTGCTGG TGGAGGCCAT CGACGTGCCC GCAGGCACTG CCACCCTCGG CCGCCGCCTG  3060
GTAAACATCA CCATCATCAA GGAGCAAGCC AGAGACGTGG TGTCCTTTGA GCAGCCTGAG  3120
TTCTCGGTCA GCCGCGGGGA CCAGGTGGCC CGCATCCCTG TCATCCGGCG TGTCCTGGAC  3180
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TACATCCCCG TGGAGGGTGA GCTGCTGTTC CAGCCTGGGG AGGCCTGGAA AGAGCTGCAG  3300
GTGAAGCTCC TGGAGCTGCA AGAAGTTGAC TCCCTCCTGC GGGGCCGCCA GGTCCGCCGT  3360
TTCCACGTCC AGCTCAGCAA CCCTAAGTTT GGGGCCCACC TGGGCCAGCC CCACTCCACC  3420
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TCACAGCCAC CCCCTCACGG CGACCTGGGC GCCCCGCAGA ACCCCAATGC TAAGGCCGCT  3540
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GTAAAGTACT GGATTCAGGG TGACTCCGAA TCCGAAGCCC ACCTGCTCGA CAGCAAGGTG  3660
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GTGCCCAGCG AGCCAGGGCG TCTGGCCTTC AATGTCGTCT CCTCCACGGT GACCCAGCTG  3840
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CTGGTCAACG ATGACAACCG ACCTATTGGG CCCATGAAGA AAGTGCTGGT TGACAACCCT  3960
AAGAACCGGA TGCTGCTTAT TGAGAACCTT CGGGAGTCCC AGCCCTACCG CTACACGGTG  4020
AAGGCGCGCA ACGGGGCCGG CTGGGGGCCT GAGCGGGAGG CCATCATCAA CCTGGCCACC  4080
CAGCCCAAGA GGCCCATGTC CATCCCCATC ATCCCTGACA TCCCTATCGT GGACCCCCAG  4140
AGCGGGGAGG ACTACGACAG CTTCCTTATG TACAGCGATG ACGTTCTACG CTCTCCATCG  4200
GGCAGCCAGA GGCCCAGCGT CTCCGATGAC ACTGAGCACC TGGTGAATGG CCGGATGGAC  4260
TTTGCCTTCC CGGGCAGCAC CAACTCCCTG CACAGGATGA CCACGACCAG TGCTGCTGCC  4320
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GACACGCCCA CCCGCCTGGT GTTCTCTGCC CTGGGGCCCA CATCTCTCAG AGTGAGCTGG  4560
CAGGAGCCGC GGTGCGAGCG GCCGCTGCAG GGCTACAGTG TGGAGTACCA GCTGCTGAAC  4620
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TTCACTGCCC TGAGCCCAGA CTCGCTGCAG CTGAGCTGGG AGCGGCCACG GAGGCCCAAT  4920
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GCATTCCGGG TGGATGGAGA CAGCCCCGAG AGCCGGCTGA CCGTGCCGGG CCTCAGCGAG  5040
AACGTGCCCT ACAAGTTCAA GGTGCAGGCC AGGACCACTG AGGGCTTCGG GCCAGAGCGC  5100
GAGGGCATCA TCACCATAGA GTCCCAGGAT GGAGGACCCT TCCCGCAGCT GGGCAGCCGT  5160
GCCGGGCTCT TCCAGCACCC GCTGCAAAGC GAGTACAGCA GCATCACCAC CACCCACACC  5220
AGCGCCACCG AGCCCTTCCT AGTGGATGGG CCGACCCTGG GGGCCCAGCA CCTGGAGGCA  5280
GGCGGCTCCC TCACCCGGCA TGTGACCCAG GAGTTTGTGA GCCGGACACT GACCACCAGC  5340
GGAACCCTTA GCACCCACAT GGACCAACAG TTCTTCCAAA CTTGACCGCA CCCTGCCCCA  5400
CCCCCGCCAT GTCCCACTAG GCGTCCTCCC GACTCCTCTC CCGGAGCCTC CTCAGCTACT  5460
CCATCCTTGC ACCCCTGGGG GCCCAGCCCA CCCGCATGCA CAGAGCAGGG GCTAGGTGTC  5520
TCCTGGGAGG CATGAAGGGG GCAAGGTCCG TCCTCTGTGG GCCCAAACCT ATTTGTAACC  5580
AAAGAGCTGG GAGCAGCACA AGGACCCAGC CTTTGTTCTG CACTTAATAA ATGGTTTTGC  5640
TACTG
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Seq ID NO: 360 Protein sequence
Protein Accession #: NP_000204.1

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CNTQAELLAA GCQRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL   120
EVFEPLESPV DLYILMDFSN SMSDDLDNLK KMGQNLARVL SQLTSDYTIG FGKFVDKVSV   180
PQTDMRPEKL KEPWPNSDPP PSFKNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL   240
QTAVCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLAGI MSRNDERCHL DTTGTYTQYR   300
TQDYPSVPTL VRLLAKHNII PIFAVTNYSY SYYEKLHTYF PVSSLGVLQE DSSNIVELLE   360
EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGEVGIYQV QLRALEHVDG   420
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THVCQLPEDQ KGNIHLKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV   480
CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN   540
FQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR   600
CHCHQQSLYT DTICEINYSA IHPGLCEDLR SCVQCQAWGT GEKKGRTCEE CNFKVKMVDE   660
LKRAEEVVVR CSFRDEDDDC TYSYTMEGDG APGPNSTVLV HKKKDCPPGS FWWLIPLLLL   720
LLPLLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFKED HYMLRENLMA SDHLDTPMLR   780
SGNLKGRDVV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTREC   840
AQLRQEVEEN LNEVYRQISG VHKLQQTKFR QQPNAGKKQD HTIVDTVLMA PRSAKPALLK   900
LTEKQVEQRA FHDLKVAPGY YTLTADQDAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL   960
LVEAIDVPAG TATLGRRLVN ITIIKEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG  1020
KSQVSYRTQD GTAQGNRDYI PVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH  1080
VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLGAP QNPNAKAAGS  1140
RKIHFNWLPP SGKPMGYRVK YWIQGDSESE AHLLDSKVPS VELTNLYPYC DYEMKVCAYG  1200
AQGEGPYSSL VSCRTHQEVP SEPGRLAFNV VSSTVTQLSW AEPAETNGEI TAYEVCYGLV  1260
NDDNRPIGPM KKVLVDNPKN RMLLIENLRE SQPYRYTVKA RNGAGWGPER EAIINLATQP  1320
KRPMSIPIIP DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPSVSDDTE HLVNGRMDFA  1380
FPGSTNSLHR MTTTSAAAYG THLSPHVPHR VLSTSSTLTR DYNSLTRSEH SHSTTLPRDY  1440
STLTSVSSHD SRLTAGVPDT PTRLVFSALG PTSLRVSWQE PRCERPLQGY SVEYQLLNGG  1500
ELHRLNIPNP AQTSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES QVHPQSPLCP  1560
LPGSAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEM AQGGGPATAF  1620
RVDGDSPESR LTVPGLSENV PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRAG  1680
LFQHPLQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEF VSRTLTTSGT  1740
LSTHMDQQFF QT
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Seq ID NO: 361 DNA sequence
Nucleic Acid Accession #: NM_013332.1
Coding sequence: 1..63

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AGTAACCGAC TTTCCTCCGG ACTCCTGCAC GACCTGCTCC TACAGCCGGC GATCCACTCC   120
CGGCTGTTCC CCCGGAGGGT CCAGAGGCCT TTCAGAAGGA GAAGGCAGCT CTGTTTCTCT   180
GCAGAGGAGT AGGGTCCTTT CAGCCATGAA GCATGTGTTG AACCTCTACC TGTTAGGTGT   240
GGTACTGACC CTACTCTCCA TCTTCGTTAG AGTGATGGAG TCCCTAGAAG GCTTACTAGA   300
GAGCCCATCG CCTGGGACCT CCTGGACCAC CAGAAGCCAA CTAGCCAACA CAGAGCCCAC   360
CAAGGGCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC   420
ATATTTTGGA ACACTGACCT AGACATGTCC AGATGGGAGT CCCATTCCTA GCAGACAAGC   480
TGAGCACCGT TGTAACCAGA GAACTATTAC TAGGCCTTGA AGAACCTGTC TAACTGGATG   540
CTCATTGCCT GGGCAAGGCC TGTTTAGGCC GGTTGCGGTG GCTCATGCCT GTAATCCTAG   600
CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCGAGA CCAGCCTCGC   660
CAACATGGCG AAACCCCATC TCTACTAAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA   720
GGCCTGTAAT CCCAGTTCCT TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCCGGGGACG   780
GAGGTTGCAG TGAACCGAGA TCGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC   840
CATCTCAAAA AAAAAAAGAA AAGAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC   900
TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCCGGG GTCTGGTGTA TGCTGTGCTT   960
TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG  1020
TGATATTTTC AACCCTACTT CCTAAACATC TGTCTGGGGT TCCTTTAGTC TTGAATGTCT  1080
TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG  1140
CAGTTGAAGA GGTTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGTT CAGTGCCCAT  1200
TTCTCATTTT ACATTTTAAA GTCGTTCCTC CAACATAGTG TGTATTGGTC TGAAGGGGGT  1260
GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA  1320
TTTTTTCTAA CTAATAAAGT GGAATATATA TTTCAAAAAA AAAAAAAAAA AA
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Seq ID NO: 362 Protein sequence
Protein Accession #: NP_037464.1

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1          11         21         31         41         51
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MKHVLNLYLL GVVLTLLSIF VRVMESLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS    60
RSM
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Seq ID NO: 363 DNA sequence
Nucleic Acid Accession #: NM_023915.1
Coding sequence: 250..1326

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GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA   180
CCCACGCCTC AATCGTCCCC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGCATCAC   240
AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC   300
CAAGAGAGTC ACAATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTCAC   360
AATGAATTTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTTGT GGCAAGCATC   420
TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA   480
TTCTATCTCA AAAACATAGT GGTTGCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA   540
ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT   600
TCAGTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT   660
GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC   720
ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC   780
ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAAGT   840
CCTTTGGGGG TCAAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC   900
GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC   960
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AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
GTGGCTGTGT TTTTTACCTG CTTTCTACCA TATCACTTGT GCAGAATTCC TTTTACTTTT 1080
AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAAA TCCTATATTA CTGCAAAGAA 1140
ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG 1200
TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCAG GAGTGAAAGC 1260
ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320
GTGTAGGCCT TTTATTGTTT GTTGGAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT 1380
TTCATTATCC TTAAAAAAAA AA

Seq ID NO: 364 Protein sequence
Protein Accession #: NP_076404

1 11 21 31 41 51

MGFNLTLAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL 120
FYANMYTSIV FLGLISIDRY LKVVKPFGDS RMYSITFTKV LSVCVWVIMA VLSLPNIILT 180
NGQPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
ISQSSRKRKH NQSIRVVVAV FFTCFLPYHL CRIPFTFSHL DRLLDESAQK ILYYCKEITL 300
FLSACNVCLD PIIYFFMCRS FSRRLFKKSN IRTRSESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 365 DNA sequence
Nucleic Acid Accession #: NM_005365.1
Coding sequence: 1..948

1 11 21 31 41 51

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TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCCAGAGT 180
CCTCAGGGAG GCGCTTCCTC CTCCATTTCC GTCTACTACA CTTTATGGAG CCAATTCGAT 240
GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTCGACCC AGCTCAGCTG 300
GAGTTCATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCCTGCTC 360
CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAAGCCT CCGAGTTCAT GCAGGTGATC 480
TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACTGCT 540
CTTGGCCTCT CGTGCGATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC 600
CTGATCATTG TCCTGGGTGT GATCCTAACC AAAGACAACT GCGCCCCTGA AGAGGTTATC 660
TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCACATGTT CTACGGGGAG 720
CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAACT ACCTGGAGTA CCGGCAGGTG 780
CCCGGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
AGCTATGAGA AGGTCATAAA TTATTTGGTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900
CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 366 Protein sequence
Protein Accession #: NP_005356.1

1 11 21 31 41 51

MSLEQRSPHC KPDEDLEAQG EDLGLMGAQE PTGEEEETTS SSDSKEEEVS AAGSSSPPQS 60
PQGGASSSIS VYYTLWSQFD EGSSSQEEEE PSSSVDPAQL EFMFQEALKL KVAELVHFLL 120
HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA 180
LGLSCDSMLG DGHSMPKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE 240
PRKLLTQDWV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYLV MLNAREPICY 300
PSLYEEVLGE EQEGV

Seq ID NO: 367 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

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GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CCGAACAAGA TGAAGACAGT 240
GAAGTGCGCG CCGGGCGTGG ACGTCTGCAC CGAGGCCGTG GGGGCGGTGG AGACCATCCA 300
CGGACAATTC TCGCTGGCAG TGCSGGGTTG CGGTTCGGGA CTCCCCGGCA AGAATGACCG 360
CGGCCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
CTGCAACGCC AAGCTCAACC TCACCTCGCG GGCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480
ATACCCGCCC AACGGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
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CTTCGACGGC AACGTCACCT TGACGGCAGC TAATGTGACT GTGTCCTTGC CTGTCCGGGG 660
CTGTGTCCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCCAGGGT TCACGCTCAG 720
TGGCTCCTGT TGCCAGGGGT CCCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCCTCAAC 840
CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAAACCCAT 900
GCCAGCGCCA ACCAGTCAGA CTCCGAGACA GGGAGTAGAA CACGAGGCCT CCCGGGATGA 960
GGAGCCCAGG TTGACTGGAG GCGCCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA 1020
TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
ATTGGCAGCC CTTCTGTTGG CCGTGGCTGC TGGTGTCCTA CTGTGAGCTT CTCCACCTGG 1140
AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCCTGTT 1200
CCCACCACTG GACTGGGCTG GCCCAGCCCC TGTTTTTCCA ACATTCCCCA GTATCCCCAG 1260
CTTCTGCTGC GCTGGTTTGC GGCTTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320

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GGGTGTTCTA GCTTTTTGAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG  1380
TCCTCTTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG  1440
AGGATGCTAA GCTTCCTACT CACTTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG  1500
GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCCT ACTCCCCGCA TCTTTGGGGA  1560
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TTGTATAGTG AAAAAAAA
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Seq ID NO: 368 Protein sequence
Protein Accession #: NP_055215

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SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT   180
AANVTVSLPV RGCVQDEFCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPPLVR   240
LPPPEPTTVA STTSVTTSTS APVRPTSTTK PMPAPTSQTP RQGVEHEASR DEEPRLTGGA   300
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Seq ID NO: 369 DNA sequence
Nucleic Acid Accession #: NM_005329.1
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Seq ID NO: 370 Protein sequence
Protein Accession #: NP_005320.1

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STFSCIMQKW GGKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG   240
VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQQFLE   300
DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRW LNQQTRWSKS   360
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IIKATYACFL RGNAEMIFMS LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNFIG   480
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Seq ID NO: 371 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

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CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA   240
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WO03042661 [file:///E:/WO03042661.pcp]


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Seq ID NO: 372 Protein sequence:
Protein Accession #: built from XP_031379

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Seq ID NO: 373 DNA sequence
Nucleic Acid Accession #: built from NM_002851
Coding sequence: 148-4518

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Protein Accession #: EOS sequence

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Seq ID NO: 379 DNA sequence
Nucleic Acid Accession #: EOS sequence
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CCCTCTTCCG TCTGGTGGAG TTATCTGGAG GCTGCATCAA GATTGATGGA GTGAGAATCA  3900
GTGATATTGG CCTTGCCGAC CTCCGAAGCA AACTCTCTAT CATTCCTCAA GAGCCGGTGC  3960
TGTTCAGTGG CACTGTCAGA TCAAATTTGG ACCCCTTCAA CCAGTACACT GAAGACCAGA  4020
TTTGGGATGC CCTGGAGAGG ACACACATGA AAGAATGTAT TGCTCAGCTA CCTCTGAAAC  4080
TTGAATCTGA AGTGATGGAG AATGGGGATA ACTTCTCAGT GGGGGAACGG CAGCTCTTGT  4140
GCATAGCTAG AGCCCTGCTC CGCCACTGTA AGATTCTGAT TTTAGATGAA GCCACAGCTG  4200
CCATGGACAC AGAGACAGAC TTATTGATTC AAGAGACCAT CCGAGAAGCA TTTGCAGACT  4260
GTACCATGCT GACCATTGCC CATCGCCTGC ACACGGTTCT AGGCTCCGAT AGGATTATGG  4320
TGCTGGCCCA GGGACAGGTG GTGGAGTTTG ACACCCCATC GGTCCTTCTG TCCAACGACA  4380
GTTCCCGATT CTATGCCATG TTTGCTGCTG CAGAGAACAA GGTCGCTGTC AAGGGCTGAC  4440
TCCTCCCTGT TGACGAAGTC TCTTTTCTTT AGAGCATTGC CATTCCCTGC CTGGGGCGGG  4500
CCCCTCATCG CGTCCTCCTA CCGAAACCTT GCCTTTCTCG ATTTTATCTT TCGCACAGCA  4560
GTTCCGGATT GGCTTGTGTG TTTCACTTTT AGGGAGAGTC ATATTTTGAT TATTGTATTT  4620
ATTCCATATT CATGTAAACA AAATTTAGTT TTTGTTCTTA ATTGCACTCT AAAAGGTTCA  4680
GGGAACCGTT ATTATAATTG TATCAGAGGC CTATAATGAA GCTTTATACG TGTAGCTATA  4740
TCTATATATA ATTCTGTACA TAGCCTATAT TTACAGTGAA AATGTAAGCT GTTTATTTTA  4800
TATTAAAATA AGCACTGTGC TAATAACAGT GCATATTCCT TTCTATCATT TTTGTACAGT  4860
TTGCTGTACT AGAGATCTGG TTTTGCTATT AGACTGTAGG AAGAGTAGCA TTTCATTCTT  4920
CTCTAGCTGG TGGTTTCACG GTGCCAGGTT TTCTGGGTGT CCAAAGGAAG ACGTGTGGCA  4980
ATAGTGGGCC CTCCGACAGC CCCCTCTGCC GCCTCCCCAC AGCCGCTCCA GGGGTGGCTG  5040
GAGACGGGTG GGCGGCTGGA GACCATGCAG AGCGCCGTGA GTTCTCAGGG CTCCTGCCTT  5100
CTGTCCTGGT GTCACTTACT GTTTCTGTCA GGAGAGCAGC GGGGCGAAGC CCAGGCCCCT  5160
TTTCACTCCC TCCATCAAGA ATGGGGATCA CAGAGACATT CCTCCGAGCC GGGGAGTTTC  5220
TTTCCTGCCT TCTTCTTTTT GCTGTTGTTT CTAAACAAGA ATCAGTCTAT CCACAGAGAG  5280
TCCCACTGCC TCAGGTTCCT ATGGCTGGCC ACTGCACAGA GCTCTCCAGC TCCAAGACCT  5340
GTTGGTTCCA AGCCCTGGAG CCAACTGCTG CTTTTTGAGG TGGCACTTTT TCATTTGCCT  5400
ATTCCCACAC CTCCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCCTTT  5460
CTCACCGCAG TCGTCGCACA GTCTCTCTCT CTCTCTCCCC TCAAAGTCTG CAACTTTAAG  5520
CAGCTCTTGC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT  5580
ACCTCAGGTT GCTGGTTGCT GTGTGGTTTG GTGTGTTCCC GCAAACCCCC TTTGTGCTGT  5640
GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCATC AGTTGAATGG TCAGCGTTGC  5700
ATGTCGTGAC CAACTAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG  5760
CAAAAATCTG AAAATGTGAA TAAAATTATT TTGGATTTTG TAAAAAAAAA AAAAAAAAAA  5820
AAAAAAAAAA AAAAAAAA
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Seq ID NO: 384 Protein sequence
Protein Accession #: NP_005679.1

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1          11         21         31         41         51
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MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECQDAL ETAARAEGLS    60
LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR   120
VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI   180
LSIVCLMITQ LAGFSGPAFM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW   240
ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG   300
PVVAILGMIY NVIILGPTGF LGSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE   360
VLTYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV   420
HMTLGFDLTA AQAFTVVTVF NSMTFALKVT PPSVKSLSEA SVAVDRFKSL FLMEEVHMIK   480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA   540
VLAEQKGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVGSG   600
KTSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS   660
CCLRPDLAIL PSSDLTEIGE RGANLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG   720
NHIFNSAIRK HLKSKTVLFV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI   780
FNNLLLGETP PVEINSKKET SCSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS   840
VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQGSGN TTVTRGNETS   900
VSDSMKDNPH MQYYASIYAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRILRSPM   960
KFFDTTPTGR ILNRFSKDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP  1020
LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL  1080
LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT  1140
GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM  1200
RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD  1260
IGLADLRSKL SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKE CIAQLPLKLE  1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT  1380
MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG
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Seq ID NO: 385 DNA sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89..631

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CTGAGAGCCG GGCAGAGGCT CCGGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC   120
GACGGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCCT GATGGCCCAG GGGGCAATGC   180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCCGGGGCG CAGGGGCAGC   240
AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG   300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCCTGC TTGAGTTCTA   360
CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA   420
GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCACTG TGTCCGGCAA   480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC   540
CTGTCTCCAG CAGCTTTCCC TGTTGATGTG GATCACCCAG TGCTTTCTGC CCGTGTTTTT   600
GGCTCAGCCT CCCTCAGGGC AGAGGCGCTA AGCCCAGCCT GGCGCCCCTT CCTAGGTCAT   660
GCCTCCTCCC CTAGGGAATG GTCCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT   720
GTTTGTCGCT GGAGGAGGAC GGCTTACATG TTTGTTTCTG TAGAAAATAA AACTGAGCTA
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Seq ID NO: 386 Protein sequence
Protein Accession #: NP_001318.1

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1          11         21         31         41         51
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PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAELARRSLA QDAPPLPVPG   120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQQLSLLM WITQCFLPVF LAQPPSGQRR
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Seq ID NO: 387 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52..459

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1          11         21         31         41         51
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GAAGGCCAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT   120
CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA   180
GGTCCCCGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCCGCGGGGT   240
CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG   300
GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC   360
ATCAGCTCCT GTCTCCAGCA GCTTTCCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCCC   420
GTGTTTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCTTCC   480
TAGGTCATGC CTCCTCCCCT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG   540
GCCTGATTGT TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTTCTGTA GAAAATAAAG   600
CTGAGCTA
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Seq ID NO: 388 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA    60
PRGPHGGAAS AQDGRCPCGA RRPDSRLLQF RLTAADHRQL QLSISSCLQQ LSLLMWITQC   120
FLPVFLAQAP SGQRR
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Seq ID NO: 389 DNA sequence
Nucleic Acid Accession #: NM_005562.1
Coding sequence: 90..3671

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AGACAGAGAC TGAGCGGCCC GGCACCGCCA TGCCTGCGCT CTGGCTGGGC TGCTGCCTCT   120
GCTTCTCGCT CCTCCTGCCC GCAGCCCCGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA   180
ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAAACT GGTAATGGAT   240
TCCGCTGCCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG   300
GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT   360
CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG   420
CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG   480
ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG   540
ACGCGGGCCG CTGTGTCTGC AAGCCAGCTG TTACTGGAGA ACGCTGTGAT AGGTGTCGAT   600
CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCCAGTGT TTCTGCTATG   660
GGCATTCAGC CAGCTGCCGC AGCTCTGCAG AATACAGTGT CCATAAGATC ACCTCTACCT   720
TTCATCAAGA TGTTGATGGC TGGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC   780
AATGGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT   840
TTGTGGCTCC TGCCAAATTT CTTGGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCCT   900
TTGACTACCG TGTGGACAGA GGAGGCAGAC ACCCATCTGC CCATGATGTG ATTCTGGAAG   960
GTGCTGGTCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTTGTGGGC  1020
TCACCAAGAC TTACACATTC AGGTTAAATG AGCATCCAAG CAATAATTGG AGCCCCCAGC  1080
TGAGTTACTT TGAGTATCGA AGGTTACTGC GGAATCTCAC AGCCCTCCGC ATCCGAGCTA  1140
CATATGGAGA ATACAGTACT GGGTACATTG ACAATGTGAC CCTGATTTCA GCCCGCCCTG  1200
TCTCTGGAGC CCCAGCACCC TGGGTTGAAC AGTGTATATG TCCTGTTGGG TACAAGGGGC  1260
AATTCTGCCA GGATTGTGCT TCTGGCTACA AGAGAGATTC AGCGAGACTG GGGCCTTTTG  1320
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GCACCTGTAT TCCTTGTAAC TGTCAAGGGG GAGGGGCCTG TGATCCAGAC ACAGGAGATT  1380
GTTATTCAGG GGATGAGAAT CCTGACATTG AGTGTGCTGA CTGCCCAATT GGTTTCTACA  1440
ACGATCCGCA CGACCCCCGC AGCTGCAAGC CATGTCCCTG TCATAACGGG TTCAGCTGCT  1500
CAGTGATGCC GGAGACGGAG GAGGTGGTGT GCAATAACTG CCCTCCCGGG GTCACCGGTG  1560
CCCGCTGTGA GCTCTGTGCT GATGGCTACT TTGGGGACCC CTTTGGTGAA CATGGCCCAG  1620
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GTGACCGGCT GACAGGCAGG TGTTTGAAGT GTATCCACAA CACAGCCGGC ATCTACTGCG  1740
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GAGCTTGCAA CTGTAACCCC ATGGGCTCAG AGCCTGTAGG ATGTCGAAGT GATGGCACCT  1860
GTGTTTGCAA GCCAGGATTT GGTGGCCCCA ACTGTGAGCA TGGAGCATTC AGCTGTCCAG  1920
CTTGCTATAA TCAAGTGAAG ATTCAGATGG ATCAGTTTAT GCAGCAGCTT CAGAGAATGG  1980
AGGCCCTGAT TTCAAAGGCT CAGGGTGGTG ATGGAGTAGT ACCTGATACA GAGCTGGAAG  2040
GCAGGATGCA GCAGGCTGAG CAGGCCCTTC AGGACATTCT GAGAGATGCC CAGATTTCAG  2100
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ACCAGAGCCG CCTGGATGAC CTCAAGATGA CTGTGGAAAG AGTTCGGGCT CTGGGAAGTC  2220
AGTACCAGAA CCGAGTTCGG GATACTCACA GGCTCATCAC TCAGATGCAG CTGAGCCTGG  2280
CAGAAAGTGA AGCTTCCTTG GGAAACACTA ACATTCCTGC CTCAGACCAC TACGTGGGGC  2340
CAAATGGCTT TAAAAGTCTG GCTCAGGAGG CCACAAGATT AGCAGAAAGC CACGTTGAGT  2400
CAGCCAGTAA CATGGAGCAA CTGACAAGGG AAACTGAGGA CTATTCCAAA CAAGCCCTCT  2460
CACTGGTGCG CAAGGCCCTG CATGAAGGAG TCGGAAGCGG AAGCGGTAGC CCGGACGGTG  2520
CTGTGGTGCA AGGGCTTGTG GAAAAATTGG AGAAAACCAA GTCCCTGGCC CAGCAGTTGA  2580
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AAGCCAATGT GACAGCAGAT GGAGCCTTGG CCATGGAAAA GGGACTGGCC TCTCTGAAGA  3240
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TGCACCATAC TCCTTGCTTC CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA  3900
ATGATCAAGG ATCTGGACCC CAAAGAATAG ACTGGATGGA AAGACAAACT GCACAGGCAG  3960
ATGTTTGCCT CATAATAGTC GTAAGTGGAG TCCTGGAATT TGGACAAGTG CTGTTGGGAT  4020
ATAGTCAACT TATTCTTTGA GTAATGTGAC TAAAGGAAAA AACTTTGACT TTGCCCAGGC  4080
ATGAAATTCT TCCTAATGTC AGAACAGAGT GCAACCCAGT CACACTGTGG CCAGTAAAAT  4140
ACTATTGCCT CATATTGTCC TCTGCAAGCT TCTTGCTGAT CAGAGTTCCT CCTACTTACA  4200
ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTTGGAGTG  4260
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GTTCTGGACC TGGGCATGAC ATCCTTTCTT TTAATGATGC CATGGCAACT TAGAGATTGC  4380
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TTACCTCCAT CCATCCTTCC AACATATATT TATTGAGTAC CTACTGTGTG CCAGGGGCTG  4740
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GCAATAACCG CTTGGTTTGC AACCTCTTTG CTCAACAGAA CATATGTTGC AAGACCCTCC  4920
CATGGGGGCA CTTGAGTTTT GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTTCTTTG  4980
CATTCCAGCT GTCACTCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA  5040
TAACACCAGT GGGAATTGCT GGAGGAACCA GAGGCACTTC CACCTTGGCT GGGAAGACTA  5100
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CAATTGTTAG ATGCC
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Seq ID NO: 390 Protein sequence
Protein Accession #: NP_005553.1

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DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCKPGVTG ARCDRCLPGF  120
HMLTDAGCTQ DQRLLDSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGGN  180
PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVDGWKA VQRNGSPAKL QWSQRHQDVF  240
SSAQRLDPVY FVAPAKFLGN QQVSYGQSLS FDYRVDRGGR HPSAHDVILE GAGLRITAPL  300
MPLGKTLPCG LTKTYTFRLN EHPSNNWSPQ LSYFEYRRLL RNLTALRIRA TYGEYSTGYI  360
DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTCIPCNCQG  420
GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRSCK PCPCHNGFSC SVMPETEEVV  480
CNNCPPGVTG ARCELCADGY FGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK  540
CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCNPMGS EPVGCRSDGT CVCKPGFGGP  600
NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL  660
QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLDDLKM TVERVRALGS QYQNRVRDTH  720
RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR  780
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ETEDYSKQAL SLVRKALHEG VGSGSGSPDG AVVQGLVEKL EKTKSLAQQL TREATQAEIE   840
ADRSYQHSLR LLDSVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG   900
NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREFDL   960
QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE  1020
IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE  1080
AQKVDTRAKN AGVTIQDTLN TLDGLLHLMD QPLSVDEEGL VLLEQKLSRA KTQINSQLRP  1140
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Seq ID NO: 391 DNA sequence
Nucleic Acid Accession #: AF101051.1
Coding sequence: 221.856

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ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAACG CGGGGCTGCA   240
GCTGTTGGGC TTCATTCTCG CCTTCCTGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT   300
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CGAGGGGCTG TGGATGTCCT GCGTGTCGCA GAGCACCGGG CAGATCCAGT GCAAAGTCTT   420
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CTAATTTACC AAGGATGAAT TCTTTCAATT CTTCATGCGT GCCCTTTTCA TATACTTATT  1440
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TTTCATTGGT CTCTATCTCC TGAATCTAAC ACATTTCATA GCCTACATTT TAGTTTCTAA  1560
AGCCAAGAAG AATTTATTAC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAAA  1620
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ACCTTTTTGT TCCCCATTCC TTAATTGTAT TGTTTTCCCA AGTGTAATTA TCATGCGTTT  1860
TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT  1920
GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAGCA AGTCACTTAA TCTTTCTACC  1980
TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTG  2040
AATATTAATT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTC  2100
TTTATTTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACCT ACACACGTAC  2160
CTTCATGTGA TTCACTGCCT TCCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAAACCTAC  2220
ACACATACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATTT CCACTGAACA  2280
AAACCTACGC ACATACCTTC ATGTGGCTCA GTGCCTTCCT CTCTCTACCA GTCTATTTCC  2340
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AGCAAGGCAT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC  2580
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TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA  3060
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TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT  3360
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AAAAGGAAAA AAAAAAAAAA AAA
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Seq ID NO: 392 Protein sequence
Protein Accession #: AAD16433.1

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QIQCKVFDSL LNLSSTLQAT RALMVVGILL GVIAIFVATV GMKCMKCLED DEVQKMRMAV   120
IGGAIFLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGGA   180
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Seq ID NO: 393 DNA sequence
Nucleic Acid Accession #: NM_006180.1
Coding sequence: 352..2820

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CCCCCTGTAA AGCGGTTCGC TATGCCGGGA CCACTGTGAA CCCTGCCGCC TGCCGGAACA   180
CTCTTCGCTC CGGACCAGCT CAGCCTCTGA TAAGCTGGAC TCGGCACGCC CGCAACAAGC   240
ACCGAGGAGT TAAGAGAGCC GCAAGCGCAG GGAAGGCCTC CCCGCACGGG TGGGGGAAAG   300
CGGCCGGTGC AGCGCGGGGA CAGGCACTCG GGCTGGCACT GGCTGCTAGG GATGTCGTCC   360
TGGATAAGGT GGCATGGACC CGCCATGGCG CGGCTCTGGG GCTTCTGCTG GCTGGTTGTG   420
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ATTCCCCTGG CAAACCTGCA GATACCCAAT TGTGGTTTGC CATCTGCAAA TCTGGCCGCA   960
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CTTAACAAAC GTAATTTGTT ATATCAGCAG ACACTCCAGT TTGCCCACCA CAACTAACAA  3240
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Seq ID NO: 394 Protein sequence
Protein Accession #: NP_006171.1

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NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAKSSPD TQDLYCLNES   180
SKNIPLANLQ IPNCGLPSAN LAAPNLTVEE GKSITLSCSV AGDPVPNMYW DVGNLVSKHM   240
NETSHTQGSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH   300
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT   360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST   420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKGPASV ISNDDDSASP   480
LHHISNGSNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDTFV QHIKRHNIVL   540
KRELGEGAFG KVFLAECYNL CPEQDKILVA VKTLKDASDN ARKDFHREAE LLTNLQHEHI   600
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VKFYGVCVEG DPLIMVFEYM KHGDLNKFLR AHGPDAVLMA EGNPPTELTQ SQMLHIAQQI   660
AAGMVYLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYYRVG GHTMLPIRWM   720
PPESIMYRKF TTESDVWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ   780
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Seq ID NO:  395 DNA sequence
Nucleic Acid Accession #:  AF410899
Coding sequence: 483..2999

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CCGCCGGTCG GTGCCCGGCG CGCCGGGCCA TGCAGCGACG GCCGCCGCGG AGCTCCGAGC   240
AGCGGTAGCG CCCCCCTGTA AAGCGGTTCG CTATGCCGGG ACCACTGTGA ACCCTGCCGC   300
CTGCCGGAAC ACTCTTCGCT CCGGACCAGC TCAGCCTCTG ATAAGCTGGA CTCGGCACGC   360
CCGCAACAAG CACCGAGGAG TTAAGAGAGC CGCAAGCGCA GGGAAGGCCT CCCCGCACGG   420
GTGGGGGAAA GCGGCCGGTG CAGCGCGGGG ACAGGCACTC GGGCTGGCAC TGGCTGCTAG   480
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Seq ID NO:  396 Protein sequence
Protein Accession #: AAL67965.1

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NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAKSSPD TQDLYCLNES   180
SKNIPLANLQ IPNCGLPSAN LAAPNLTVEE GKSITLSCSV AGDPVPNMYW DVGNLVSKHM   240
NETSHTQGSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH   300
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT   360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST   420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKDFSWF GFGKVKSRQG   480
VGPASVISND DDSASPLHHI SNGSNTPSSS EGGPDAVIIG MTKIPVIENP QYFGITNSQL   540
KPDTFVQHIK RHNIVLKREL GEGAFGKVFL AECYNLCPEQ DKILVAVKTL KDASDNARKD   600
PHREAELLTN LQHEHIVKFY GVCVEGDPLI MVFEYMKHGD LNKFLRAHGP DAVLMAEGNP   660
PTELTQSQML HIAQQIAAGM VYLASQHFVH RDLATRNCLV GENLLVKIGD FGMSRDVYST   720
DYYRVGGHTM LPIRWMPPES IMYRKFTTES DVWSLGVVLW EIFTYGKQPW YQLSNNEVIE   780
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Seq ID NO: 397 DNA sequence
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Coding sequence: 74..814

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CATCACCGTC ATCCCTAAGT TCAGACCTGG ACCACGGTGG TGTGCCGTTC AAGGCCAGGT   240
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SFHYFSMGDC IGWLEDFLMG MDSTLEPSAG APLAMSSGTT QLRATATTLI LCCLLIILPC   240
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Seq ID NO: 399 DNA sequence
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Coding sequence: 57..482

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|          |          |          |          |          |
GGCTCTCACC CTCCTCTCCT GCAGCTCCAG CTTTGTGCTC TGCCTCTGAG GAGACCATGG    60
CCCAGTATCT GAGTACCCTG CTGCTCCTGC TGGCCACCCT AGCTGTGGCC CTGGCCTGGA   120
GCCCCAAGGA GGAGGATAGG ATAATCCCGG GTGGCATCTA TAACGCAGAC CTCAATGATG   180
AGTGGGTACA GCGTGCCCTT CACTTCGCCA TCAGCGAGTA TAACAAGGCC ACCAAAGATG   240
ACTACTACAG ACGTCCGCTG CGGGTACTAA GAGCCAGGCA ACAGACCGTT GGGGGGGTGA   300
ATTACTTCTT CGACGTAGAG GTGGGCCGCA CCATATGTAC CAAGTCCCAG CCCAACTTGG   360
ACACCTGTGC CTTCCATGAA CAGCCAGAAC TGCAGAAGAA ACAGTTGTGC TCTTTCGAGA   420
TCTACGAAGT TCCCTGGGAG AACAGAAGGT CCCTGGTGAA ATCCAGGTGT CAAGAATCCT   480
AGGGATCTGT GCCAGGCCAT TCGCACCAGC CACCACCCAC TCCCACCCCC TGTAGTGCTC   540
CCACCCCTGG ACTGGTGGCC CCCACCCTGC GGGAGGCCTC CCCATGTGCC TGCGCCAAGA   600
GACAGACAGA GAAGGCTGCA GGAGTCCTTT GTTGCTCAGC AGGGCGCTCT GCCCTCCCTC   660
CTTCCTTCTT GCTTCTAATA GCCCTGGTAC ATGGTACACA CCCCCCCACC TCCTGCAATT   720
AAACAGTAGC ATCGCC
```

Seq ID NO: 400 Protein sequence
Protein Accession #: NP_001889.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQRALHF AISEYNKATK    60
DDYYRRPLRV LRARQQTVGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKKQLCSF   120
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EIYEVPWENR RSLVKSRCQE S

Seq ID NO: 401 DNA sequence
Nucleic Acid Accession #: NM_003976.2
Coding sequence: 299.961

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1          11         21         31         41         51
|          |          |          |          |          |
CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAAAAA GGGGATTAAA CCATTTACCT    60
CATGGAGTTG TGAAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG   120
CTACTTCTGC TGGGTTGAGT CTAGCTGTGT AGGCCCCTTG TTCCTCACCT GGAGAAACTG   180
GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTTGCAA GCTGCCTCAA   240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCCTGGTGT TGATAGAGAT   300
GGAACTTGGA CTTGGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GGCGGCAGCC   360
TGCCCTGTGG CCCACCCTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGCAG AGGCCTCCCT   420
GGGCTCCGCG CCCCGCAGCC CTGCCCCCCG CGAAGGCCCC CCGCCTGTCC TGGCGTCCCC   480
CGCCGGCCAC CTGCCGGGGG GACGCACGGC CCGCTGGTGC AGTGGAAGAG CCCGGCGGCC   540
GCCGCCGCAG CCTTCTCGGC CCGCGCCCCC GCCGCCTGCA CCCCCATCTG CTCTTCCCCG   600
CGGGGGCCGC GCGGCGCGGG CTGGGGGCCC GGGCAGCCGC GCTCGGGCAG CGGGGGCGCG   660
GGGCTGCCGC CTGCGCTCGC AGCTGGTGCC GGTGCGCGCG CTCGGCCTGG GCCACCGCTC   720
CGACGAGCTG GTGCGTTTCC GCTTCTGCAG CGGCTCCTGC CGCCGCGCGC GCTCTCCACA   780
CGACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCG   840
GCCCGTCAGC CAGCCCTGCT GCCGACCCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT   900
CAACAGCACC TGGAGAACCG TGGACCGCCT CTCCGCCACC GCCTGCGGCT GCCTGGGCTG   960
AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCCTGGGAC  1020
CCTCCCGCAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCCT CAAAGCTGAG  1080
AGGCCCCTAC CGGTGGGTGA TGGATATCAT CCCCGAACAG GTGAAGGGAC AACTGACTAG  1140
CAGCCCCAGA GCCCTCACCC TGCGGATCCC AGCCTAAAAG ACACCAGAGA CCTCAGCTAT  1200
GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCCTCG AACCTGGGAC  1260
CCCTCCTCTG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCCGCCCAGG CCCTGTAGGG  1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTTGGTTGAA AGTGCCTGTG CTGGAACTGG  1380
CCTGTACTCA CTCATGGGAG CTGGCCCC
```

Seq ID NO: 402 Protein sequence
Protein Accession #: NP_003967.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS    60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA   120
RGCRLRSQLV PVRAILGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS  180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG
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Seq ID NO: 403 DNA sequence
Nucleic Acid Accession #: NM_057091.1
Coding sequence: 783..1445

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1          11         21         31         41         51
|          |          |          |          |          |
ACTGGCCGCT GAGAGAAGAA TCGGGTGGAG CAGAGAGCAG CTGCTGCAGG GCAGACAGCC    60
GGACCCCCAA ATCTGCACGT ACCAGCAGTC AGCCGCCCCA CGCAGGGACC GGCTTACCCC   120
TCGCTCCCCG CCCTCACTCA CTTTCTCCCG CCCTCGGCCC GGCCTCCCAG CTCTCTACTT   180
CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCCTCTC CACCGCTCGA GTTCTCTACT   240
CTCCATATCC GAGGGGCCCC TCCCAGCATC TACCCCCCTC CCAACCTCGG GGGACCTAGC   300
CAAGCTAGGG GGGACTGGAT CCGACGGGTG GAGCAGCCAG GTGAGCCCCG AAAGGTGGGG   360
CGGGGCAGGG GCGCTCCCAG CCCCACCCCG GGATCTGGTG ACGCTGGGGC TGGAATTTGA   420
CACCGGACGG CTGCGGCGGC GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCC   480
CAGACAAGGC CCGGGGGCTC CGCCAGCAGC AGGTCCCTCG GGCCCCAGCC CTCGCTGCCA   540
CCCGGGCCTG GAGCCCCACA CCCGAGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC   600
TAAAAGAGGC ACTGCCAGGT GTACAGTCCT GGGCATGCGC TGTTTGAGCT TCGGGGGAGA   660
GCCCAGCACT GGTCCCCGGA AAGGTGCCTA GAAGAACAAG GTGCAGGACC CCGTGCTGCC   720
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GGCGCTCCTG GTGTTGATAG   780
AGATGGAACT TGGACTTGGA GGCCTCTCCA CGCTGTCCCA CTGCCCCTGG CCTAGGCGGC   840
AGCCTGCCCT GTGGCCCACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT   900
CCCTGGGCTC CGCGCCCCGC AGCCCTGCCC CCCGCGAAGG CCCCCCGCCT GTCCTGGCGT   960
CCCCCGCCGG CCACCTGCCG GGGGGACGCA CGGCCCGCTG GTGCAGTGGA AGAGCCCGGC  1020
GGCCGCCGCC GCAGCCTTCT CGGCCCGCGC CCCCGCCGCC TGCACCCCCA TCTGCTCTTC  1080
CCCGCGGGGG CCGCGCGGCG CGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG  1140
CGCGGGGCTG CCGCCTGCGC TCGCAGCTGG TGCCGGTGCG CGCGCTCGGC CTGGGCCACC  1200
GCTCCGACGA GCTGGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCCGCCGC GCGCGCTCTC  1260
CACACGACCT CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCCGGGCT  1320
CCCGGCCCGT CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG  1380
ACGTCAACAG CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG  1440
GCTGAGGGCT CGCTCCAGGG CTTTGCAGAC TGGACCCTTA CCGGTGGCTC TTCCTGCCTG  1500
GGACCCTCCC GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC  1560
TGAGAGGCCC CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA  1620
CTAGCAGCCC CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG  1680
CTATGGAGCC CTTCGGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG  1740
GGACCCCTCC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT  1800
AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA  1860
CTGGCCTGTA CTCACTCATG GGAGCTGGCC CC
```

Seq ID NO: 404 Protein sequence
Protein Accession #: NP_003967.1

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1          11         21         31         41         51
|          |          |          |          |          |
MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS    60
PAGHLPGGRT ARWCSGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA   120
RGCRLRSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS   180
RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG
```

Seq ID NO: 405 DNA sequence
Nucleic Acid Accession #: NM_057160.1
Coding sequence: 1..714

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC    60
CACCTGGGTG CCCTCTTTCT CCCTCAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG   120
TGGCCCACCC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC   180
GCGCCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCCGCCTG TCCTGGCGTC CCCCGCCGGC   240
CACCTGCCGG GGGGACGCAC GGCCCGCTGG TGCAGTGGAA GAGCCCGGCG GCCGCCGCCG   300
CAGCCTTCTC GGCCCGCGCC CCCGCCGCCT GCACCCCCAT CTGCTCTTCC CCGCGGGGGC   360
CGCGCGGCGC GGGCTGGGGG CCCGGGCAGC CGCGCTCGGG CAGCGGGGGC GCGGGGCTGC   420
CGCCTGCGCT CGCAGCTGGT GCCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCCGACGAG   480
CTGGTGCGTT TCCGCTTCTG CAGCGGCTCC TGCCGCCGCG CGCGCTCTCC ACACGACCTC   540
AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCCCGGGCTC CCGGCCCGTC   600
AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC   660
ACCTGGAGAA CCGTGGACCG CCTCTCCGCC ACCGCCTGCG GCTGCCTGGG CTGAGGGCTC   720
GCTCCAGGGC TTTGCAGACT GGACCCTTAC CGGTGGCTCT TCCTGCCTGG GACCCTCCCG   780
CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGGCCCC   840
TACCGGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC   900
AGAGCCCTCA CCCTGCGGAT CCCAGCCTAA AAGACACCAG AGACCTCAGC TATGGAGCCC   960
TTCGGACCCA CTTCTCACAG ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCCT  1020
CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCCGCCC AGGCCCTGTA GGGACAGCAT  1080
TTGAAGGACA CATATTGCAG TTGCTTGGTT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC  1140
TCACTCATGG GAGCTGGCCC C
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Seq ID NO: 406 Protein sequence
Protein Accession #: NP_476501.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS    60
APRSPAPREG PPPVLASPAG HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG   120
RAARAGGPGS RARAAGARGC RLRSQLVPVR ALGLGHRSDE LVRFRFCSGS CRRARSPHDL   180
SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG
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Seq ID NO: 407 DNA sequence
Nucleic Acid Accession #: NM_057090.1
Coding sequence: 29..715

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1          11         21         31         41         51
|          |          |          |          |          |
CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACTTGGA CTTGGAGGCC TCTCCACGCT    60
GTCCCACTGC CCCTGGCCTA GGCGGCAGGC TCCACTTGGT CTCTCCGCGC AGCCTGCCCT   120
GTGGCCCACC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCCT CCCTGGGCTC   180
CGCGCCCCGC AGCCCTGCCC CCCGCGAAGG CCCCCCGCCT GTCCTGGCGT CCCCCGCCGG   240
CCACCTGCCG GGGGGACGCA CGGCCCGCTG GTGCAGTGGA AGAGCCCGGC GGCCGCCGCC   300
GCAGCCTTCT CGGCCCGCGC CCCCGCCGCC TGCACCCCCA TCTGCTCTTC CCCGCGGGGG   360
CCGCGCGGCG CGGGCTGGGG GCCCGGGCAG CCGCGCTCGG GCAGCGGGGG CGCGGGGCTG   420
CCGCCTGCGC TCGCAGCTGG TGCCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCCGACGA   480
GCTGGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCCGCCGC GCGCGCTCTC CACACGACCT   540
CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCCGGGCT CCCGGCCCGT   600
CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG   660
CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGGCT   720
CGCTCCAGGG CTTTGCAGAC TGGACCCTTA CCGGTGGCTC TTCCTGCCTG GGACCCTCCC   780
GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCCC   840
CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC   900
CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC   960
CTTCGGACCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GGACCCCTCC  1020
TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA  1080
TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA CTGGCCTGTA  1140
CTCACTCATG GGAGCTGGCC CC
```

Seq ID NO: 408 Protein sequence
Protein Accession #: NP_476431.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MELGLGGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE    60
GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG   120
SRARAAGARG CRLRSQLVPV RALGLGHRSD ELVRFRFCSG SCRRARSPHD LSLASLLGAG   180
ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG
```

Seq ID NO: 409 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCACTGA AGCATTATCT CCTTTTGCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG    60
GCCTACCATG GCTGCCCTAG CGAGTGTACC TGCTCCAGGG CCTCCCAGGT GGAGTGCACC   120
GGGGCACGCA TTGTGGCGGT GCCCACCCCT CTGCCCTGGA ACGCCATGAG CCTGCAGATC   180
CTCAACACGC ACATCACTGA ACTCAATGAG TCCCCGTTCC TCAATATCTC AGCCCTCATC   240
GCCCTGAGGA TTGAGAAGAA TGAGCTGTCG CGCATCACGC CTGGGGCCTT CCGAAACCTG   300
GGCTCGCTGC GCTATCTCAG CCTCGCCAAC AACAAGCTGC AGGTTCTGCC CATCGGCCTC   360
TTCCAGGGCC TGGACAGCCT TGAGTCTCTC CTTCTGTCCA GTAACCAGCT GTTGCAGATC   420
CAGCCGGCCC ACTTCTCCCA GTGCAGCAAC CTCAAGGAGC TGCAGTTGCA CGGCAACCAC   480
CTGGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCACGAA GCTCAATCTG   540
GGCAAGAATA GCCTCACCCA CATCTCACCC AGGGTCTTCC AGCACCTGGG CAATCTCCAG   600
GTCCTCCGGC TGTATGAGAA CAGGCTCACG GATATCCCCA TGGGCACTTT TGATGGGCTT   660
GTTAACCTGC AGGAACTGGC TCTACAGCAG AACCAGATTG GACTGCTCTC CCCTGGTCTC   720
TTCCACAACA ACCACAACCT CCAGAGACTC TACCTGTCCA ACAACCACAT CTCCCAGCTG   780
CCACCCAGCA TCTTCATGCA GCTGCCCCAG CTCAACCGTC TTACTCTCTT TGGGAATTCC   840
CTGAAGGAGC TCTCTCTGGG GATCTTCGGG CCCATGCCCA ACCTGCGGGA GCTTTGGCTC   900
TATGACAACC ACATCTCTTC TCTACCCGAC AATGTCTTCA GCAACCTCCG CCAGTTGCAG   960
GTCCTGATTC TTAGCCGCAA TCAGATCAGC TTCATCTCCC CGGGTGCCTT CAACGGGCTA  1020
ACGGAGCTTC GGGAGCTGTC CCTCCACACC AACGCACTGC AGGACCTGGA CGGGAATGTC  1080
TTCCGCATGT TGGCCAACCT GCAGAACATC TCCCTGCAGA ACAATCGCCT CAGACAGCTC  1140
CCAGGGAATA TCTTCGCCAA CGTCAATGGC CTCATGGCCA TCCAGCTGCA GAACAACCAG  1200
CTGGAGAACT TGCCCCTCGG CATCTTCGAT CACCTGGGGA AACTGTGTGA GCTGCGGCTG  1260
TATGACAATC CCTGGAGGTG TGACTCAGAC ATCCTTCCGC TCCGCAACTG GCTCCTGCTC  1320
AACCAGCCTA GGTTAGGGAC GGACACTGTA CCTGTGTGTT TCAGCCCAGC CAATGTCCGA  1380
GGCCAGTCCC TCATTATCAT CAATGTCAAC GTTGCTGTTC CAAGCGTCCA TGTCCCTGAG  1440
GTGCCTAGTT ACCCAGAAAC ACCATGGTAC CCAGACACAC CCAGTTACCC TGACACCACA  1500
TCCGTCTCTT CTACCACTGA GCTAACCAGC CCTGTGGAAG ACTACACTGA TCTGACTACC  1560
ATTCAGGTCA CTGATGACCG CAGCGTTTGG GGCATGACCC AGGCCCAGAG CGGGCTGGCC  1620
ATTGCCGCCA TTGTAATTGG CATTGTCGCC CTGGCCTGCT CCCTGGCTGC CTGCGTCGGC  1680
TGTTGCTGCT GCAAGAAGAG GAGCCAAGCT GTCCTGATGC AGATGAAGGC ACCCAATGAG  1740
TGTTAAAGAG GCAGGCTGGA GCAGGGCTGG GGAATGATGG GACTGGAGGA CCTGGGAATT  1800
TCATCTTTCT GCCTCCACCC CTGGGTCCAT GGAGCTTTCC CGTGATTGCT CTTTCTGGCC  1860
CTAGATAAAG GTGTGCCTAC CTCTTCCTGA CTTGCCTGAT TCTCCCGTAG AGAAGCAGGT  1920
CGTGCCGGAC CTTCCTACAA TCAGGAAGAT AGATCCAACT GGCCATGGCA AAAGCCCTGG  1980
GGATTTCCGA TTCATACCCC TGGGCTTCCT TCGAGAGGGC TCTTCCTCCA AATCCTCCCC  2040
ACCTGTCCTC CAAGAACAGC CTTCCCTGCG CCCAGGCCCC CTCCGGGCCT CTGTAGACTC  2100
AGTTAGTCCA CAGCCTGCTC ACTTCGTGGG AATAGTTCTC CGCTGAGATA GCCCCTCTCG  2160
CCTAAGTATT ATGTAAGTTG ATTTCCCTTC TTTTGTTTCT CTTGTTTGTG CTATGGCTTG  2220
ACCCAGCATG TCCCCTCAAA TGAAAGTTCT CCCCTTGATT TTCTGCTCCT GAAGGCAGGG  2280
TGAGTTCTCT CCTCAAAGAA GACTTCAAAC CATTTAACTG GTTTCTTAAG AGCCGTCAAT  2340
CAGCCTGGTT TTGGGGATGC TATGAAAGAG AGAAGGAAAA TCATGCCGCT CAGTTCCTGG  2400
AGACAGAAGA GCCGTCATCA GTGTCTCACT TGTGATTTTT ATCTGGAAAA GGAAGAAACA  2460
CCCCAGCACA GCAAGCTCAG CCTTTTAGAG AAGGATATTT CCAAACTGCA AACTTTGCTT  2520
TGAAAAGTTT AGCCCTTTAA GGAATGAAAT CATGTAGAAT TTTGGACTTC TAAAAACATT  2580
AAAATCAGCT TATTAATACG GGATAGAGAA AGAAATCTGG TGCCTGGGGG TCCCTGTGTT  2640
CACCCCTAGA GTTTGTTTTA AAATTTTTAA TTGAAGCATG TGAAGTGTAC STGCAGAAAA  2700
GTGGGAACAT GATAGTGTAT GGCTTGGTGG ATTTTCACAA ACTGAACATA CCTGTGTAAT  2760
CAGCATCTAG ACCCAGACCC AGAGCATCAC AAATATCCCC CATCCTGGGC TTTTCCCAGA  2820
GGAGATGGGG GCTTCTGAAG ATGGACTTAC CTGGGACCTG CCCCCCATGA GCCAGGACGG  2880
TCCCCCCACA GTCAGCCTGT GCAAAGGCCC CGTGGCCAGG GGTGGAGGAG AATATGTGGG  2940
TGTGGACAGG ATGGGAGACT GTGGCCTGAA CAGGAGATTT TATTATATCT GGAGACCCTG  3000
AGAGACCCTG AGACCTGGGG CACCATGGCT GGCCAGGTCA GAAGCATCCT GACTGCAGAG  3060
GTCCGTGCAG CCACACCCTC TTCCCTGCCA GCAAGTTGTC TGCGGCTCAT CGGAGGCCCC  3120
TCCGCCTGGA GCCTTCTATG GACGTGATAT GCCTGTATCT GTTTTTAATT TTCATTCTTC  3180
ACTTAGGGGA AGTGAAATCG CTCAGAGATG AGATCCTTTA ATTGAAAACG AAGTGTAACG  3240
GAATCTAGTG TCTTTCTAAT GTGGTAAAAT TCTCCATCAA CATCACAGTC AGCTGGCAGC  3300
TGAACTTCAG AATCTCACTT ACAGCAGGCG ACACGGGGGT ACACCGATGG GTCACACTGG  3360
GTCTGGGGGC TCCCTGGAGC TCCTCCTGCG TGTGGTCTGG TTAGGAGTTG AGTTGTTTGC  3420
TCCAGGGTTA TTCTCCTCCT CGAGTCACAG TCACACGAAT ACCTGCCTTC TCTGGCTTTC  3480
CTGCTATACA CATATTCACA TGGCGCTCAA GAAGTTAGGC TCATGGCAAC GTGTGTCTTT  3540
CTCTGGACAA CTGGCCCAGT TTACAGTGAA ATGGAGAATT TCAGGTCTCC ACGTCTGCCC  3600
AGGAAAGAAC TTCAGCTGAC TCCACGGGGA TCTGGAAATC CACGACCAAT CCCGATCGGC  3660
TCTTATTAGC TCCCCGCTCC ACAAGACACC TGTGCTTTGG AAATCCACCA CCAATCCCGA  3720
TCGGCTCTTA TTAGCTCCCC GCTCCACAAG ACACCTGTGA TCTGGAAATC TACCACCAAT  3780
CCCGATCGGC TCTTATTAGC TCCCCGCTCC ACAAGACACC TGTGACATCC TCCAGGGCCA  3840
CAGGAGCACG TGCTGACCAG TTTTCCCTTC CAGTTCCTGC ACAAAAAGTG TCCAGAGGGC  3900
TGTTTGCAAA CACTAGTGCA CTTTGTAGCT TTTCACCCTC TGTCCCAGGG AATCTAGGAG  3960
AGATGAGGCC CGTCAGAGTC AAGAGATGTC ATCCCCCCAG GGTCTCCAAG GCATTTCCAC  4020
ACTATTGGTG GCACCTGGAG GACATGCACC AAGGCTTGCC AGAGCCAACA GGAAGTGAGC  4080
CCAGAGCATG GCACATGAGC ATCACCCGCT GATGGTGGCC TGCTGTGCCT GGTGCCAACA  4140
GGGGCATCCC GGCCCGTACC CCTCCAGACA GGAAGCATGG GTTTGCCCAC AGACCTGTCG  4200
GGTGCTCCTG TGAGTGGCCT CCAGATGTCT TTGTGCATAG GCACAAGTGG GCCAGGGCTG  4260
GAGGGAGGTG GGAAACCTCA TCATCCGGTG GGCCCTGCCA ATCTTAACCC AGAACCCTTA  4320
GGTATTCCTG GCAGTAGCCA TGACATTGGA GCACCTTCCT CTCCAGCCAG AGGCTGACCT  4380
GAGGGCCACT GTCCTCAGAT GACACCACCC AGGAGCACCC TAGGTGAGGG GTGAGGGCCC  4440
CCTTATGTGA ACCTCTTGCC TCTTCCTTTC TCCCATCAGA GTGGTTGGAT GGAGCCATTG  4500
GCCTCCTTTT CTTCAGCGGG CCCTTCAACC TCTCTGCACC ATGTTGTCTG GCTGAGGAGC  4560
TACTAGAAAA GCTGAGTGGA GTCTCCTTTC CAACAGGATG ATGCATTTGC TCAATTCTCA  4620
GGGCTGGAAT GAGCCGGCTG GTCCCCCAGA AAGCTGGAGT GGGGTACAGA GTTCAGTTTT  4680
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CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA  4740
GTGTTGGAGA AGAAACAACA AAAGCCAATT AGAACCACTA TTTTTAAAAA GTGCTTACTG  4800
TGCACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC  4860
GGTAGGAGTG CCGCCTCTAC CCACTTGTGA TGGGGTACAG AGGCACTTGC TCTTCTGCAT  4920
GGTGTTCAAT AGGCTGGGAG TTTTATTTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC  4980
TTGTCTTGGG CTTTCGTCAT TAAACCAAAG GAAATGGAAG CCATTCCCCT GTTGCTCTCC  5040
TTAGTCTTGG TCATCAGAAC CTCACTTGGT ACCATATAGA TCAAAAGCTT TGTAACCACA  5100
GGAAAAAATA AACTCTTCCA TCCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT  5160
TGGGCTGTAT GTATATTGTT CTTCCTCCTT AGAATTTAGA GATACAAGAG TTCTACTTAG  5220
AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA  5280
GAACTTCCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGGACCCAG  5340
AGTTGGTCGA CAGATGTTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA  5400
GCCCCCAGAT CCCACAGTCA GAACTGAATC TGCGTTGTTG GGAAGCCAGC AGTGGCCTTG  5460
GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA  5520
CTCCTTCCGC CCCAGGTTTC TTCTTCTCTT AAGGAGAGAT TGTTCTCACC AACCCGCTGC  5580
CTTCATGCTG CCTTCAAAGC TAGATCATGT TTGCCTTGCT TAGAGAATTA CTGCAAATCA  5640
GCCCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCCC TCAGGGTTTT GTAGAGTGTG  5700
AGCCCTGGTG GGCAGGGTTG GGGGGTCTGT CTTCTGCTGG ATGCTGCTTG TAATCCATTT  5760
GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT
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Seq ID NO: 410 Protein sequence
Protein Accession #: BAB84587.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPLKHYLLLL VGCQAWGAGL AYHGCPSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI    60
LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL   120
FQGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFD HLVGLTKLNL   180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL   240
FHNNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL   300
YDNHISSLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLDGNV   360
FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCELRL   420
YDNPWRCDSD ILPLRNWLLL NQPRLGTDTV PVCFSPANVR GQSLIIINVN VAVPSVHVPE   480
VPSYPETPWY PDTPSYPDTT SVSSTTELTS PVEDYTDLTT IQVTDDRSVW GMTQAQSGLA   540
IAAIVIGIVA LACSLAACVG CCCCKKRSQA VLMQMKAPNE C
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Seq ID NO: 411 DNA sequence
Nucleic Acid Accession #: XM_098151
Coding sequence: 1..447

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1          11         21         31         41         51
|          |          |          |          |          |
ATGATGCATT TGCTCAATTC TCAGGGCTGG AATGAGCCGG CTGGTCCCCC AGAAAGCTGG    60
AGTGGGGTAC AGAGTTCAGT TTTCCTCTCT GTTTACAGCT CCTTGACAGT CCCACGCCCA   120
TCTGGAGTGG GAGCTGGGAG TCAGTGTTGG AGAAGAAACA ACAAAAGCCA ATTAGAACCA   180
CTATTTTTAA AAAGTGCTTA CTGTGCACAG ATACTCTTCA AGCACTGGAC GTGGATTCTC   240
TCTCTAGCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCTC TACCCACTTG TGATGGGGTA   300
CAGAGGCACT TGCTCTTCTG CATGGTGTTC AATAGGCTGG GAGTTTTATT TATCTCTTCA   360
AACTTTGTAC AAGAGCTCAT GGCTTGTCTT GGGCTTTCGT CATTAAACCA AAGGAAATGG   420
AAGCCATTCC CCTGTTGCTC TCCTTAG
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Seq ID NO: 412 Protein sequence
Protein Accession #: XP_098151

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1          11         21         31         41         51
|          |          |          |          |          |
MMHLLNSQGW NEPAGPPESW SGVQSSVFLS VYSSLTVPRP SGVGAGSQCW RRNNKSQLEP    60
LFLKSAYCAQ ILFKHWTWIL SLALSTPAVG VPPLPTCDGV QRHLLFCMVF NRLGVLFISS   120
NFVQELMACL GLSSLNQRKW KPPPCCSP
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Seq ID NO: 413 DNA sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77..1372

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1          11         21         31         41         51
|          |          |          |          |          |
GTCCCCGCAG CGCCGTCGCG CCCTCCTGCC GCAGGCCACC GAGGCCGCCG CCGTCTAGCG    60
CCCCGACCTC GCCACCATGA GAGCCCTGCT GGCGCGCCTG CTTCTCTGCG TCCTGGTCGT   120
GAGCGACTCC AAAGGCAGCA ATGAACTTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA   180
TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA   240
GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG   300
TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA   360
CTCTGCCACT GTCCTTCAGC AAACGTACCA TGCCCACAGA TCTGATGCTC TTCAGCTGGG   420
CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCCT GGTGCTATGT   480
GCAGGTGGGC CTAAAGCCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA   540
AAAGCCCTCC TCTCCTCCAG AAGAATTAAA ATTTCAGTGT GGCCAAAAGA CTCTGAGGCC   600
CCGCTTTAAG ATTATTGGGG GAGAATTCAC CACCATCGAG AACCAGCCCT GGTTTGCGGC   660
CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG   720
CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCATTGAT TACCCAAAGA AGGAGGACTA   780
CATCGTCTAC CTGGGTCGCT CAAGGCTTAA CTCCAACACG CAAGGGGAGA TGAAGTTTGA   840
GGTGGAAAAC CTCATCCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA   900
CATTGCCTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGGACTAT   960
ACAGACCATC TGCCTGCCCT CGATGTATAA CGATCCCCAG TTTGGCACAA GCTGTGAGAT  1020
CACTGGCTTT GGAAAAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAAATGAC  1080
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TGTTGTGAAG CTGATTTCCC ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT  1140
CACCACCAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCCT GCCAGGGAGA  1200
CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGCATG ACTTTGACTG GAATTGTGAG  1260
CTGGGGCCGT GGATGTGCCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT  1320
CTTACCCTGG ATCCGCAGTC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC  1380
AGGGAGGAAA CGGGCACCAC CCGCTTTCTT GCTGGTTGTC ATTTTTGCAG TAGAGTCATC  1440
TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG  1500
CACCACCAGG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC  1560
CAGACCCTCT GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT  1620
TGTCTTTTTC TGGACTGAAG CCTGCAGGAG TTAAAAAGGG CAGGGCATCT CCTGTGCATG  1680
GGCTCGAAGG GAGAGCCAGC TCCCCCGACC GGTGGGCATT TGTGAGGCCC ATGGTTGAGA  1740
AATGAATAAT TTCCCAATTA GGAAGTGTAA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC  1800
AATGTGGGAG CAGCGGTTTG GGGAGCAGAG ACACTAACGA CTTCAGGGCA GGGCTCTGAT  1860
ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTTGTGTGG  1920
GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCCTT  1980
AAACTGTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC  2040
CTGGGGCCTC TTGGGTCCCC CACGTGACAG TGCCTGGGAA TGTACTTATT CTGCAGCATG  2100
ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT  2160
ATCCCTTCCT TTTAGCCTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT  2220
ACACTGAATA TTTATATTTC ACTATTTTTA TTTATATTTT TGTAATTTTA AATAAAAGTG  2280
ATCAATAAAA TGTGATTTTT CTGA
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Seq ID NO: 414 Protein sequence
Protein Accession #: NP_002649.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRALLARLLL CVLVVSDSKG SNELHQVPSN CDCLNGGTCV SNKYFSNIHW CNCPKKFGGQ    60
HCEIDKSKTC YEGNGHFYRG KASTDTMGRP CLPWNSATVL QQTYHAHRSD ALQLGLGKHN   120
YCRNPDNRRR PWCYVQVGLK PLVQECMVHD CADGKKPSSP PEELKFQCGQ KTLRPRFKII   180
GGEFTTIENQ PWFAAIYRRH RGGSVTYVCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG   240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHHNDIALLK IRSKEGRCAQ PSRTIQTICL   300
PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVKLI SHRECQQPHY YGSEVTTKML   360
CAADPQWKTD SCQGDSGGPL VCSLQGRMTL TGIVSWGRGC ALKDKPGVYT RVSHFLPWIR   420
SHTKEENGLA L
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Seq ID NO: 415 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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1          11         21         31         41         51
|          |          |          |          |          |
CGCCAAAGGA AAAGCCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC    60
CTCTCCGCGC GCCCCACCTC CTCCGCCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC   120
GCTCCGGCCG CGGCCCTCGC CCCGCGGAGC CCTCCTACCC CGGCCCGACG CTCGGCCCGC   180
GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCCT CCGGCTCCTG GAACGGAGCC   240
CTCTGCCGGC TGCTCCTGCT GACCCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAAA   300
AATGTGACAT TACATGTTCC CTCCAAACTA GATGCCGAGA AACTTGTTGG TAGAGTTAAC   360
CTGAAAGAGT GCTTTACAGC TGCAAATCTA ATTCATTCAA GTGATCCTGA CTTCCAAATT   420
TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT   480
TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTTG   540
GAGCATCAAA CAAAGGTCCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC   600
AAGAGAAGAT GGGCTCCAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA   660
CTTTTCCTTC AACAGGTTCA ATCTGACACG GCCCAAAACT ATACCATATA CTATTCCATA   720
AGAGGTCCTG GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA   780
AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC   840
TTTGCAACAA CTCCAGATGG GTATACTCCA GAACTTCCAC TGCCCCTAAT AATCAAAATA   900
GAGGATGAAA ATGATAACTA CCCAATTTTT ACAGAAGAAA CTTATACTTT TACAATTTTT   960
GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT  1020
GACACGATGC ACACACGCCT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCCACC  1080
CTATTTTCTA TGCATCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA  1140
GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT  1200
GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA  1260
ACATTTACTC GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAAATC  1320
TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAACTGGAG AGCTAATTAT  1380
ACCATTTTAA AGGGCAATGA AAATGGCAAT TTTAAAATTG TAACAGATGC CAAAACCAAT  1440
GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG  1500
CAAATTGGTG TAGTTAATGA AGCTCCATTT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG  1560
AGCACAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACCCT  1620
CCAATACAGA CTGTTCGCAT GAAAGAAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT  1680
AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAACTGAT  1740
CCAACAGGGT GGGTCACCAT TGATGAAAAT ACAGGATCAA TCAAAGTTTT CAGAAGCCTG  1800
GATAGAGAGG CAGAGACCAT CAAAAATGGC ATATATAATA TTACAGTCCT TGCATCAGAC  1860
CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC  1920
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ATTGTTGCGG TTGATCCTGA TGAGCCTATC CATGGCCCAC CCTTTGACTT TAGTCTGGAG  2040
AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA  2100
CGTCTTTCCT ATCAGAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA  2160
GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC  2220
GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGA  2280
AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGCAT CCTGTTTACG  2340
CTGGTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC  2400
CAGCAGAACC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG  2460
AATGGCTTCA CAACCCAAAC TGTGGGCGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA  2520
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TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAAGGAGG ACACCAGACC  2580
TCGGAATCCT GCCGGGGGGC TGGCCACCAT CACACCCTGG ACTCCTGCAG GGGAGGACAC  2640
ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTTAC TCAGCCCCGT  2700
CTTGGTGAAA AAGTGTATCT GTGTAATCAA GATGAAAATC ACAAGCATGC CCAAGACTAT  2760
GTCCTGACAT ATAACTATGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTTGCAGT  2820
GAACGACAAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA  2880
CTAGCAGAAG CATGCATGAA GAGATGAGTG TGTTCTAATA AGTCTCTGAA AGCCAGTGGC  2940
TTTATGACTT TTAAAAAAAA TTACAAACCA AGAATTTTTT AAAGCAGAAG ATGCTATTTG  3000
TGGGGGTTTT TCTCTCATTA TTTGGATGGA ATCTCTTTGG TCAAATGCAC ATTTACAGAG  3060
AGACACTATA AACAAGTACA CAAATTTTTC AATTTTTACA TATTTTTAAA TTACTTATCT  3120
TCTATCCAAG GAGGTCTACA GAGAAATTAA AGTCTGCCTT ATTTGTTACA TTTGGGTATA  3180
ATGACAACAG CCAATTTATA GTGCAATAAA ATGTAATTAA TTCAAGTCCT TATTATAGAC  3240
TATTTGAAGC ACAACCTAAT GGAAAATTGT AGAGACCTTG CTTTAACATT ATCTCCAGTT  3300
AATTAAGTGT TCATGTGGTG CTTGGAAACT GTTGTTTTCC TGAACATCTA AAGTGTGTAG  3360
ACTGCATTCT TGCTATTATT TTATTCTTGT AATGTGACCT TTTCACTGTG CAAAGGGAGA  3420
TTTCTAGCCA GGCATTGACT ATTACAATTT CATT
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Seq ID NO: 416 Protein sequence
Protein Accession #: NP_077740.1

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1          11         21         31         41         51
|          |          |          |          |          |
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ANLIHSSDPD FQILEDGSVY TTNTILLSSE KRSFTILLSN TENQEKKKIF VFLEHQTKVL   120
KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ   180
EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAPATTPDG YTPELPLPLI IKIEDENDNY   240
PIFTEETYTF TIFENCRVGT TVGQVCATDK DEPDTMHTRL KYSIIGQVPP SPTLFSMHPT   300
TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDDVND HLPTFTRTSY   360
VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNE NGNFKIVTDA KTNEGVLCVV   420
KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM   480
KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI   540
KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD   600
EPIHGPPFDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFGSYVVPI TVRDRLGMSS   660
VTSLDVTLCD CITENDCTHR VDPRIGGGGV QLGKWAILAI LLGIALLFCI LFTLVCGASG   720
TSKQPKVIPD DLAQQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG   780
QETIEMVKGG HQTSESCRGA GHHHTLDSCR GGHTEVDNCR YTYSEWHSFT QPRLGEKVYL   840
CNQDENHKHA QDYVLTYNYE GRGSVAGSVG CCSERQEEDG LEFLDNLEPK FRTLAEACMK   900
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Seq ID NO: 417 DNA sequence
Nucleic Acid Accession #: NM_004949.1
Coding sequence: 202..2745

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|          |          |          |          |          |
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CTCTCCGCGC GCCCCACCTC CTCCGCCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC   120
GCTCCGGCCG CGGCCCTCGC CCCGCGGAGC CCTCCTACCC CGGCCCGACG CTCGGCCCGC   180
GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCCT CCGGCTCCTG GAACGGAGCC   240
CTCTGCCGGC TGCTCCTGCT GACCCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAAA   300
AATGTGACAT TACATGTTCC CTCCAAACTA GATGCCGAGA AACTTGTTGG TAGAGTTAAC   360
CTGAAAGAGT GCTTTACAGC TGCAAATCTA ATTCATTCAA GTGATCCTGA CTTCCAAATT   420
TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT   480
TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTTG   540
GAGCATCAAA CAAAGGTCCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC   600
AAGAGAAGAT GGGCTCCAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA   660
CTTTTCCTTC AACAGGTTCA ATCTGACACG GCCCAAAACT ATACCATATA CTATTCCATA   720
AGAGGTCCTG GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA   780
AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC   840
TTTGCAACAA CTCCAGATGG GTATACTCCA GAACTTCCAC TGCCCCTAAT AATCAAAATA   900
GAGGATGAAA ATGATAACTA CCCAATTTTT ACAGAAGAAA CTTATACTTT TACAATTTTT   960
GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT  1020
GACACGATGC ACACACGCCT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCCACC  1080
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CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC  1920
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ATTGTTGCGG TTGATCCTGA TGAGCCTATC CATGGCCCAC CCTTTGACTT TAGTCTGGAG  2040
AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA  2100
CGTCTTTCCT ATCAGAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA  2160
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GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGA  2280
AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGCAT CCTGTTTACG  2340
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CTGGTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC 2400
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CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 3000
AAAAAATTAC AAACCAAGAA TTTTTTAAAG CAGAAGATGC TATTTGTGGG GGTTTTTCTC 3060
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AGTACACAAA TTTTTCAATT TTTACATATT TTTAAATTAC TTATCTTCTA TCCAAGGAGG 3180
TCTACAGAGA AATTAAAGTC TGCCTTATTT GTTACATTTG GGTATAATGA CAACAGCCAA 3240
TTTATAGTGC AATAAAATGT AATTAATTCA AGTCCTTATT ATAGACTATT TGAAGCACAA 3300
CCTAATGGAA AATTGTAGAG ACCTTGCTTT AACATTATCT CCAGTTAATT AAGTGTTCAT 3360
GTGGTGCTTG GAAACTGTTG TTTTCCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420
ATTATTTTAT TCTTGTAATG TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480
TTGACTATTA CAATTTCATT

Seq ID NO: 418 Protein sequence
Protein Accession #: NP_004940.1

1 11 21 31 41 51

MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFTA 60
ANLIHSSDPD FQILEDGSVY TTNTILLSSE KRSFTILLSN TENQEKKKIF VFLEHQTKVL 120
KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPELPLPLI IKIEDENDNY 240
PIFTEETYTF TIFENCRVGT TVGQVCATDK DEPDTMHTRL KYSIIGQVPP SPTLFSMHPT 300
TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDDVND HLPTFTRTSY 360
VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNE NGNFKIVTDA KTNEGVLCVV 420
KPLNYEEKQQ MILQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540
KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD 600
EPIHGPPFDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFGSYVVPI TVRDRLGMSS 660
VTSLDVTLCD CITENDCTHR VDPRIGGGGV QLGKWAILAI LLGIALLFCI LFTLVCGASG 720
TSKQPKVIPD DLAQQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
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GHTLIKN

Seq ID NO: 419 DNA sequence
Nucleic Acid Accession #: NM_002722.1
Coding sequence: 14..301

1 11 21 31 41 51

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ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCCAGTA TGCAGCTGAT CTCCGTAGAT 180
ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAAGACA CAAAGAGGAC ACGCTGGCCT 240
TCTCGGAGTG GGGGTCCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT 300
AATGCCACCT TCTGTCTCCT ACGACTCCAT GAGCAGCGCC AGCCCAGCTC TCCCCTCTGC 360
ACCCTTGGCT CTGGCCAAAG CTTGCTCCCT GCTCCCACAC AGGCTCAATA AAGCAAGTCA 420
AAGCC

Seq ID NO: 420 Protein sequence
Protein Accession #: NP_002713.1

1 11 21 31 41 51

MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60
TRPRYGKRHK EDTLAFSEWG SPHAAVPREL SPLDL

Seq ID NO: 421 DNA sequence
Nucleic Acid Accession #: NM_032545.1
Coding sequence: 46..718

1 11 21 31 41 51

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CCATGTCAGG CTTCTGTTTA CGGTCAGTTT GGCATTACAG ATCATCAATT TGGGAAACAG 120
CTATCAAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180
GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240
CGAGGGCTGG GGGCCGGAGG AGCCGCTCCC CTACTCCCGG GCTTTCGGAG AGGGTGCGTC 300
CGCGCGGCCG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG 360
CCCGGCCCAC TTCACCGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420
CCTGGAGCAC GGAGCCTGGA CCCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGGC 480
CCTGCACTGC CTCCCCCTCC AGACGCCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540
CCACGCTCAC GGGCCGAGCG CCGGGGGCGC GCCCAGCCTG CTACTCTTGC TGCCCTGCGC 600
ACTCCTGCAC CGCCTCCTGC GCCCGGATGC GCCCGCGCAC CCTCGGTCCC TGGTCCCTTC 660
CGTCCTCCAG CGGGAGCGGC GCCCCTGCGG AAGGCCGGGA CTTGGGCATC GCCTTTAATT 720
TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780

TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840
AAAAAA

Seq ID NO: 422 Protein sequence
Protein Accession #: NP_115934.1

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1          11         21         31         41         51
|          |          |          |          |          |
MTWRHHVRLL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSHFGE   60
VTGSAEGWGP EEPLPYSRAF GEGASARPRC CRNGGTCVLG SFCVCPAHFT GRYCEHDQRR  120
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL  180
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPCGRPGLG HRL
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Seq ID NO: 423 DNA sequence
Nucleic Acid Accession #: NM_006533.1
Coding sequence: 72..467

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AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT    60
CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT   120
TCTCCGGACC TGGTGTCAGG GGTGGTCCTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG   180
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC   240
CCGACTGCCG ATTCCTGACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA   300
AGGGCCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG   360
CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG   420
GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG   480
CTGGCCCTGC CGTTTCCCCT CCTTGGGTTT ATGCAAATAC AATCAGCCCA GTGCAAAC
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Seq ID NO: 424 Protein sequence
Protein Accession #: NP_006524.1

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1          11         21         31         41         51
|          |          |          |          |          |
MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LQDYMAPDCR    60
FLTIHRGQVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD   120
VKTDKWDFYC Q
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Seq ID NO: 425 DNA sequence
Nucleic Acid Accession #: NM_080870.1
Coding sequence: 3..710

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1          11         21         31         41         51
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AGAAAACCAC AAGAACCCCA GAAAAGCCTA CGCTATACTC AGAGAAGACC ATATGCACCA   120
AAGGGAAAAA CACACCAGTC CCAGAAAAGC CTACAGAAAA CCTGGGGAAC ACCACACTGA   180
CCACTGAGAC CATAAAAGCC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG   240
TCACAAAGAC TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT   300
CTTCTCATCT AAATAAAACT GAAGTTACTC ATCAGGTGCC CACTGGTTCT TTCACCCTCA   360
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CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAATG   480
ATTCATTCCC TGCATGGGCC ATAGTTATTG TGGTCCTGGT GGCTGTGATT CTCCTCCTGG   540
TGTTCCTTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACACGCCGC ACACTAACCC   600
AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAATTCCTAC CCGGTCTACC   660
TGATGGAGCA GCAGAATCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGGAGTA   720
GGCGCCCAGC CCTGGCTCTT CCATGCTCTG CCCCTTTCCT GGATGAGGAA CCGGACTCAC   780
AATTTCTATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAACC   840
CTTCATCTGT TCTTGAAACT GGTTGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT   900
AGGGGACAAA GAAGAAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGGT   960
CTGAGAATGA AAAGGTGTTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC  1020
TGAGTCCTAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG  1080
GGTTTATGGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTTCAGGA CAGCATTATG  1140
TTATTTCCAT TCACTATTAC TTAAGAGTTT GTGTGTAAAC AGGCTCATCT CTGAGTTCTC  1200
AGGACCCTTG CCCCCACCCC CATTTTTTTA ATGAAAAAAA AAAACAAAAA AAACGGATCC  1260
AAGAAGAAAA GAGAATTTAT TTCCTTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAAGT  1320
CCAGAAGAAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTTCCT CCCAAATCCC  1380
TTAGTTTTCC TAAATGTCTA CAGTGGACGC CCTGTTGGTT TGGCTTGCTG GGTTGTGGGT  1440
GGACACGCAA GGAGGGGATT TTTATTTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA  1500
GACCTTCCCT GATTGGTGTC TCAGCATTTA TTTTCCTGTC TCTTCCACCA AAAGCCAGCT  1560
GTAGCTTTAT CTCGTAAAAG TTACCCATCT TCTCTACTGT CCCCATTCTC TCTCCTCCCA  1620
CCTTCACCCC AGATTCAAGT TTTCCTCCTT GTAGGCATTT CATCTGTGTG TGTTTTCTGG  1680
ATTTTCTCTC TCTCTTCTTA TGGCCATTTC ACCTTATTAC TGATTGGGTA GAGGGGGAAA  1740
AGGAGAATGA TGATGATAGT TTCCTTCTGT CTATTGACCT TTTTTATAAT AAAGTATAAC  1800
ATGTT
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Seq ID NO: 426 Protein sequence
Protein Accession #: NP_543146.1

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1          11         21         31         41         51
|          |          |          |          |          |
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TETIKAPVKS TENPEKTAAV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI   120
TSRTKLSSIT SEATGNESHP YLNKDGSQKG IHAGQMGEND SFPAWAIVIV VLVAVILLLV   180
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FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSPR

Seq ID NO: 427 DNA sequence
Nucleic Acid Accession #: XM_069480.1
Coding sequence: 1..4383

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1          11         21         31         41         51
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CCCCAGAAGG ACTCTGTCTC AGACTGGGCC ATTGTGTTGA TCACTCTCAC TTTGGTGGCA   120
GCAATTGTCA GCCTAATGTA CGGTATCAAG AAGGCCTGCC AGTTCCGGAG GGAGATGAGT   180
CTGGGGTGTG GCTGTGGCTC TGTGACCCCT TACAGCAGCC ACCATGAGGG GGAGGCTGCC   240
AGCCAGCGCT ACTCTTGTCA AATGAAAGCT TCTTGGGGGG CAGGTGCTAC TACATTCCAA   300
GAATATCAGA AAACTGGGGA ACTCTCAACA TCCGATCACA TATTTCCCCT CACTCCAGGC   360
CTTGTTTATA GTATCCCTTT TGATCACATT GTTCTGCATT CAGGACAAAG ACCTCCAGAG   420
CTCCCTAAAT CTACAGAAAT CCATGAGCAA AAACGCCACT GCAACACCAC ACGCCATTCT   480
AAGCCAACTG ACAAGCCTAC AGGCAACTCC AAAACTATAG ACCACAAAAG CTCTACAGAT   540
AATCATGAGG CTCCTCCCAC TTCTGAAGAA AACTCCAGCA ACCAAGGGAA AGACCCAATG   600
ATCCGGAACC AGCGCTCTGT TGATCCTGCT GACTCCACTA CCACACATAA AGAATCCGCT   660
GGAAAAAAAC ATATAACGCC AGCACCCAAG AGCAAAATAA ACTGTCGTAA GTCCACAACA   720
GGCAAATCAA CGGTAACAAG AAAATCAGAT AAAACTGGAA GACCTTTGGA AAAGTCCATG   780
AGTACTTTGG ATAAGACAAG TACCAGCTCA CATAAGACTA CAACTTCCTT CCACAACTCA   840
GGCAATTCAC AGACCAAGCA AAAAAGCACA TCTTTTCCAG AAAAAATCAC AGCAGCCTCA   900
AAAACAACAT ACAAGACCAC AGGAACCCCA GAAGAGTCAG AAAAAACTGA AGATTCCAGA   960
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AACACCGCAC CATTCCCAGC AGGGCCTACA GAAAATAGAG AAATGACAGC CAATGAGAAT  1260
ACCACACTAT TCCCAGCAGA GCCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAACACC  1320
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CCATCCCCAG CAGAGCCTAC AGAACATGGA GAAAGGACCC CATTTGCCAA TGACAAAACC  1440
ACATCATCCT CAGCAGAGTC TACAGAACAT GGAGAAAGGA CCCCACTGGC CAACGAGAAC  1500
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ACACCATCCC CAGCAGGGCC TACAGAAAAC AGAGAAACGA CAGCCAACGA GAAGACCACA  1620
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TCCCCAGCAG AGCCTACAGA AAATGGACAA AGGACCCCAT TTGCCAATGA GAAAACCACA  1740
TCATCCTCAG CAGAGCCTAC AGAACAGGA GAAAGGACCC CACTGGCCAA TGAGAACACC  1800
ACACCATCCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAAGACCACA  1860
CCATCCCCAG CAGAGCCTAC AGAAAATGGA GACAGGACTC CTTTGGCCAA TGAGAAGACC  1920
ACGCCATCTC TAGCAGAGCC TACAGAAAAT GGACAAAGGA CCCCATTTGC CAATGAGAAG  1980
ACCACATCAT CCTCAGCAGA GCCTACAGAA CACGAAGAAA GGACTCCACT GGCCAATGAG  2040
AACACCACAC CATCCCCGGC AGAGCCTACA GAAAATAGAG AAAGGACAGC CAATGAGAAC  2100
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ACACCATTCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAACACCACA  2460
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ACACCATCTC TAGCAGAGCC TACAGAAAAT GGAAAAAGGA CCCCATTTGC CAATGAGAAG  2580
ACCACATCAT CCTCAGCAGA GCCTACAGAA CACGCAGAAA GGACTCCACT GGCCAATGAG  2640
AACACCACAT CATCCCCAGC AGAGCCTACA GAAAATAGAG AAAGGACAGC CAATGAGAAG  2700
ACCACACAAT TCCCAGCAGA GCCTACAGAA AATAGAGAAA GCACAGCCAA TGAGAAGACC  2760
ACACCATTCC CAGCAGAGCC TACAGAAAAT AGAGAATGGA CAGCCAATGA GAACACCACA  2820
CTATCCCCAG CAGAGCCTAC AGAACATGAA GAAATGACCC CATTGGCCAA TGAGAAGACC  2880
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ACCACACCAT CCTCAGCAGA GCCTACAGAA CATGGAGAAA GGACCCCACT GGCCAATGAG  3000
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GCCACACCAT CCCCAGCAAA GCCTACAGAA CATGGAGAAA CGACAGTCAA TGAGGACACC  3120
ACACCATCCT CAGCAGAGCC TACAGAAAAT GGAGAAAGGA CCCCACTGGC CAATGAGAAC  3180
ACCACAACAT CCCCAACAGA GTCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAAGACC  3240
ACACCATCCC CAGCAGAGCC TACAGAACAT GGAGAAAGGA CACCATCAGC CAATGAGAAG  3300
ACCATACCAT CTCCAGCAAA GCCTACAGAA CACGAAGAAA TGACCCCATC GGCCAATGAG  3360
AACACCACAC CATCCCCAGT AAAGCCTACA GAACATGGAG AAAAGACTAC ATTGGCCAAT  3420
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AATGAGAAGA TCACACCATC CCTAGCAAAG CCTACAGAAC ATGGAGAAAG GACCACATCA  3540
CCCAATGACA AGATCACCTC ATCTGCAGCA GAGTCTACAG AACATAGAGA TAGGGCTACA  3600
TCAGCCAATG TGATCACACC AGCCCCAGCA GAGCCTATAA AACATGCAAA AAGGACCACA  3660
TTGGCCCATG AGAAGATGAC ACAAGTCACA GAAAAGTCCA CAGAACACCC AGAAAAGACC  3720
ACGTCAACCA CAGAGAAAAC CACAAGAACC CCAGAAAAGC CTACGCTATA CTCAGAGAAG  3780
ACCATATGCA CCAAAGGGAA AAACACACCA GTCCCAGAAA AGCCTACAGA AAACCTGGGG  3840
AACACCACAC TGACCACTGA GACCATAAAA GCCCCAGTAA AGTCCACAGA AAACCCAGAA  3900
AAAACAGCAG CAGTCACAAA GACTATAAAA CCTTCAGTCA AGGTCACAGG AGACAAATCT  3960
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TCTTTCACCC TCATTACATC TAGAACGAAG CTGAGTTCTA TCACATCAGA AGCCACAGGA  4080
AACGAGAGCC ATCCATACCT CAATAAAGAT GGCTCACAGA AAGGTATCCA CGCTGGACAG  4140
ATGGGAGAGA ATGATTCATT CCCTGCATGG GCCATAGTTA TTGTGGTCCT GGTGGCTGTG  4200
ATTCTCCTCC TGGTGTTCCT TGGCCTGATC TTCTTGGTCT CCTATATGAT GCGGACACGC  4260
CGCACACTAA CCCAGAACAC CCAGTACAAT GATGCAGAGG ATGAGGGTGG CCCCAATTCC  4320
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TGA
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Seq ID NO: 428 Protein sequence
Protein Accession #: XP_069480.1

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LGCGCGSVTP YSSHHEGEAA SQRYSCQMKA SWGAGATTFQ EYQKTGELST SDHIFPLTPG   120
LVYSIPFDHI VLHSGQRPPE LPKSTEIHEQ KRHCNTTRHS KPTDKPTGNS KTIDHKSSTD   180
NHEAPPTSEE NSSNQGKDPM IRNQRSVDPA DSTTTHKESA GKKHITPAPK SKINCRKSTT   240
GKSTVTRKSD KTGRPLEKSM STLDKTSTSS HKTTTSFHNS GNSQTKQKST SFPEKITAAS   300
KTTYKTTGTP EESEKTEDSR TTVASDKLLT KTTKNIQETI SANELTQSLA EPTEHGGRTA   360
NENNTPSPAE PTENRERTAN ENTTLSPAEP TENRERTANE NTAPFPAGPT ENREMTANEN   420
TTLFPAEPTE HGERTANENT TPSPAEPTEH GERTANENTT PSPAEPTEHG ERTPFANDKT   480
TSSSAESTEH GERTPLANEN TTPSPAEPTE NRERTANENT TPSPAGPTEN RETTANEKTT   540
LSPVEPTENR ETTANEKTTP SPAEPTENGQ RTPFANEKTT SSSAEPTEHG ERTPLANENT   600
TPSPAEPTEN RERTANEKTT PSPAEPTENG DRTPLANEKT TPSLAEPTEN GQRTPFANEK   660
TTSSSAEPTE HEERTPLANE NTTPSPAEPT ENRERTANEN TTPSPAGPTE NREMTANEKT   720
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TPSLAEPTEN GKRTPFANEK TTSSSAEPTE HAERTPLANE NTTSSPAEPT ENRERTANEK   900
TTQFPAEPTE NRESTANEKT TPFPAEPTEN REWTANENTT LSPAEPTEHE EMTPLANEKT   960
TLSPAEPTEN GERTPFTNEK TTPSSAEPTE HGERTPLANE ITTPSRAEPT EHGERIANEK  1020
ATPSPAKPTE HGETTVNEDT TPSSAEPTEN GERTPLANEN TTTSPTESTE HGERTANEKT  1080
TPSPAEPTEH GERTPSANEK TIPSPAKPTE HEEMTPSANE NTTPSPVKPT EHGEKTTLAN  1140
EKITLSPEGP TEHGAKTTSA NEKITPSLAK PTEHGERTTS PNDKITSSAA ESTEHRDRAT  1200
SANVITPAPA EPIKHAKRTT LAHEKMTQVT EKSTEHPEKT TSTTEKTTRT PEKPTLYSEK  1260
TICTKGKNTP VPEKPTENLG NTTLTTETIK APVKSTENPE KTAAVTKTIK PSVKVTGDKS  1320
LTTTSSHLNK TEVTHQVPTG SFTLITSRTK LSSITSEATG NESHPYLNKD GSQKGIHAGQ  1380
MGENDSFPAW AIVIVVLVAV ILLLVFLGLI FLVSYMMRTR RTLTQNTQYN DAEDEGGPNS  1440
YPVYLMEQQN LGMGQIPSPR
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Seq ID NO: 429 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..10674

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TTTCAGCAGA TGTCCCCGTC GCGCAATTTC AGCTTCCGCC TCTTCCCCGA GACCGCGCCC   120
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GTGGAGCGGC TGGGCCAGGC GTTCCGGCGA CGCGTGCGGC TGCTGCGGGA GCTCAGCGAG   240
CGCCTGGAGC TTGTCTTCCT GGTGGATGAT TCGTCCAGCG TGGGCGAAGT CAACTTCCGC   300
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CGCGTGGCCA TCGTGACCTT CTCGTCCAAG AACTACGTGG TGCCGCGCGT CGATTACATC   420
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TCCTACCGAG GTGGCGGCAC CTACACCAAG GGCGCCTTCC AGCAAGCCGC GCAAATTCTT   540
CTTCATGCTA GAGAAAACTC AACAAAAGTT GTATTTCTCA TCACTGATGG ATATTCCAAT   600
GGGGGAGACC CTAGACCAAT TGCAGCGTCA CTGCGAGATT CAGGAGTGGA GATCTTCACT   660
TTTGGCATAT GGCAAGGGAA CATTCGAGAG CTGAATGACA TGGCTTCCAC CCCAAAGGAG   720
GAGCACTGTT ACCTGCTACA CAGTTTTGAA GAATTTGAGG CTTTAGCTCG CCGGGCATTG   780
CATGAAGATC TACCTTCTGG GAGTTTTATT CAAGATGATA TGGTCCACTG CTCATATCTT   840
TGTGATGAAG GCAAGGACTG CTGTGACCGA ATGGGAAGCT GCAAATGTGG GACACACACA   900
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GACGTGGAGG CTCCTCAAAT CAACTGTCCT AAGGACATAG AGGCTAAGAC TCTGGAACAG  1740
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GCTATCGTAT ACACGGCAAC TGACCTATCC GGCAACCAGG CCAGCTGCAT TTTCCATATC  1920
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GTCTCGGAGA AGGTACATGC CGCAAGCTGG GATGAGCCTC AGTTCTCAGA CAACTCAGGG  2040
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GAAGGGTCTA CTGACAAGTA TTATTGTGCT TATGAAGATG GCGTCTGGAA ACCAACATAT  2340
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GCATTTGAGA CGACCCTGGG AAAAATGGTC CCATCATTTT GTAGTGATGC AGAGGACATT  2520
GACTGCAGAC TGGAGGAGAA CCTGACCAAA AAATATTGCC TAGAATATAA TTATGACTAT  2580
GAAAATGGCT TTGCAATTGG ACCAGGTGGC TGGGGTGCAG CTAATAGGCT GGATTACTCT  2640
TACGATGACT TCCTGGACAC TGTGCAAGAA ACAGCCACAA GCATCGGCAA TGCCAAGTCC  2700
TCACGGATTA AAAGAAGTGC CCCATTATCT GACTATAAAA TTAAGTTAAT TTTTAACATC  2760
ACAGCTAGTG TGCCATTACC CGATGAAAGA AATGATACCC TTGAATGGGA AAATCAGCAA  2820
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CGACTCCTTC AGACATTGGA AACTATCACA AATAAACTGA AAAGGACTCT CAACAAAGAC 2880
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GGATCCTATC AAGATGAAGA AGGGCAACTT GAGTGCAAGC TTTGCCCCTC TGGGATGTAC 3120
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CTGGCCTGTC CCTTTTATGG AACTACCCCA TTCGCTGGTT CCAGATCCAT CACAGAATGT 3480
TCAACTTCAG TTCTGAATAT TACTATTTTC GGTGGATTTG GGCATCTGGA GTTGTTAAAT 3540
TGTCCTTCTG AGGTTTTCCA TGAATGCTTC TTTAACCCTT GCCACAATAG TGGAACCTGC 3600
CAGCAACTTG GGCGTGGTTA TGTTTGTCTC TGTCCACTTG GATATACAGG CTTAAAGTGT 3660
GAAACAGACA TCGATGAGTG CAGCCCACTG CCTTGCCTCA ACAATGGAGT TTGTAAAGAC 3720
CTAGTTGGGG AATTCATTTG TGAGTGCCCA TCAGGTTACA CAGGTCAGCG GTGTGAAGAA 3780
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Seq ID NO: 430 Protein sequence
Protein Accession #: FGENESH predicted

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TTGAGTTTTG AGTACCTCTT TTCCCATATA CAATCTTCCT TCCTTAGGTA ATTTGGAAGA  2760
AAACTATGAC CCATTTAATT TCTATTGTGT TTCACCAAAT TCAGTGTTGT TCATTATACC  2820
TCTCTGAAAT ATAGGTTTAA TTTCAAATAG AATATGGACT TAAATGTTAA TGAGAAACTG  2880
GCTTTAATCA ATTCTAGCAT TTTATTACTG TAATACAGGG CTGATAGAGT GATTTTGTCT  2940
TATATGAGTC AGTTACTACT TACAGGTGAT AACTTGCATA CTATTGGAAG ATAAAGTTGT  3000
CAAACTTGTC AAGAATGAGA AAAGCCAAAT TAGAAAATCC TATGTCCTAG TTTCCTTACC  3060
AAGGATAATT AAATATATCA CTAAGAGCTT TATATATTGA TTATATATTG TTGACAACTG  3120
GTTTAAGCAT CATAGCCTAT GATGATAAAC ACTGCCTATA TATGTAAATA GCTTTTCATC  3180
AATTCTTAAA TTTCTTAACC TAGGCTTCAG GGAGCATATG AAACCAAAAT TATATGGAAC  3240
ATTTTCTGTG TGTACATGTA CATGCATTTT TCTAGGGAGA GAGTCCGTAG GTTTATCAGA  3300
ATATCAAGGA AAACTGTGAC CCAAAGAAGT TTAAGAATCA CATACAGTGC TGCTGGCTTT  3360
TTGTGCTTGG CAAATGAGTG ACAATAGAAG AAATAATTTT TCTTACACAT TTTAAAACGT  3420
TTTCTCTTCC TTGTGATTGA AGATGAAAGG AGTAAGAAAT TAAGGCATTT GTTTAATTTA  3480
TACTGGTAAC TTATTTAGGG GGGAGGGGAC ATGAAGGTAG GTAAATAGGT AGGCCTCTAA  3540
TTGAACCACC TCTCTAAGTT ATGTACGTAT ATATAAGCTG AAATTGTGTT TGACATTCTG  3600
AGGGTTTTCT TTTTCTTTTT CCTTTTTTTT TTTTTTGGT GGGGGGCTGG GGGTCAGAGT  3660
CTTGTTCTGT TGCCTGGGCT GGAGTGCAGT GGCATGATCT CAGCTCACTG CAACCTCTGC  3720
CTTCTGGATT CAAGTGATTC TCCTGCCTCA GCCTCTTGAG TAGCTGGGAC TACAGGTGCC  3780
CGCCACCACA CCAGCTAATT TTTGTATTTT TAGTAGAGGC GAAGTTTCCC CATGTTGGCC  3840
AGGCTGGTCT TGAACTCCCG ACCTCAAGTG ATCTGTCTAC CTCGGCCTCC TAAAGTGCTG  3900
AGATTACAGG TGTGAGCCAC CGTGCCCGGC CCATTCTAAG GGTTTTCTTT GAAGACAGGT  3960
CAAATGCTGT TAGTAAGTTT CAGGAGATTG TTAATTCCTC AGTTATACCA GATTTTATAA  4020
AATATTTGAG AATAGATGGC TAACAAGAGG TTAGAAATAC TTTTCCTTAA TTTTAATCCA  4080
CAGTATGTTA CATGCATTCT ACCACTACAT TTTGGTGCTA TTTAAGGTGT GCAATTTTCT  4140
ATAGGTGACT TTTGCAATTC AGGGAAGATT TGGGCATATT AAATGAAAGA ATATCTAATT  4200
GGGGGAGGTG TGAAGGGAAA GAAATTCTTT TCAAAAGCTG ACCACAAAGA GTAGTTAAAA  4260
GTTTTTGTCA CTATCTTCAC AAGTGTGTAA AGCACAGATT TCAACAGAGT GCTTGGCATA  4320
TTGTAGGGTG CTCAATGGTG GTTTTTATTA TTATTACTCA GATTCCACAG TGGCAAGAAA  4380
CATCATTCTA CATAATGGAA AACATTTACA TCAAATCCCA CTTACTTTAA TGCGAACTTG  4440
GAGATAATTT ATGGTATTGT ATTGTAAACC ATTAATGAAA ACTTTTTCAC AGTTGAGTGA  4500
AATTAAAATC ACTATATCTC
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Seq ID NO: 434 Protein sequence
Protein Accession #: NP_009162.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDKLKCPSFF KCREKEKVSA SSENFHVGEN DENQDRGNWS KKSDYLLSMI GYAVGLGNVW    60
RFPYLTYSNG GGAFLIPYAI MLALAGLPLF FLECSLGQFA SLGPVSVWRI LPLFQGVGIT   120
MVLISIFVTI YYNVIIAYSL YYMFASFQSE LPWKNCSSWS DKNCSRSPIV THCNVSTVNK   180
GIQEIIQMNK SWVDINNFTC INGSEIYQPG QLPSEQYWNK VALQRSSGMN ETGVIVWYLA   240
LCLLLAWLIV GAALFKGIKS SGKVVYFTAL FPYVVLLILL VRGATLEGAS KGISYYIGAQ   300
SNFTKLKEAE VWKDAATQIF YSLSVAWGGL VALSSYNKFK NNCFSDAIVV CLTNCLTSVF   360
AGFAIFSILG HMAHISGKEV SQVVKSGFDL AFIAYPEALA QLPGGPFWSI LFFFMLLTLG   420
LDSQFASIET ITTTIQDLFP KVMKKMRVPI TLGCCLVLFL LGLVCVTQAG IYWVHLIDHF   480
CAGWGILIAA ILELVGIIWI YGGNRFIEDT EMMIGAKRWI FWLWWRACWF VITPILLIAI   540
FIWSLVQFHR PNYGAIPYPD WGVALGWCMI VFCIIWIPIM AIIKIIQAKG NIFQRLISCC   600
RPASNWGPYL EQHRGERYKD MVDPKKEADH EIPTVSGSRK PE
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Seq ID NO: 435 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 51..1085

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC     60
CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCCTGCTC ACAGCCTCAC    120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA    180
ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCCACAA CCTGCCCCAG AATCGTATTG    240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA    300
TAGGAACTCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA    360
ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG    420
TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC    480
TGCCCAAGCC CTCCATCTCC AGCAACAACT CCAACCCCGT GGAGGACAAG GATGCTGTGG    540
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CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA   600
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA   660
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA   720
ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCC   780
CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA   840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC   900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT   960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG  1020
TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA  1080
TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT  1140
GAATTCTTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG  1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA  1260
ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT  1320
GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA  1380
AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC  1440
TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA  1500
GGGTAACTTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAATAAG  1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC  1620
AAATGTACAG TGGTCCTTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT  1680
TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG  1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTTGAACAT GGCTAAATAC AATGGGTATC  1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAAATGG CTACACTCAT  1860
CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA  1920
CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT  1980
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT  2040
GGCTGGAATT ACAAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG  2100
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC  2160
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT  2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAC CAATTTAAAA AAAAAAAAGA  2280
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT  2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC  2400
TGTTTCCTTG TTCCAATTTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG  2460
CTATCACTGT ACTTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT  2520
TAGCTCTATA ACT
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Seq ID NO: 436 Protein sequence
Protein Accession #: AAA59907.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGPPSAPPCR LHVPWKEVLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLAHNLPQ    60
NRIGYSWYKG ERVDGNSLIV GYVIGTQQAT PGPAYSGRET IYPNASLLIQ NVTQNDTGFY   120
TLQVIKSDLV NEEATGQFHV YPELPKPSIS SNNSNPVEDK DAVAFTCEPE VQNTTYLWWV   180
NGQSLPVSPR LQLSNGNMTL TLLSVKRNDA GSYECEIQNP ASANRSDPVT LNVLYGPDVP   240
TISPSKANYR PGENLNLSCH AASNPPAQYS WFINGTFQQS TQELFIPNIT VNNSGSYMCQ   300
AHNSATGLNR TTVTMITVSG SAPVLSAVAT VGITIGVLAR VALI
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Seq ID NO: 437 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 1355..1657

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC    60
CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCCTGCTC ACAGCCTCAC   120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA   180
ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCCACAA CCTGCCCCAG AATCGTATTG   240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA   300
TAGGAACTCA ACAAGCTACC CCAGGCCCCG CATACAGTGG TCGAGAGACA ATATACCCCA   360
ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG   420
TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC   480
TGCCCAAGCC CTCCATCTCC AGCAACAACT CCAACCCCGT GGAGGACAAG GATGCTGTGG   540
CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA   600
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA   660
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA   720
ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCC   780
CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA   840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC   900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT   960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG  1020
TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA  1080
TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT  1140
GAATTCTTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG  1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA  1260
ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT  1320
GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA  1380
AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC  1440
TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA  1500
GGGTAACTTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAATAAG  1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC  1620
AAATGTACAG TGGTCCTTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT  1680
TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG  1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTTGAACAT GGCTAAATAC AATGGGTATC  1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAAATGG CTACACTCAT  1860
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CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA  1920
CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT  1980
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT  2040
GGCTGGAATT ACAAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG  2100
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC  2160
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT  2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAC CAATTTAAAA AAAAAAAAGA  2280
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT  2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC  2400
TGTTTCCTTG TTCCAATTTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG  2460
CTATCACTGT ACTTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT  2520
TAGCTCTATA ACT
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Seq ID NO: 438 Protein sequence
Protein Accession #: AAA59908.1

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1           11          21          31          41          51
|           |           |           |           |           |
MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SFAWQDDAVI SISQEVASEG NLTECQIYLV    60
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELDF
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Seq ID NO: 439 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 2370..2501

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1           11          21          31          41          51
|           |           |           |           |           |
GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC    60
CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCCTGCTC ACAGCCTCAC   120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA   180
ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCCACAA CCTGCCCCAG AATCGTATTG   240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA   300
TAGGAACTCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA   360
ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG   420
TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC   480
TGCCCAAGCC CTCCATCTCC AGCAACAACT CCAACCCCGT GGAGGACAAG GATGCTGTGG   540
CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA   600
GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA   660
GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA   720
ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCC   780
CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA   840
ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC   900
TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT   960
CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG  1020
TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA  1080
TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT  1140
GAATTCTTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG  1200
CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA  1260
ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT  1320
GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA  1380
AACAAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC  1440
TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA  1500
GGGTAACTTA ACAGAGTGTC AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAATAAG  1560
AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC  1620
AAATGTACAG TGGTCCTTTT CAGAGTTGGA CTTCTAGACT CACCTGTTCT CACTCCCTGT  1680
TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG  1740
GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTTGAACAT GGCTAAATAC AATGGGTATC  1800
GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAAATGG CTACACTCAT  1860
CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA  1920
CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT  1980
CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT  2040
GGCTGGAATT ACAAAACTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG  2100
ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC  2160
TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT  2220
GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAC CAATTTAAAA AAAAAAAAGA  2280
ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT  2340
TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC  2400
TGTTTCCTTG TTCCAATTTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG  2460
CTATCACTGT ACTTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT  2520
TAGCTCTATA ACT
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Seq ID NO: 440 Protein sequence
Protein Accession #: AAA59909.1

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1           11          21          31          41          51
|           |           |           |           |           |
MLTNVFISVV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS
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Seq ID NO: 441 DNA sequence
Nucleic Acid Accession #: NM_002381.2
Coding sequence: 64..1524

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1           11          21          31          41          51
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AAATCCGAGC CTCGCGTGGG CTCCTGGCCC CCGACGGACA CCACCAGGCC CACGGAGCCC    60
ACCATGCCGC GCCCGGCCCC CGCGCGCCGC CTCCCGGGAC TCCTCCTGCT GCTCTGGCCG   120
CTGCTGCTGC TGCCCTCCGC CGCCCCCGAC CCCGTGGCCC GCCCGGGCTT CCGGAGGCTG   180
GAGACCCGAG GTCCCGGGGG CAGCCCTGGA CGCCGCCCCT CTCCTGCGGC TCCCGACGGC   240
GCGCCCGCTT CCGGGACCAG CGAGCCTGGC CGCGCCCGCG GTGCAGGTGT TTGCAAGAGC   300
AGACCCTTGG ACCTGGTGTT TATCATTGAT AGTTCTCGTA GCGTACGGCC CCTGGAATTC   360
ACCAAAGTGA AAACTTTTGT CTCCCGGATA ATCGACACTC TGGACATTGG GCCAGCCGAC   420
ACGCGGGTGG CAGTGGTGAA CTATGCTAGC ACTGTGAAGA TCGAGTTCCA ACTCCAGGCC   480
TACACAGATA AGCAGTCCCT GAAGCAGGCT GTGGGTCGAA TCACACCCTT GTCAACAGGC   540
ACCATGTCAG GCCTAGCCAT CCAGACAGCA ATGGACGAAG CCTTCACAGT GGAGGCAGGG   600
GCTCGAGAGC CCTCTTCTAA CATCCCTAAG GTGGCCATCA TTGTTACAGA TGGGAGGCCC   660
CAGGACCAGG TGAATGAAGT GGCGGCTCGG GCCCAAGCAT CTGGTATTGA GCTCTATGCT   720
GTGGGCGTGG ACCGGGCAGA CATGGCGTCC CTCAAGATGA TGGCCAGTGA GCCCCTAGAG   780
GAGCATGTTT TCTACGTGGA GACCTATGGG GTCATTGAGA AACTTTCCTC TAGATTCCAG   840
GAAACCTTCT GTGCGCTGGA CCCCTGTGTG CTTGGAACAC ACCAGTGCCA GCACGTCTGC   900
ATCAGTGATG GGGAAGGCAA GCACCACTGT GAGTGTAGCC AAGGATACAC CTTGAATGCC   960
GACAAGAAAA CGTGTTCAGC TCTTGATAGG TGTGCTCTTA ACACCCACGG ATGTGAGCAC  1020
ATCTGTGTGA ATGACAGAAG TGGCTCTTAT CATTGTGAGT GCTATGAAGG TTATACCTTG  1080
AATGAAGACA GGAAAACTTG TTCAGCTCAA GATAAATGTG CTTTGGGTAC CCATGGGTGT  1140
CAGCACATTT GTGTGAATGA CAGAACAGGG TCCCATCATT GTGAATGCTA TGAGGGCTAC  1200
ACTCTGAATG CAGATAAAAA AACATGTTCA GTCCGTGACA AGTGTGCCCT AGGCTCTCAT  1260
GGTTGCCAGC ACATTTGTGT GAGTGATGGG GCCGCATCCT ACCACTGTGA TTGCTATCCT  1320
GGCTACACCT TAAATGAGGA CAAGAAAACA TGTTCAGCCA CTGAGGAAGC ACGAAGACTT  1380
GTTTCCACTG AAGATGCTTG TGGATGTGAA GCTACACTGG CATTCCAGGA CAAGGTCAGC  1440
TCGTATCTTC AAAGACTGAA CACTAAACTT GATGACATTT TGGAGAAGTT GAAAATAAAT  1500
GAATATGGAC AAATACATCG TTAAATTGCT CCAATTTCTC ACCTGAAAAT GTGGACAGCT  1560
TGGTGTACTT AATACTCATG CATTCTTTTG CACACCTGTT ATTGCCAATG TTCCTGCTAA  1620
TAATTTGCCA TTATCTGTAT TAATGCTTGA ATATTACTGG ATAAATTGTA TGAAGATCTT  1680
CTGCAGAATC AGCATGATTT TTCCAAGGAA ATACATATGC AGATACTTAT TAAGAGCAAA  1740
CTTTAGTGTC TCTAAGTTAT GACTGTGAAA TGATTGGTAG GAAATAGAAT GAAAAGTTTA  1800
GTGTTTCTTT ATCTACTAAT TGAGCCATTT AATTTTTAAA TGTTTATATT AGATAACCAT  1860
ATTCACAATG GAAACTTTAG GTCTAGTTTC TTTTGATAGT ATTTATAATA TAAATCAATC  1920
TTATTACTGA GAGTGCAAAT TGTACAAGGT ATTTACACAT ACAACTTCAT ATAACTGAGA  1980
TGAATGTAAT TTTGAACTGT TTAACACTTT TTGTTTTTTG CTTATTTTGT TGGAGTATTA  2040
TTGAAGATGT GATCAATAGA TTGTAATACA CATATCTAAA AATAGTTAAC ACAGATCAAG  2100
TGAACATTAC ATTGCCATTT TTAATTCATT CTGGTCTTTG AAAGAAATGT ACTACTAAAG  2160
AGCACTAGTT GTGAATTTAG GGTGTTAAAC TTTTTACCAA GTACAAAAAT CCCAAATTCA  2220
CTTTATTATT TTGCTTCAGG ATCCAAGTGA CAAAGTTATA TATTTATAAA ATTGCTATAA  2280
ATCGACAAAA TCTAATGTTG TCTTTTTAAT GTTAGTGATC CACCTGCCTC AGCCTCCCAA  2340
AGTGCTGGGA TTACAGGCTT GAAAGTCTAA CTTTTTTTTA CTTATATATT TGATACATAT  2400
AATTCTTTTG GCTTTGAAAC TTGCAACTTT GAGAACAAAA CAGTCCTTTA AATTTTGCAC  2460
TGCTCAATTC TGTTTTTCGT TTGCATTGTC TTTAATATAA TAAAAGTTAT TACCTTTACA  2520
TATTATCATG TCTATTTTTG ATGACTCATC AATTTTGTCT ATTAAAGATA TTTCTTTAAA  2580
TTAAAAAAAA AAAAAAAAA
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Seq ID NO: 442 Protein sequence
Protein Accession #: NP_002372.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPRPAPARRL PGLLLLLWPL LLLPSAAPDP VARPGFRRLE TRGPGGSPGR RPSPAAPDGA    60
PASGTSEPGR ARGAGVCKSR PLDLVFIIDS SRSVRPLEFT KVKTFVSRII DTLDIGPADT   120
RVAVVNYAST VKIEFQLQAY TDKQSLKQAV GRITPLSTGT MSGLAIQTAM DEAFTVEAGA   180
REPSSNIPKV AIIVTDGRPQ DQVNEVAARA QASGIELYAV GVDRADMASL KMMASEPLEE   240
HVFYVETYGV IEKLSSRFQE TFCALDPCVL GTHQCQHVCI SDGEGKHHCE CSQGYTLNAD   300
KKTCSALDRC ALNTHGCEHI CVNDRSGSYH CECYEGYTLN EDRKTCSAQD KCALGTHGCQ   360
HICVNDRTGS HHCECYEGYT LNADKKTCSV RDKCALGSHG CQHICVSDGA ASYHCDCYPG   420
YTLNEDKKTC SATEEARRLV STEDACGCEA TLAFQDKVSS YLQRLNTKLD DILEKLKINE   480
YGQIHR
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Seq ID NO: 443 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

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CGGTTGCTGC GGCTCCTCGT GCTGGGGCTC TGGCTGGCGT TGCTGCGCTC CGTGGCCGGG   120
GAGCAAGCGC CAGGCACCGC CCCCTGCTCC CGCGGCAGCT CCTGGAGCGC GGACCTGGAC   180
AAGTGCATGG ACTGCGCGTC TTGCAGGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC   240
GCTGCAGCAC CTCCTGCCCC CTTCCGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC   300
CTGACCTTCG TGCTGGGGCT GCTTTCTGGC TTTTTGGTCT GGAGACGATG CCGCAGGAGA   360
GAGAAGTTCA CCACCCCCAT AGAGGAGACC GGCGGAGAGG GCTGCCCAGC TGTGGCGCTG   420
ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTCATCCA   480
TTCTAGAGCC AGTCTCTGCC TCCCAGACGC GGCGGGAGCC AAGCTCCTCC AACCACAAGG   540
GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA   600
AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC   660
ACAAAACAGC TGACACTGAC TAAGGAACTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT   720
CCTTCCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC   780
TCACTCAGAT GTCCTGAAAT TCCACCACGG GGGTCACCCT GGGGGGTTAG GGACCTATTT   840
TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCCAACTC   900
CCCAAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT   960
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AATAAAAGAA TCTTTAACTT TAAAAAAAAA AAAAAAAA

Seq ID NO: 444 Protein sequence
Protein Accession #: NP_057723.1

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SDFCLGCAAA PPAPFRLLWP ILGGALSLTF VLGLLSGFLV WRRCRRREKF TTPIEETGGE   120
GCPAVALIQ
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Seq ID NO: 445 DNA sequence
Nucleic Acid Accession #: AF322916.1
Coding sequence: 50..4300

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CAAGTCCCGC CTGAGGAGGC AGGACGTGCC CGGCCCCGCG TCGTCTGGCG CCGCCGCCGC   120
CAGCGCGCAT GCAGCAGATT GGAATAAATA TGATGACCGA TTGATGAAAG CAGCAGAAAG   180
GGGGGATGTA GAAAAAGTGA CCTCAATCCT TGCTAAAAAG GGGGTCAATC CAGGCAAACT   240
AGATGTGGAA GGCAGATCTG TCTTCCATGT TGTGACCTCA AAGGGGAATC TTGAGTGTTT   300
GAATGCCATC CTTATACATG GAGTTGATAT TACAACCAGT GACACTGCAG CGAGAAATGC   360
TCTTCACCTG GCTGCTAAGT ATGGACATGC ATTGTGCCTA CAAAAACTTC TACAGTACAA   420
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AGATTGTCCT TCTAGCATAC AGCTGCTTTG TGACCATGGG GCCTCTGTGA ATGCCAAAGA   540
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CATGCTAGGT TGCGAATATG GTTGCAGAGA TGCAGTAGAA GTCTTAATTA AAAATGGTGC   720
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CAATCTGGAC ATTCTAACCT TGTTGAAGAC TGCATCGGAA AATACCAACA AAGGGAGAGA   840
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AAATGTGAAG TCACATCAGA GGGAGCATCA AAATATTCAG GATTTGGAGA TTGAAAATGA   960
AGATTTGAAA GAGAGGTTGA GAAAAATTCA GCAAGAACAA AGAATACTTT TGGATAAAGT  1020
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GAGAGAAAAG CTGAAGTCCC TTTTGGCAGC TAAAGAAAAG CAACATGAAG AAAGCTTAAG  1140
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AAGTCATTTC AGTAACCGAA AAGAAGATAT GCTTCTTAAA CAAGGTCAGA TGTATATGGC  1260
AGACTCACAG TGTACTTCCC CAGGTATACC AGCCCATATG CAAAGCAGAT CTATGTTAAG  1320
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AGAGTTAGAA GCAATGCGAA CTTTCTGTGA GTCAGCAAAA CAAGACCGAC TGAAGCTCCA  1440
AAATGAACTG GCACACAAAG TGGCAGAATG CAAAGCTTTA GCATTAGAAT GTGAAAGGGT  1500
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TCAGTTGAAA GACTTGAAAG TAAAATATGA AGGTGCTTCA GCAGAAGTGG GGAAATTAAG  1740
AAACCAAATC AAACAAAATG AGATGATAGT AGAAGAGTTT AAGAGGGATG AAGGCAAGCT  1800
GATAGAAGAA AATAAGCGAT TACAGAAGGA ACTTAGTATG TGTGAAATGG AGCGAGAGAA  1860
GAAAGGAAGA AAGGTCACAG AGATGGAAGG CCAGGCAAAA GAATTGTCAG CGAAGTTGGC  1920
CCTTTCCATT CCAGCTGAAA AATTTGAAAA CATGAAGAGC TCATTATCAA ATGAAGTGAA  1980
TGAGAAAGCA AAAAAATTAG TAGAAATGGA AAGAGAACAT GAAAAATCAC TTAGTGAAAT  2040
TAGACAGTTA AAGAGAGAAC TTGAGAATGT TAAGGCCAAG CTTGCTCAGC ACGTCAAACC  2100
AGAGGAACAT GAACAGGTTA AGAGCAGATT AGAACAGAAA TCAGGAGAAC TTGGGAAGAA  2160
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GGATAATAAG CTCCTCAAGG AGCAAGCACA TAACTTAACA ATTGAAATGA AAAATCATTA  2280
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ATTGCTACTG GAAAATGACA GCTTAAGTAA GGATGTAAGC CGCCTAGAAA CTGTGTTTGT  2460
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TGAAATATTA AAAAGAAACC TGGAAAACAC TCAGAACCAA ATAAAAGCTG AGTACATCAG  2820
CCTGGCAGAG CACGAGGCAA AGATGAGCTC GCTAAGTCAG AGCATGAGAA AGGTGCAGGA  2880
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TGCCGAAATT AAAGCCCAGA AGAAGGAGCT CGACACAATA CAAGAATGCA TTAAGGTAAA  3000
ATATGCCCCA ATTGTCAGCT TTGAGGAGTG CGAGAGAAAA TTTAAAGCAA CAGAGAAAGA  3060
ACTAAAAGAC CAGTTATCAG AGCAGACACA AAAGTATAGT GTCAGTGAAG AAGAAGTCAA  3120
GAAAAACAAG CAAGAGAATG ACAAGTTAAA GAAGGAGATT TTTACCCTTC AGAAAGATTT  3180
GAGAGATAAG ACAGTTCTCA TTGAGAAGTC TCATGAAATG GAAAGAGCAT TAAGCAGAAA  3240
AACAGACGAG CTAAACAAAC AGTTAAAAGA CTTGTCACAG AAATACACGG AAGTAAAGAA  3300
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AGCCAGCTTG AGAGAAAAGG AAGAAGAAAG CCAAAACAAA ATGGAAGAAG TCTCCAAACT  3660
TCAGTCGGAG GTTCAGAATA CTAAACAAGC ATTAAAAAAA TTAGAGACTA GAGAGGTAGT  3720
TGACTTGTCT AAATATAAAG CAACAAAAAG TGATTTGGAG ACACAGATTT CTAGCTTAAA  3780
TGAAAAATTG GCCAATCTGA ATAGAAAGTA TGAGGAAGTA TGTGAGGAAG TTTTGCATGC  3840
CAAAAAGAAG GAAATATCTG CAAAAGATGA GAAGGAATTA CTGCATTTCA GCATTGAGCA  3900
AGAAATTAAG GATCAGAAGG AACGATGTGA TAAGTCCTTA ACAACAATCA CAGAGTTACA  3960
AAGAAGAATA CAAGAATCTG CTAAACAAAT AGAAGCAAAA GATAATAAGA TAACTGAACT  4020
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WO03042661 [file:///E:/WO03042661.pcp]


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GCTTAATGAT GTGGAAAGAT TAAAACAGGC ACTCAATGGC CTTTCCCAAC TCACCTACAC  4080
AAGTGGGAAC CCCACCAAGA GGCAGAGCCA GCTGATTGAC ACTCTGCAGC ACCAAGTGAA  4140
ATCTCTGGAG CAACAGCTGG CCGATGCTGA CAGACAGCAC CAAGAAGTAA TTGCAATTTA  4200
TCGGACACAC CTTCTTAGTG CTGCACAGGG TCACATGGAT GAAGATGTTC AGGAGGCTCT  4260
GCTCCAGATC ATACAAATGC GGCAGGGGCT TGTGTGCTAG CCGTTAGCAC TGACTGCCAG  4320
TATCTGTTTT ATCTTGCTGG TGCTGAACAT TCTTTGTGCA ACTCCATGGT CTTTCTGGGC  4380
CTTACTGTGC TGGTATAATT AAAATAAAAT ATATTTTGTT CTGGGTGT
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Seq ID NO: 446 Protein sequence
Protein Accession #: AAG49577.1

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LQYNCPTEHA DLQGRTALQK KAMADCPSSI QLLCDHGASV NAKDVKGRTP LVLATQMSRP   180
TICQLLIDRG ADVNSRDKQN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSSYYA   240
RIGDNLDILT LLKTASENTN KGRELWKKGP SLQQRNLTHM QDEVNVKSHQ REHQNIQDLE   300
IENEDLKERL RKIQQEQRIL LDKVNGLQLQ LNEEVMVADD LESEREKLKS LLAAKEKQHE   360
ESLRTIEALK NRFKYFESDH LGSGSHFSNR KEDMLLKQGQ MYMADSQCTS PGIPAHMQSR   420
SMLRPLELSL PSQTSYSENE ILKKELEAMR TFCESAKQDR LKLQNELAHK VAECKALALE   480
CERVKEDSDE QIKQLEDALK DVQKRMYESE GKVKQMQTHF LALKEHLTSE AASGNHRLTE   540
ELKDQLKDLK VKYEGASAEV GKLRNQIKQN EMIVEEFKRD EGKLIEENKR LQKELSMCEM   600
EREKKGRKVT EMEGQAKELS AKLALSIPAE KFENMKSSLS NEVNEKAKKL VEMEREHEKS   660
LSEIRQLKRE LENVKAKLAQ HVKPEEHEQV KSRLEQKSGE LGKKITELTL KNQTLQKEIE   720
KVYLDNKLLK EQAHNLTIEM KNHYVPLKVS EDMKKSHDAI IDDLNRKLLD VTQKYTEKKL   780
EMEKLLLEND SLSKDVSRLE TVFVPPEKHE KEIIALKSNI VELKKQLSEL KKKCGEDQEK   840
IHALTSENTN LKKMMSNQYV PVKTHEEVKM TLNDTLAKTN RELLDVKKKF EDINQEFVKI   900
KDKNEILKRN LENTQNQIKA EYISLAEHEA KMSSLSQSMR KVQDSNAEIL ANYRKGQEEI   960
VTLHAEIKAQ KKELDTIQEC IKVKYAPIVS FEECERKFKA TEKELKDQLS EQTQKYSVSE  1020
EEVKKNKQEN DKLKKEIFTL QKDLRDKTVL IEKSHEMERA LSRKTDELNK QLKDLSQKYT  1080
EVKNVKEKLV EENAKQTSEI LAVQNLLQKQ HVPLEQVEAL KKSLNGTIEN LKEELKSMQR  1140
CYEKEQQTVT KLHQLLENQK NSSVPLAEHL QIKEAFEKEV GIIKASLREK EEESQNKMEE  1200
VSKLQSEVQN TKQALKKLET REVVDLSKYK ATKSDLETQI SSLNEKLANL NRKYEEVCEE  1260
VLHAKKKEIS AKDEKELLHF SIEQEIKDQK ERCDKSLTTI TELQRRIQES AKQIEAKDNK  1320
ITELLNDVER LKQALNGLSQ LTYTSGNPTK RQSQLIDTLQ HQVKSLEQQL ADADRQHQEV  1380
IAIYRTHLLS AAQGHMDEDV QEALLQIIQM RQGLVC
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Seq ID NO: 447 DNA sequence
Nucleic Acid Accession #: NM_003020.1
Coding sequence: 29..664

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CCCTGACCGG GTCTCAGAAG CAGATATCCA GAGGCTGCTT CATGGTGTTA TGGAGCAATT   180
GGGCATTGCC AGGCCCCGAG TGGAATATCC AGCTCACCAG GCCATGAATC TTGTGGGCCC   240
CCAGAGCATT GAAGGTGGAG CTCATGAAGG ACTTCAGCAT TTGGGTCCTT TTGGCAACAT   300
CCCCAACATC GTGGCAGAGT TGACTGGAGA CAACATTCCT AAGGACTTTA GTGAGGATCA   360
GGGGTACCCA GACCCTCCAA ATCCCTGTCC TGTTGGAAAA ACAGATGATG GATGTCTAGA   420
AAACACCCCT GACACTGCAG AGTTCAGTCG AGAGTTCCAG TTGCACCAGC ATCTCTTTGA   480
TCCGGAACAT GACTATCCAG GCTTGGGCAA GTGGAACAAG AAACTCCTTT ACGAGAAGAT   540
GAAGGGAGGA GAGAGACGAA AGCGGAGGAG TGTCAATCCA TATCTACAAG GACAGAGACT   600
GGATAATGTT GTTGCAAAGA AGTCTGTCCC CCATTTTTCA GATGAGGATA ACGATCCAGA   660
GTAAAGAGAA GATGCTAGAC GAAAACCCAC ATTACCTGTT AGGCCTCAGC ATGGCTTATG   720
TGCACGTGTA AATGGAGTCC CTGTGAATGA CAGCATGTTT CTTACATAGA TAATTATGGA   780
TACAAAGCAG CTGTATGTAG ATAGTGTATT GTCTTCACAC CGATGATTCT GCTTTTTGCT   840
AAATTAGAAT AAGAGCTTTT TTGTTTCTTG GGTTTTTAAA ATGTGAATCT GCAATGATCA   900
TAAAAATTAA AATGTGAATG TCAACAATAA AAAGCAAGAC TATGAAAGGC TCAGATTTCT   960
TGCAGTTTAA AATGGTGTCT GAGGTTGTAC TATTTTGGCC AAGTCTGTAG AAAGCTGTCA  1020
TTTGATTTTG ATTATGTAGT TCATCCAGCC CTTGGGCATT GTTATACACC AGTAAAGAAG  1080
GCTGTACTCA AGAGGAGGAG CTGACACATT TCACTTGGCT GCGTCTTAAT AAACATGAAT  1140
GCAAGCATTG GC
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Seq ID NO: 448 Protein sequence
Protein Accession #: NP_003011.1

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1          11         21         31         41         51
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PAHQAMNLVG PQSIEGGAHE GLQHLGPFGN IPNIVAELTG DNIPKDFSED QGYPDPPNPC   120
PVGKTDDGCL ENTPDTAEFS REFQLHQHLF DPEHDYPGLG KWNKKLLYEK MKGGERRKRR   180
SVNPYLQGQR LDNVVAKKSV PHFSDEDKDP E
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Seq ID NO: 449 DNA sequence
Nucleic Acid Accession #: NM_003816.1
Coding sequence: 79..2538

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CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC   120
CGGTGGTTGC TGTTGCTTGG CCTGGTGGGC CCAGTCCTCG GTGCGGCGCG GCCAGGCTTT   180
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CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTTGGAGATT AACTAGAGAA   240
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AAAGAGCATA TTATTCACTT GGAAAGGAAC AAAGACCTTT TGCCTGAAGA TTTTGTGGTT   360
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CATTATCGGG GCTATGTGGA GGGAGTTCAT AATTCATCCA TTGCTCTTAG CGACTGTTTT   480
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CCCAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGGTATGTG   720
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GGGATGGTTA ACGAAGGCAC AAAATGTGGT GCTGGAAAGA TCTGTAGAAA CTTCCAGTGT  1980
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CATGAATAAG CAAATATTGT CTTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCATA  3120
TTATTTTGAA AGTACAAAAT ATACTAAAAG AGTGTGTGTG TATTCACGCA GTTACTCGCT  3180
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GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTCGTT CACAATAGCA CTATTTTAAA  3300
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CTTGAGAATT TCATGAGCAC TTTAAAATCT GAACTTTCAA AGCTTGCTAT TAAATCATTT  3480
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AAAGTTTAAT AATAGGTTTA TTAACTGAAT TTCATTAGTT TTTTAAAAGT GTTTTTGGTT  3780
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AAAAAAAAAA AAAAAAAAAA AAAAA
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Seq ID NO: 450 Protein sequence
Protein Accession #: NP_003807.1

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EGVHNSSIAL SDCFGLRGLL HLENASYGIE PLQNSSHFEH IIYRMDDVYK EPLKCGVSNK   180
DIEKETAKDE EEEPPSMTQL LRRRRAVLPQ TRYVELFIVV DKERYDMMGR NQTAVREEMI   240
LLANYLDSMY IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS   300
AQLVLKKGFG GTAGMAFVGT VCSRSHAGGI NVFGQITVET FASIVAHELG HNLGMNHDDG   360
RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTLNKGGN CLLNIPKPDE AYSAPSCGNK   420
LVDAGEECDC GTPKECELDP CCEGSTCKLK SPAECAYGDC CKDCRFLPGG TLCRGKTSEC   480
DVPEYCNGSS QFCQPDVFIQ NGYPCQNNKA YCYNGMCQYY DAQCQVIFGS KAKAAPKDCF   540
IEVNSKGDRF GNCGFSGNEY KKCATGNALC GKLQCENVQE IPVFGIVPAI IQTPSRGTKC   600
WGVDFQLGSD VPDPGMVNEG TKCGAGKICR NFQCVDASVL NYDCDVQKKC HGHGVCNSNK   660
NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL VFFFLIVPLI VCAIFIFIKR   720
DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSPV TPPREVPIYA NRFAVPTYAA   780
KQPQQFPSRP PPPQPKVSSQ GNLIPARPAP APPLYSSLT
```

Seq ID NO: 451 DNA sequence
Nucleic Acid Accession #: NM_016650.1
Coding sequence: 196..789

```
1          11         21         31         41         51
|          |          |          |          |          |
GGTTTCAATA TATGCAGATG TCTCGATATA GGAATGAAAT TACGTCTTTG GAACAACTTA    60
AATAAGTCAA ATATACTTGG AGCTTTAAAA ATTAAAAGGA GAGAGATTCG AGCACCTTTT   120
CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGGTGTG   180
CCCCAGCTGG GAAACATGGC TGTCATACAT TCACATCTGT GGAAAGGATT GCAAGAGAAG   240
TTCTTGAAGG GAGAACCCAA AGTCCTTGGG GTTGTGCAGA TTCTGACTGC CCTGATGAGC   300
CTTAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCCTATT   360
TCCGTGCATA TCGGGTACAC AATTTGGGGG TCAGTAATGT TTATTATTTC AGGATCCTTG   420
TCAATTGCAG CAGGAATTAG AACTACAAAA GGCCTGGTCC GAGGTAGTCT AGGAATGAAT   480
ATCACCAGCT CTGTACTGGC TGCATCAGGG ATCTTAATCA ACACATTTAG CTTGGCGTTT   540
TATTCATTCC ATCACCCTTA CTGTAACTAC TATGGCAACT CAAATAATTG TCATGGGACT   600
ATGTCCATCT TAATGGGTCT GGATGGCATG GTGCTCCTCT TAAGTGTGCT GGAATTCTGC   660
ATTGCTGTGT CCCTCTCTGC CTTTGGATGT AAAGTGCTCT GTTGTACCCC TGGTGGGGTT   720
GTGTTAATTC TGCCATCACA TTCTCACATG GCAGAAACAG CATCTCCCAC ACCACTTAAT   780
GAGGTTTGAG GCCAACAAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG   840
ACACAAGAGC CTCACATGAG AAATTACCAG TATCCAACTT CGATACTGAT AGACGTGTTG   900
ATATTATTAT TATATGTAAT CCAATTATGA ACTGTGTGTG TATAGAGAGA TAATAAATTC   960
AAAATTATGT TCTCATTTTT TTCCCTGGAA CTCAATAACT CACTTCACTG GCTCTTTATC  1020
GAGAGTACTA GGAGTTAAAT TAATAAATAA TGCATTTAAT GAGGCCACAG GAAAAA
```

Seq ID NO: 452 Protein sequence
Protein Accession #: NP_057734.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAVIHSHLWK GLQEKFLKGE PKVLGVVQIL TALMSLSMGI TMMCMASNTY GSNPISVHIG    60
YTIWGSVMFI ISGSLSIAAG IRTTKGLVRG SLGMNITSSV LAASGILINT FSLAFYSFHH   120
PYCNYYGNSN NCHGTMSILM GLDGMVLLLS VLEFCIAVSL SAFGCKVLCC TPGGVVLILP   180
SHSHMAETAS PTPLNEV
```

Seq ID NO: 453 DNA sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..503

```
1          11         21         31         41         51
|          |          |          |          |          |
AGTCTCTGCT CTTCCCAGCC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GGACCATGCG    60
CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCCTC TGCCTAGCGC CCCGGGGGCG   120
AGCGGTCCCG CTGCCTGCGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA   180
CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC   240
TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG   300
GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA   360
GGCCTTGGGC AATCAGCAGC CTTCGTGGGA TTCAGAGGAT AGCAGCAACT TCAAAGATGT   420
AGGTTCAAAA GGCAAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA   480
CCCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC   540
TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA   600
AAATATTTGA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT   660
CTTCTGGTTT AAACTTGTTT GCTGTGAACA ATTGTCGAAA AGAGTCTTCC AATTAATGCT   720
TTTTTATATC TAGGCTACCT GTTGGTTAGA TTCAAGGCCC CGAGCTGTTA CCATTCACAA   780
TAAAAGCTTA AACACAT
```

Seq ID NO: 454 Protein sequence
Protein Accession #: NP_002082.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTKMYPR GNHWAVGHLM GKKSTGESSS    60
VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQQPS WDSEDSSNFK   120
DVGSKGKVGR LSAPGSQREG RNPQLNQQ
```

Seq ID NO: 455 DNA sequence
Nucleic Acid Accession #: NM_016522.1
Coding sequence: 265..1299

```
1          11         21         31         41         51
|          |          |          |          |          |
GCGGAAGCAG CGAGGAGGGA GCCCCCTTTG GCCGTCCTCC GTGGAACCGG TTTTCCGAGG    60
CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC   120
TTTTCTCCTC CCCGCGCCTC CCGGTCGCCG CGGGTTCACC GCTCAGTCCC CGCGCTCGCT   180
CCGCACCCCA CCCACTTCCT GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG CTGCCGGAGT   240
TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCCT GCCCTGGAAG   300
TGCCTCGTGG TCGTGTCTCT CAGGCTGCTG TTCCTTGTAC CCACAGGAGT GCCCGTGCGC   360
AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAACGTGA CGGTCCGGCA GGGGGAGAGC   420
GCCACCCTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCCTGGCT AAACCGCAGC   480
ACCATCCTCT ATGCTGGGAA TGACAAGTGG TGCCTGGATC CTCGCGTGGT CCTTCTGAGC   540
AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT   600
TACACCTGCT CGGTGCAGAC AGACAACCAC CCAAAGACCT CTAGGGTCCA CCTCATTGTG   660
CAAGTATCTC CCAAAATTGT AGAGATTTCT TCAGATATCT CCATTAATGA AGGGAACAAT   720
ATTAGCCTCA CCTGCATAGC AACTGGTAGA CCAGAGCCTA CGGTTACTTG GAGACACATC   780
```

```
TCTCCCAAAG CGGTTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC   840
CGGGAACAGT CAGGGGACTA CGAGTGCAGT GCCTCCAATG ACGTGGCCGC GCCCGTGGTA   900
CGGAGAGTAA AGGTCACCGT GAACTATCCA CCATACATTT CAGAAGCCAA GGGTACAGGT   960
GTCCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA  1020
TTCCAGTGGT ACAAGGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA  1080
AACAGACCTT TCCTCTCAAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC  1140
TACACTTGCG TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTTGGT  1200
CCAGGCGCCG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG  1260
CTGCCTCTTC TGGTCTTGCA CCTGCTTCTC AAATTTTGAT GTGAGTGCCA CTTCCCCACC  1320
CGGGAAAGGC TGCCGCCACC ACCACCACCA ACACAACAGC AATGGCAACA CCGACAGCAA  1380
CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA  1440
GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAAATTG  1500
CCTTGCAGAT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA  1560
CCCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG  1620
GGCTCAGCCT CTCTGCCCAC AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC  1680
AAATTCAATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT  1740
CCGGCCCAAG CGTGGCGCTG CGGGCACTTT GGTAGACTGT GCCACCACGG CGTGTGTTGT  1800
GAAACGTGAA ATAAAAAGAG CAAAAAAAAA AAAAAAAAA
```

Seq ID NO: 456 Protein sequence
Protein Accession #: NP_057606.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGVCGYLFLP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID    60
NRVTRVAWLN RSTILYAGND KWCLDPRVVL LSNTQTQYSI EIQNVDVYDE GPYTCSVQTD   120
NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCIAT GRPEPTVTWR HISPKAVGFV   180
SEDEYLEIQG ITREQSGDYE CSASNDVAAP VVRRVKVTVN YPPYISEAKG TGVPVGQKGT   240
LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VENRPFLSKL IFFNVSEHDY GNYTCVASNK   300
LGHTNASIML FGPGAVSEVS NGTSRRAGCV WLLPLLVLHL LLKF
```

Seq ID NO: 457 DNA sequence
Nucleic Acid Accession #: NM_012261.1
Coding sequence: 203..1045

```
1          11         21         31         41         51
|          |          |          |          |          |
GATTTGCTCT GCCAGCAGCT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC    60
ACAGAATACG CGCTCCCTCC CTCCCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC   120
CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG   180
CCTCATTCGG GGCACTGCGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG   240
ACTTCGAGTT CTCCTGATGT TGTTCCATAC AATGGCTCAA ATCATGGCAG AACAAGAAGT   300
GGAAAATCTC TCAGGCCTTT CCACTAACCC TGAAAAAGAT ATATTTGTGG TGCGGGAAAA   360
TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG   420
GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCCGAT ATCGCATTGA CCCGGGGAGC   480
TGAGGTGAAG GGCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTTCT GGGTGGATCG   540
CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA   600
GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT   660
CAAAGACGCA GTCAGTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT   720
CACCCCCGCT GGGAAGTCCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG   780
TGATCCGCAG AAGACGGTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTTGACAT   840
TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT   900
GGAAGAAACC TTGCCCCTGA TTTTGGGGCT CATCTTGGGC CTCGTCATCA TGGTAACACT   960
CGCGATTTAC CACGTCCACC ACAAAATGAC TGCCAACCAG GTGCAGATCC CTCGGGACAG  1020
ATCCCAGTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCCTAT TCCTGCTCCC  1080
CCAACTGGAT CAGGTAGAAC AACAAAAGCA CTTTTCCATC TTGTACACGA GATACACCAA  1140
CATAGCTACA ATCAAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA  1200
AACCCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC  1260
ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT  1320
TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA  1380
TTGAAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCTT  1440
TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC  1500
TCATGCTCCC TGCAGCAAGA CCCCTGAAAG TGATTCATGC TTCTGGCTGG CATTCTGCAT  1560
GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG  1620
AAAACGACTA ATGTAACTAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC  1680
GGGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AAACACACTA  1740
TTCTCTGGC
```

Seq ID NO: 458 Protein sequence
Protein Accession #: NP_036393.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA    60
EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELQVFW VDRAYALKML   120
FVKESHNMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY   180
ECQAQQTISL ASSDPQKTVT MILSAVHIQP FDIISDFVFS EEHKCPVDER EQLEETLPLI   240
LGLILGLVIM VTLAIYHVHH KMTANQVQIP RDRSQYKHMG
```

Seq ID NO: 459 DNA sequence
Nucleic Acid Accession #: NM_001169.1
Coding sequence: 85..870

```
1          11         21         31         41         51
```

```
TAGGAGATAA GAGTATCTTG CACAGCAGGT GCAGGTTTCC CAGCAGCTCA GGCAAGAGTC    60
CGATGTTTGT GCCATCTGAT CCTGATGTCT GGAGAGATAG CCATGTGTGA GCCTGAATTT   120
GGCAATGACA AGGCCAGGGA GCCGAGCGTG GGTGGCAGGT GGCGAGTGTC CTGGTACGAA   180
CGGTTTGTGC AGCCATGTCT GGTCGAACTG CTGGGCTCTG CTCTCTTCAT CTTCATCGGG   240
TGCCTGTCGG TCATTGAGAA TGGGACGGAC ACTGGGCTGC TGCAGCCGGC CCTGGCCCAC   300
GGGCTGGCTT TGGGGCTCGT GATTGCCACG CTGGGGAATA TCAGTGGTGG ACACTTCAAC   360
CCTGCGGTGT CCCTGGCAGC CATGCTGATC GGAGGCCTCA ACCTGGTGAT GCTCCTCCCG   420
TACTGGGTCT CACAGCTGCT CGGGGGGATG CTCGGGGCTG CCTTGGCCAA GGTGGTGAGT   480
CCTGAGGAGA GGTTCTGGAA TGCATCTGGG GCGGCCTTTG TGACAGTCCA GGAGCAGGGG   540
CAGGTGGCAG GGGCGTTGGT GGCAGAGATC ATCCTGACGA CGCTGCTGGC CCTGGCTGTA   600
TGCATGGGTG CCATCAATGA GAAGACAAAG GGCCCTCTGG CCCCGTTCTC CATCGGCTTT   660
GCCGTCACCG TGGATATCCT GGCTGGGGGC CCTGTGTCTG GAGGCTGCAT GAATCCCGCC   720
CGTGCTTTTG GACCTGCGGT GGTGGCCAAC CACTGGAACT TCCACTGGAT CTACTGGCTG   780
GGCCCACTCC TGGCTGGCCT GCTTGTTGGA CTGCTCATTA GGTGCTTCAT TGGAGATGGG   840
AAGACCCGCC TCATCCTGAA GGCTCGGTGA GCAGAGCTCG TGGGATTCCT GCTGCTCCAG   900
GTGTCCTCAG CTCACCTGTC CCAGACTGAG GACAGGGGAG TTCCTGCATT TCCTGCCAGG   960
GCAGAGGCCC AGAGGAGCGA CCCCCTGCTT CCACTGCTTG GGCCTGCTTT CTCAGATAGA  1020
CTGACTGCTG AGGAGGCTCT AGGTTCTTGG AATTCCTTTG TGCTCATCAG AGACCCCAGC  1080
CTGGGGAACA CGCTGCCCGC ACTGCCCAGA GAGCAGTGCA AACACCACAA CACGAGCGTG  1140
TTTCTTGAGA GGAATGTCCC CGAGTTGGAC AAGGAGGCTG TTTCTGCACA TCAGCTCATT  1200
TCCCGCACCC CATTTCTTGC TTGATTGCTT TGTTGGGGGC CTGGCCACTT CCTTGCTTCT  1260
CAAGCTGACA ATTCTCACTT TGCAATAAAT AGTCCAGTGT TTCCTTCAT
```

Seq ID NO: 460 Protein sequence
Protein Accession #: NP_001160.1

```
MSGEIAMCEP EFGNDKAREP SVGGRWRVSW YERFVQPCLV ELLGSALFIF IGCLSVIENG    60
TDTGLLQPAL AHGLALGLVI ATLGNISGGH FNPAVSLAAM LIGGLNLVML LPYWVSQLLG   120
GMLGAALAKV VSPEERFWNA SGAAFVTVQE QGQVAGALVA EIILTTLLAL AVCMGAINEK   180
TKGPLAPFSI GFAVTVDILA GGPVSGGCMN PARAFGPAVV ANHWNFHWIY WLGPLLAGLL   240
VGLLIRCFIG DGKTRLILKA R
```

Seq ID NO: 461 DNA sequence
Nucleic Acid Accession #: NM_003226.1
Coding sequence: 2..226

```
GATGCTGGGG CTGGTCCTGG CCTTGCTGTC CTCCAGCTCT GCTGAGGAGT ACGTGGGCCT    60
GTCTGCAAAC CAGTGTGCCG TGCCGGCCAA GGACAGGGTG GACTGCGGCT ACCCCCATGT   120
CACCCCCAAG GAGTGCAACA ACCGGGGCTG CTGCTTTGAC TCCAGGATCC CTGGAGTGCC   180
TTGGTGTTTC AAGCCCCTGA CTAGGAAGAC AGAATGCACC TTCTGAGGCA CCTCCAGCTG   240
CCCCTGGGAT GCAGGCTGAG CACCCTTGCC CGGCTGTGAT TGCTGCCAGG CACTGTTCAT   300
CTCAGTTTTT CTGTCCCTTT GCTCCCGGCA AGCTTTCTGC TGAAAGTTCA TATCTGGAGC   360
CTGATGTCTT AACGAATAAA GGTCCCATGC TCCACCCG
```

Seq ID NO: 462 Protein sequence
Protein Accession #: NP_003217.1

```
MLGLVLALLS SSSAEEYVGL SANQCAVPAK DRVDCGYPHV TPKECNNRGC CFDSRIPGVP    60
WCFKPLTRKT ECTF
```

Seq ID NO: 463 DNA sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

```
GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC    60
ACTATGAGCC TCCCGTCCAG CCGCGCGGCC CGTGTCCCGG GTCCTTCGGG CTCCTTGTGC   120
GCGCTGCTCG CGCTGCTGCT CCTGCTGACG CCGCCGGGGC CCCTCGCCAG CGCTGGTCCT   180
GTCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTTTAC GCGTTACGCT GAGAGTAAAC   240
CCCAAAACGA TTGGTAAACT GCAGGTGTTC CCCGCAGGCC CGCAGTGCTC CAAGGTGGAA   300
GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA   360
AAGAAAGTCA TCCAGAAAAT TTTGGACAGT GGAAACAAGA AAAACTGAGT AACAAAAAAG   420
ACCATGCATC ATAAAATTGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC   480
CAGTAAGAAT AAGAAGGAAG GGTTGGTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT   540
GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA   600
CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCTTTGG   660
CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT   720
TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCTTACCGAA AAGGCTGTGG   780
ATTTCGTATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTTGTTCTT   840
ACTCACTCTT CTCATAAAAT AGGAAATATT TTAGTTCTGT TTTCTTGGGG AATATGTTAC   900
TCTTTACCCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACTGGGTG TGTCATACCG   960
TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG  1020
CTAATATATT CTCTTCCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT  1080
CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACTATAG GATGACTATA  1140
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ATTCTGGTCA CTAAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC  1200
TGATTGCTAA TTTACATAGA AATGTATTCT CTTGGTTTTT TAAATAAAAG CAAAATTAAC  1260
AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT  1320
CATTTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT  1380
TTTAAAGGTT TTGACCATTT TGTTATGAGG AATTATACAT GTATCACATT CACTATATTA  1440
AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCATT  1500
TGGAGAAACA ATAAAAGATT TCTAAACCAA AAAAAAAAAA AAAAAAA
```

Seq ID NO: 464 Protein sequence
Protein Accession #: NP_002984.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSLPSSRAAR VPGPSGSLCA LLALLLLLTP PGPLASAGPV SAVLTELRCT CLRVTLRVNP    60
KTIGKLQVFP AGPQCSKVEV VASLKNGKQV CLDPEAPFLK KVIQKILDSG NKKN
```

Seq ID NO: 465 DNA sequence
Nucleic Acid Accession #: NM_002038.2
Coding sequence: 108..500

```
1          11         21         31         41         51
|          |          |          |          |          |
GAACCGTTTA CTCGCTGCTG TGCCCATCTA TCAGCAGGCT CCGGGCTGAA GATTGCTTCT    60
CTTCTCTCCT CCAAGGTCTA GTGACGGAGC CCGCGCGCGG CGCCACCATG CGGCAGAAGG   120
CGGTATCGCT TTTCTTGTGC TACCTGCTGC TCTTCACTTG CAGTGGGGTG GAGGCAGGTA   180
AGAAAAAGTG CTCGGAGAGC TCGGACAGCG GCTCCGGGTT CTGGAAGGCC CTGACCTTCA   240
TGGCCGTCGG AGGAGGACTC GCAGTCGCCG GGCTGCCCGC GCTGGGCTTC ACCGGCGCCG   300
GCATCGCGGC CAACTCGGTG GCTGCCTCGC TGATGAGCTG GTCTGCGATC CTGAATGGGG   360
GCGGCGTGCC CGCCGGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGGCAGCA   420
GCGTCGTCAT AGGTAATATT GGTGCCCTGA TGGGCTACGC CACCCACAAG TATCTCGATA   480
GTGAGGAGGA TGAGGAGTAG CCAGCAGCTC CCAGAACCTC TTCTTCCTTC TTGGCCTAAC   540
TCTTCCAGTT AGGATCTAGA ACTTTGCCTT TTTTTTTTTT TTTTTTTTTT TTTGAGATGG   600
GTTCTCACTA TATTGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC   660
ACTGCAGCCT CCAACTCCTA GCCTCAAGTG ATCCTCCTGT CTCAACCTCC CAAGTAGGAT   720
TACAAGCATG CGCCGACGAT GCCCAGAATC CAGAACTTTG TCTATCACTC TCCCCAACAA   780
CCTAGATGTG AAAACAGAAT AAACTTCACC CAGAAAA
```

Seq ID NO: 466 Protein sequence
Protein Accession #: NP_002029.3

```
1          11         21         31         41         51
|          |          |          |          |          |
MRQKAVSLFL CYLLLFTCSG VEAGKKKCSE SSDSGSGFWK ALTFMAVGGG LAVAGLPALG    60
FTGAGIAANS VAASLMSWSA ILNGGGVPAG GLVATLQSLG AGGSSVVIGN IGALMGYATH   120
KYLDSEEDEE
```

Seq ID NO: 467 DNA sequence
Nucleic Acid Accession #: NM_003469.2
Coding sequence: 92..1945

```
1          11         21         31         41         51
|          |          |          |          |          |
GAAACGGCCC GAGAAGCTCG CCCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC    60
CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG   120
AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT   180
TCAGAGAAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAAAATG TCCAAAAGTT   240
TCCCAGTCCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAAGCTCA   300
TAAGGAAGAA AGCAGCCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA   360
AAAAGAAAAT GGCGATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG   420
GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCACCAAA   480
AGAAAATAAG CCCTATGCCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA   540
TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA   600
TGAAGAGAAT TCCAGGGATA ACCCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA   660
TACTCCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG   720
ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACTTTATA CGGATGATGA   780
AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG   840
GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAAGA   900
GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT   960
CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT  1020
AATTGCCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA  1080
AAATGGGGAA AGGGCCACCA GGCTTTTTGA GAAACCTCTT GATTCTCAGT CTATTTATCA  1140
GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCCAGAA GACTTAATTG AGATGCTCAA  1200
AACTGGGGAG AAGCCGAATG GATCAGTGGA ACCGGAGCGG GAGCTTGACC TTCCTGTTGA  1260
CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT  1320
CTCCAAGAGT GGCTACCCTA AAACACCTGG TCGTGCTGGG ACTGAGGCCC TACCAGACGG  1380
GCTCAGTGTT GAGGATATTT TAAATCTTTT AGGGATGGAG AGTGCAGCAA ATCAGAAAAC  1440
GTCGTATTTT CCCAATCCAT ATAACCAGGA GAAAGTTCTG CCAAGGCTCC CTTATGGTGC  1500
TGGAAGATCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCCACATG TTGAAAACAG  1560
ACAGATGGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG  1620
GATGCTAGTT AAATACCCTG AGATCATTAA TTCAAACCAA GTGAAGCGAG TTCCTGGTCA  1680
AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAAGAGCA  1740
TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC  1800
TGTGGGGCCC CCGAAGAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT  1860
AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC  1920
```

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TAAGAGAGCA ATGGAAAATA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCCTCC  1980
CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTTGA CTTCTATCCT GTTAACACTG  2040
TAATATCTTT AAATGATGTA CAGGCAGATG AAACCAGGTC ACTGGGGAGT CTGCTTCATT  2100
TCCTCTGAGC TGTTATCTTG TGTATGGATA TGTGTAAATG TTATGACTCC TTGATAAAAA  2160
ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT  2220
GGCTGTGGCA TTGTTGATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG  2280
TTTTTAATAT TTATTGAATT ATTTTGTTAC TGTCTGTAGC GTTTTGTGGA GTACTGGACC  2340
AAAAAAATAA AGCATTATAA ATATA
```

Seq ID NO: 468 Protein sequence
Protein Accession #: NP_003460.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAEAKTHWLG AALSLIPLIF LISGAEAASF QRNQLLQKEP DLRLENVQKF PSPEMIRALE    60
YIENLRQQAH KEESSPDYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ   120
AENEPQSAPK ENKPYALNSE KNFPMDMSDD YETQQWPERK LKHMQFPPMY EENSRDNPFK   180
RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EEQKLYTDDE DDIYKANNIA   240
YEDVVGGEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSGQLGI QEEDLRKESK   300
DQLSDDVSKV IAYLKRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRNLQI   360
PPEDLIEMLK TGEKPNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKTPG   420
RAGTEALPDG LSVEDILNLL GMESAANQKT SYFPNPYNQE KVLPRLPYGA GRSRSNQLPK   480
AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPGQ GSSEDDLQEE   540
EQIEQAIKEH LNQGSSQETD KLAPVSKRFP VGPPKNDDTP NRQYWDEDLL MKVLEYLNQE   600
KAEKGREHIA KRAMENM
```

Seq ID NO: 469 DNA sequence
Nucleic Acid Accession #: NM_006398.1
Coding sequence: 19..516

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCCCCTTGT CTGCAGAGAT GGCTCCCAAT GCTTCCTGCC TCTGTGTGCA TGTCCGTTCC    60
GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA   120
GAACATGTCC GGTCTAAGAC CAAGGTTCCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC   180
AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC   240
CACCTTACCC TGAAAGTGGT GAAGCCCAGT GATGAGGAGC TGCCCTTGTT TCTTGTGGAG   300
TCAGGTGATG AGGCAAAGAG GCACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGGCACAA   360
GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC   420
AATGGAAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC   480
TTACTCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTTGGC   540
AGGGGTCAAA AAGCTTATTT CTTTTAATCT CTTACTCAAC GAACACATCT TCTGATGATT   600
TCCCAAAATT AATGAGAATG AGATGAGTAG AGTAAGATTT GGGTGGGATG GGTAGGATGA   660
AGTATATTGC CCAACTCTAT GTTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT   720
TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTTAA GGCAAAATAG AGCATTC
```

Seq ID NO: 470 Protein sequence
Protein Accession #: NP_006389.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAPNASCLCV HVRSEEWDLM TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR    60
RSLSSYGIDK EKTIHLTLKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE   120
TKTGIIPETQ IVTCNGKRLE DGKMMADYGI RKGNLLFLAS YCIGG
```

Seq ID NO: 471 DNA sequence
Nucleic Acid Accession #: XM_094741.1
Coding sequence: 1..948

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGAAGGCCA ACTACAGCGC AGAGGAGCGC TTTCTCCTGC TGGGTTTCTC CGACTGGCCT    60
TCCCTGCAGC CGGTCCTCTT CGCCCTTGTC CTCCTGTGCT ACCTCCTGAC CTTGACGGGC   120
AACTCGGCGC TGGTGCTGCT GGCGGTGCGC GACCCGCGCC TGCACACGCC CATGTACTAC   180
TTCCTCTGCC ACCTGGCCTT GGTAGACGCG GGCTTCACTA CTAGCGTGGT GCCGCCGCTG   240
CTGGCCAACC TGCGCGGACC AGCGCTCTGG CTGCCGCGCA GCCACTGCAC GGCCCAGCTG   300
TGCGCATCGC TGGCTCTGGG TTCGGCCGAA TGCGTCCTCC TGGCGGTGAT GGCTCTGGAC   360
CGCGCGGCCG CAGTGTGCCG CCCGCTGCGC TATGCGGGGC TCGTCTCCCC GCGCCTATGT   420
CGCACGCTGG CCAGCGCCTC CTGGCTAAGC GGCCTCACCA ACTCGGTTGC GCAAACCGCG   480
CTCCTGGCTG AGCGGCCGCT GTGCGCGCCC CGCCTGCTGG ACCACTTCAT CTGTGAGCTG   540
CCGGCGTTGC TCAAGCTGGC CTGCGGAGCC GACGGAGACA CTACCGAGAA CCAGATGTTC   600
GCCGCCCGCG TGGTCATCCT GCTGCTGCCG TTTGCCGTCA TCCTGGCCTC CTACGGTGCC   660
GTGGCCCGAG CTGTCTGTTG CATGCGGTTC AGCGGAGGCC GGAGGAGGGC GGTGGGCACG   720
TGTGGGTCCC ACCTGACAGC CGTCTGCCTG TTCTACGGCT CGGCCATCTA CACCTACCTG   780
CAGCCCGCGC AGCGCTACAA CCAGGCACGG GGCAAGTTCG TATCGCTCTT CTACACCGTG   840
GTCACACCTG CTCTCAACCC GCTCATCTAC ACCCTCAGGA ATAAGAAAGT GAAGGGGGCA   900
GCGAGGAGGC TGCTGCGGAG TCTGGGGAGA GGCCAGGCTG GGCAGTGA
```

Seq ID NO: 472 Protein sequence
Protein Accession #: XP_094741.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKANYSAEER FLLLGFSDWP SLQPVLFALV LLCYLLTLTG NSALVLLAVR DPRLHTPMYY    60
```

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FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASLALGSAE CVLLAVMALD   120
RAAAVCRPLR YAGLVSPRLC RTLASASWLS GLTNSVAQTA LLAERPLCAP RLLDHFICEL   180
PALLKLACGG DGDTTENQMF AARVVILLLP FAVILASYGA VARAVCCMRF SGGRRRAVGT   240
CGSHLTAVCL FYGSAIYTYL QPAQRYNQAR GKFVSLFYTV VTPALNPLIY TLRNKKVKGA   300
ARRLLRSLGR GQAGQ
```

Seq ID NO: 473 DNA sequence
Nucleic Acid Accession #: NM_001062.1
Coding sequence: 76..1380

```
1          11         21         31         41         51
|          |          |          |          |          |
GCTCTCATTA CCTTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG    60
TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT   120
TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC   180
CTAAAACCTC TGTTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC   240
AATGTTGTGT TGTCCCTCAA ACTTGTTGGA ATCCAGATCC AAACCCTGAT GCAAAAGATG   300
ATCCAACAAA TCAAATACAA TGTGAAAAGC AGATTGTCAG ATGTAAGCTC GGGAGAGCTT   360
GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACTT AATATATGAT   420
TACCACCTGA CTGACAAGCT AGAAAATAAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA   480
CACAATGGCA CTCCCCTGAC TAACTACTAC CAGCTCAGCC TGGACGTTTT GGCCTTGTGT   540
CTGTTCAATG GGAACTACTC AACCGCCGAA GTTGTCAACC ACTTCACTCC TGAAAATAAA   600
AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG   660
ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG   720
AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAAT   780
GGTCTCATTG GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA   840
GACTATTATA ATGAAAATGA CTGGAATTGC CAACAAACTC TGAATACAGT GCTCACGGAA   900
ATTTCTCAAG GAGCATTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG   960
GGAAAGACCT TCTTGGATAT TAACAAAGAC TCTTCTTGCG TCTCTGCTTC AGGTAACTTC  1020
AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC  1080
GTCAATTACT CTGTGAGAAT CAATGAAACA TATTTCACCA ATGTCACTGT GCTAAATGGT  1140
TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC  1200
ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACCTGTA TTCAGGGCCT ATGTGCCAAC  1260
AATAATGACA GAACCTACTG GGAACTTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT  1320
GGTAGTTACG TTGTCCGCAA TGGAGAAAAC TTGGAGGTTC GCTGGAGCAA ATACTAATAA  1380
GCCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCCATG TTTATTGTCC  1440
TTATGCCTTC TTCTTCATTT ATCCCAGTAC GAGCAGGAGA GTTAATAACC TCCCCTTCTC  1500
TCTCTACATG TTCAATAAAA GTTGTTGAAA GATTAAC
```

Seq ID NO: 474 Protein sequence
Protein Accession #: NP_001053.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRQSHQLPLV GLLLFSFIPS QLCEICEVSE ENYIRLKPLL NTMIQSNYNR GTSAVNVVLS    60
LKLVGIQIQT LMQKMIQQIK YNVKSRLSDV SSGELALIIL ALGVCRNAEE NLIYDYHLTD   120
KLENKFQAEI ENMEAHNGTP LTNYYQLSLD VLALCLFNGN YSTAEVVNHF TPENKNYYFG   180
SQFSVDTGAM AVLALTCVKK SLINGQIKAD EGSLKNISIY TKSLVEKILS EKKENGLIGN   240
TFSTGEAMQA LFVSSDYYNE NDWNCQQTLN TVLTEISQGA FSNPNAAAQV LPALMGKTFL   300
DINKDSSCVS ASGNFNISAD EPITVTPPDS QSYISVNYSV RINETYFTNV TVLNGSVFLS   360
VMEKAQKMND TIFGFTMEER SWGPYITCIQ GLCANNNDRT YWELLSGGEP LSQGAGSYVV   420
RNGENLEVRW SKY
```

Seq ID NO: 475 DNA sequence
Nucleic Acid Accession #: NM_004852.1
Coding sequence: 89..1546

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1          11         21         31         41         51
|          |          |          |          |          |
GCCCCCGCCC GCCCCGGGCC CTGATGGACT GAATGAAGGC TGCCTACACC GCCTATCGAT    60
GCCTCACCAA AGACCTAGAA CGTGCGCCAT GAACCCGGAG CTGACAATGG AAAGTCTGGG   120
CACTTTGCAC GGCGCGCGCG GCGGCGGCAG TGGCGGGGGC GGCGGCGGGG GCGGCGGGGG   180
CGGCGGCGGG GGCCCGGGCC ATGAGCAGGA GCTGCTGGCC AGCCCCAGCC CCCACCACGC   240
GCGCCGCGGC CCGCGTGGCT CGCTGCGGGG CCCTCCGCCG CCTCCAACCG CGCACCAGGA   300
GCTGGGCACG GCGGCAGCGG CGGCAGCGGC GGCGTCGCGC TCGGCCATGG TCACCAGCAT   360
GGCCTCGATC CTGGACGGCG GCGACTACCG GCCCGAGCTC TCCATCCCGC TGCACCACGC   420
CATGAGCATG TCCTGCGACT CGTCTCCGCC TGGCATGGGC ATGAGCAACA CCTACACCAC   480
GCTGACACCG CTCCAGCCGC TGCCACCCAT CTCCACCGTG TCTGACAAGT TCCACCACCC   540
TCACCCGCAC CACCATCCGC ACCACCACCA CCACCACCAC CACCAGCGCC TGTCCGGCAA   600
CGTCAGCGGC AGCTTCACCC TCATGCGCGA CGAGCGCGGG CTCCCGGCCA TGAACAACCT   660
CTACAGTCCC TACAAGGAGA TGCCCGGCAT GAGCCAGAGC CTGTCCCCGC TGGCCGCCAC   720
GCCGCTGGGC AACGGGCTAG GCGCCTCCA CAACGCGCAG CAGAGTCTGC CCAACTACGG   780
TCCGCCGGGC CACGACAAAA TGCTCAGCCC CAACTTCGAC GCGCACCACA CTGCCATGCT   840
GACCCGCGGT GAGCAACACC TGTCCCGCGG CCTGGGCACC CCACCTGCGG CCATGATGTC   900
GCACCTGAAC GGCCTGCACC ACCCGGGCCA CACTCAGTCT CACGGGCCGG TGCTGGCACC   960
CAGTCGCGAG CGGCCACCCT CGTCCTCATC GGGCTCGCAG GTGGCCACGT CGGGCCAGCT  1020
GGAAGAAATC AACACCAAAG AGGTGGCCCA GCGCATCACA GCGGAGCTGA AGCGCTACAG  1080
TATCCCCCAG GCGATCTTTG CGCAGAGGGT GCTGTGCCGG TCTCAGGGGA CTCTCTCCGA  1140
CCTGCTCCGG AATCCAAAAC CGTGGAGTAA ACTCAAATCT GGCAGGGAGA CCTTCCGCAG  1200
GATGTGGAAG TGGCTTCAGG AGCCCGAGTT CCAGCGCATG TCCGCCTTAC GCCTGGCAGC  1260
GTGCAAACGC AAAGAGCAAG AACCAAACAA AGACAGGAAC AATTCCCAGA AGAAGTCCCG  1320
CCTGGTGTTC ACTGACCTCC AACGCCGAAC ACTCTTCGCC ATCTTCAAGG AGAACAAACG  1380
CCCGTCAAAG GAGATGCAGA TCACCATTTC CCAGCAGCTG GGCCTGGAGC TCACAACCGT  1440
CAGCAACTTC TTCATGAACG CCCGGCGCCG CAGCCTGGAG AAGTGGCAAG ACGATCTGAG  1500
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CACAGGGGGC TCCTCGTCCA CCTCCAGCAC GTGTACCAAA GCATGATGGA AGGACTCTCA  1560
CTTGGGCACA AGTCACCTCC AAATGAGGAC AACAGATACC AAAAGAAAAC AAAGGAAAAA  1620
GACACCGGAT TCCTAGCTGG GGCCCTTCAC TGGTG
```

Seq ID NO: 476 Protein sequence
Protein Accession #: NP_004843.1

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1          11         21         31         41         51
|          |          |          |          |          |
MNPELTMESL GTLHGARGGG SGGGGGGGGG GGGGGPGHEQ ELLASPSPHH ARRGPRGSLR    60
GPPPPPTAHQ ELGTAAAAAA AASRSAMVTS MASILDGGDY RPELSIPLHH AMSMSCDSSP   120
PGMGMSNTYT TLTPLQPLPP ISTVSDKFHH PHPHHHPHHH HHHHHQRLSG NVSGSFTLMR   180
DERGLPAMNN LYSPYKEMPG MSQSLSPLAA TPLGNGLGGL HNAQQSLPNY GPPGHDKMLS   240
PNFDAHHTAM LTRGEQHLSR GLGTPPAAMM SHLNGLHHPG HTQSHGPVLA PSRERPPSSS   300
SGSQVATSGQ LEEINTKEVA QRITAELKRY SIPQAIFAQR VLCRSQGTLS DLLRNPKPWS   360
KLKSGRETFR RMWKWLQEPE FQRMSALRLA ACKRKEQEPN KDRNNSQKKS RLVFTDLQRR   420
TLFAIFKENK RPSKEMQITI SQQLGLELTT VSNFFMNARR RSLEKWQDDL STGGSSSTSS   480
TCTKA
```

Seq ID NO: 477 DNA sequence
Nucleic Acid Accession #: NM_013271.1
Coding sequence: 27..809

```
1          11         21         31         41         51
|          |          |          |          |          |
TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTCGCC GCTGCTCTGG GGGCCGCGGG    60
CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCCGCGC   120
TCTGCGCGCG GCCGGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG   180
AGACTGGCGC TCCTCGCCGC TTCCGGCGGT CAGTGCCCCG AGGTGAGGCG GCGGGGGCGG   240
TGCAGGAGCT GGCGCGGGCG CTGGCGCATC TGCTGGAGGC CGAACGTCAG GAGCGGGCGC   300
GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG   360
TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCCGACGCGC   420
CTGCAGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCCTGCC GCCCTAGCAG   480
CCCAGCTTGT CCCCGCGCCC GTCCCCGCCG CGGCGCTCCG ACCCCGGCCC CCGGTCTACG   540
ACGACGGCCC CGCGGGCCCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC   600
CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG   660
TGGCAGCCCC GCGCCGCCTC CGCCGTGCCG CCGACCACGA TGTGGGCTCT GAGCTGCCCC   720
CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAAACGCCT AGAGACCCCG GCGCCCCAGG   780
TGCCTGCACG CCGCCTCTTG CCACCCTGAG CACTGCCCGG ATCCCGTGCA CCCTGGGACC   840
CAGAAGTGCC CCCGCCATCC CGCCACCAGG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC   900
TTACCCCGGC CAGCCAGCCC TCTCACCCGA GGATCCCTAC CCCCTGGCCC ACAATAACAT   960
GATCTGAGC
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Seq ID NO: 478 Protein sequence
Protein Accession #: NP_037403.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAGSPLLWGP RAGGVGLLVL LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR    60
RSVPRGEAAG AVQELARALA HLLEAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD   120
PALGLDDDPD APAAQLARAL LRARLDPAAL AAQLVPAPVP AAALRPRPPV YDDGPAGPDA   180
EEAGDETPDV DPELLRYLLG RILAGSADSE GVAAPRRLRR AADHDVGSEL PPEGVLGALL   240
RVKRLETPAP QVPARRLLPP
```

Seq ID NO: 479 DNA sequence
Nucleic Acid Accession #: NM_002214
Coding sequence: 681..2990

```
1          11         21         31         41         51
|          |          |          |          |          |
CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG    60
CTGCCGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT   120
GTTGGCCTCC CTGCCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT   180
TCCCCTCGAC CTCGCCGGCG TACCCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT   240
TAGGGTGGTT TCCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG   300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT   360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT   420
TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG   480
GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT   540
CCGAGCCGCG GGGTCCGCCT GCTAGGCCTG CGGAAAACGT CCTAGCGACA CTCGCCCGCG   600
GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGCGC   660
GGGGCGGGCT GTTTTGCATT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTTG   720
TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTCCT CTGGGCAGCC TGGGTGTTTT   780
CACTTGTTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT   840
CCTGTGCCAG GTGCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA   900
TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT   960
GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA  1020
TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA  1080
ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTTG  1140
ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTTAT  1200
CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTCGTCTTGG ATTTGGCTCA TACGTTGATA  1260
AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT  1320
ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA  1380
TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG  1440
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AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA  1500
AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA  1560
GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACGTCT  1620
ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG  1680
ACAACAACAT TAATGTCATC TTTGCAGTTC AAGGAAAACA ATTTCATTGG TATAAGGATC  1740
TTCTACCCCT CTTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA  1800
ATAATTTGGT AGTGGAAGCC TATCAGAAGC TCATTTCAGA AGTGAAAGTT CAGGTGGAAA  1860
ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC  1920
CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG  1980
TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAACTA TGCAATAATC AAACCTATTG  2040
GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCAG TGTGAGGACA  2100
ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACTTTTCT AGATTCCAAG TGTTTCCAGT  2160
GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC  2220
ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC  2280
ACAAAATTAA GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC  2340
CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT  2400
GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG  2460
TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT  2520
GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT  2580
GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTCACCCTCA CAATTTGTCT CAGGCTATAC  2640
TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAACAACA GCATTATGTC GACCAAACTT  2700
CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTTT CATCATTTTC ATAGTTACAT  2760
TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAATAGTA  2820
ATAAAATTAA GTCCTCATCA GATTACAGAG TGTCAGCCTC AAAAAAGGAT AAGTTGATTC  2880
TGCAAAGTGT TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA  2940
TGGATATCAG CAAATTAAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATTT  3000
TTAAACACTT AATGGGAAAC TGGAATTGTT AATAATTGCT CCTAAAGATT ATAATTTTAA  3060
AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC  3120
GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA  3180
AAAATGTGTC TTACTACTGT TTGAGACTAG TGTCGTTGTA GCACTTTACT GTAATATATA  3240
ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG  3300
TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT  3360
CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAAATA ATCTGGCAAG  3420
TATATTCTAA GGTTGCCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG  3480
ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA  3540
AAAGATTATT GCTTTTTAAA GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT  3600
TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTTT GCCTTTATGT TTTGTTTTCT  3660
TTTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC  3720
TACTGCCATA AAAAACTAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT  3780
GAATGTTAA
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Seq ID NO: 480 Protein sequence
Protein Accession #: NP_002205

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1          11         21         31         41         51
|          |          |          |          |          |
MCGSALAFFT AAFVCLQNDR RGPASFLWAA WVFSLVLGLG QGEDNRCASS NAASCARCLA    60
LGPECGWCVQ EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP   120
GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF   180
SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA   240
VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRLL LVMTDQTSHL ALDSKLAGIV   300
VPNDGNCHLK NNVYVKSTTM EHPSLGQLSE KLIDNNINVI FAVQGKQFHW YKDLLPLLPG   360
TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR   420
NVTSNDEVLF NVTVTMKKCD VTGGKNYAII KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK   480
CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDQPVC SGRGVCVCGK CSCHKIKLGK   540
VYGKYCEKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRCQCPSAAA QHCVNSKGQV   600
CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS   660
CALMEQQHYV DQTSECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKIKSSS   720
DYRVSASKKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF
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Seq ID NO: 481 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

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ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAAC   180
AACCCAGAGG ACTGGTTGAG TTTGTTGCTC AAACTAGAGA AAAACAGTGT TCCGCTAAGT   240
GATGCTCTTT TAAATAAATT GATTGGTCGT TACAGTCAAG CAATTGAAGC GCTTCCCCCA   300
GATAAATATG GCCAAAATGA GAGTTTTGCT AGAATTCAAG TGAGATTTGC TGAATTAAAA   360
GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAACTGCAAG   420
AAATTTGCTT TTGTTCATAT ATCTTTTGCA CAATTTGAAC TGTCACAAGG TAATGTCAAA   480
AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCACT AGAAATGCTG   540
GAAATTGCCC TGCGGAATTT AAACCTCCAA AAAAAGCAGC TGCTTTCAGA GGAGGAAAAG   600
AAGAATTTAT CAGCATCTAC GGTATTAACT GCCCAAGAAT CATTTTCCGG TTCACTTGGG   660
CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT   720
TTATATGGAG AGAACATGCC ACCACAAGAT GCAGAAATAG GTTACCGGAA TTCATTGAGA   780
CAAACTAACA AAACTAAACA GTCATGCCCA TTTGGAAGAG TCCCAGTTAA CCTTCTAAAT   840
AGCCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTTGTTTTAT GAAAAGACAA   900
ACCTCTAGAT CAGAATGCCG AGATTTGGTT GTGCCTGGAT CTAAACCAAG TGGAAATGAT   960
TCCTGTGAAT TAAGAAATTT AAAGTCTGTT CAAAATAGTC ATTTCAAGGA ACCTCTGGTG  1020
TCAGATGAAA AGAGTTCTGA ACTTATTATT ACTGATTCAA TAACCCTGAA GAATAAAACG  1080
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GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGGTTCCA  1140
GAGAGTAACC AGAAACAGTG GCAATCTAAG AGAAAGTCAG AGTGTATTAA CCAGAATCCT  1200
GCTGCATCTT CAAATCACTG GCAGATTCCG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG  1260
AAACATACCA CTTTTGAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA  1320
ACATCTAAAT GGTTTGACCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGGAT  1380
GATTACATGA GCTGTTTTAG AACTCCAGTT GTAAAGAATG ACTTTCCACC TGCTTGTCAG  1440
TTGTCAACAC CTTATGGCCA ACCTGCCTGT TTCCAGCAGC AACAGCATCA AATACTTGCC  1500
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GATAACCAAA CTCTTGATAG TTACCGGAAC GAAATAGCTT ATTTGAATAA ACTACAACAA  1740
CACAGTGATA AGATCATCCG ACTTTATGAT TATGAAATCA CGGACCAGTA CATCTACATG  1800
GTAATGGAGT GTGGAAATAT TGATCTTAAT AGTTGGCTTA AAAAGAAAAA ATCCATTGAT  1860
CCATGGGAAC GCAAGAGTTA CTGGAAAAAT ATGTTAGAGG CAGTTCACAC AATCCATCAA  1920
CATGGCATTG TTCACAGTGA TCTTAAACCA GCTAACTTTC TGATAGTTGA TGGAATGCTA  1980
AAGCTAATTG ATTTTGGGAT TGCAAACCAA ATGCAACCAG ATACAACAAG TGTTGTTAAA  2040
GATTCTCAGG TTGGCACAGT TAATTATATG CCACCAGAAG CAATCAAAGA TATGTCTTCC  2100
TCCAGAGAGA ATGGGAAATC TAAGTCAAAG ATAAGCCCCA AAAGTGATGT TTGGTCCTTA  2160
GGATGTATTT TGTACTATAT GACTTACGGG AAAACACCAT TTCAGCAGAT AATTAATCAG  2220
ATTTCTAAAT TACATGCCAT AATTGATCCT AATCATGAAA TTGAATTTCC CGATATTCCA  2280
GAGAAAGATC TTCAAGATGT GTTAAAGTGT TGTTTAAAAA GGGACCCAAA ACAGAGGATA  2340
TCCATTCCTG AGCTCCTGGC TCATCCCTAT GTTCAAATTC AAACTCATCC AGTTAACCAA  2400
ATGGCCAAGG GAACCACTGA AGAAATGAAA TATGTTCTGG GCCAACTTGT TGGTCTGAAT  2460
TCTCCTAACT CCATTTTGAA AGCTGCTAAA ACTTTATATG AACACTATAG TGGTGGTGAA  2520
AGTCATAATT CTTCATCCTC CAAGACTTTT GAAAAAAAAA GGGGAAAAAA ATGA
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Seq ID NO: 482 Protein sequence
Protein Accession #: NP_003309.1

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NPEDWLSLLL KLEKNSVPLS DALLNKLIGR YSQAIEALPP DKYGQNESFA RIQVRFAELK  120
AIQEPDDARD YFQMARANCK KFAFVHISFA QFELSQGNVK KSKQLLQKAV ERGAVPLEML  180
EIALRNLNLQ KKQLLSEEEK KNLSASTVLT AQESFSGSLG HLQNRNNSCD SRGQTTKARF  240
LYGENMPPQD AEIGYRNSLR QTNKTKQSCP PGRVPVNLLN SPDCDVKTDD SVVPCFMKRQ  300
TSRSECRDLV VPGSKPSGND SCELRNLKSV QNSHFKEPLV SDEKSSELII TDSITLKNKT  360
ESSLLAKLEE TKEYQEPEVP ESNQKQWQSK RKSECINQNP AASSNHWQIP ELARKVNTEQ  420
KHTTFEQPVF SVSKQSPPIS TSKWFDPKSI CKTPSSNTLD DYMSCFRTPV VKNDFPPACQ  480
LSTPYGQPAC FQQQQHQILA TPLQNLQVLA SSSANECISV KGRIYSILKQ IGSGGSSKVF  540
QVLNEKKQIY AIKYVNLEEA DNQTLDSYRN EIAYLNKLQQ HSDKIIRLYD YEITDQYIYM  600
VMECGNIDLN SWLKKKKSID PWERKSYWKN MLEAVHTIHQ HGIVHSDLKP ANFLIVDGML  660
KLIDFGIANQ MQPDTTSVVK DSQVGTVNYM PPEAIKDMSS SRENGKSKSK ISPKSDVWSL  720
GCILYYMTYG KTPFQQIINQ ISKLHAIIDP NHEIEFPDIP EKDLQDVLKC CLKRDPKQRI  780
SIPELLAHPY VQIQTHPVNQ MAKGTTEEMK YVLGQLVGLN SPNSILKAAK TLYEHYSGGE  840
SHNSSSSKTF EKKRGKK
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Seq ID NO: 483 DNA sequence
Nucleic Acid Accession #: NM_003667.1
Coding sequence: 1..2651

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GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT GCCCCACACA CTGTCATTGC   120
GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTCGGAGCTG   180
CCTTCCAACC TCAGCGTCTT CACCTCCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG   240
CTGCTCCCGA ATCCCCTGCC CAGTCTCCGC TTCCTGGAGG AGTTACGTCT TGCGGGAAAC   300
GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCTTATG   360
CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC TGCAGAATTT GCGAAGCCTT   420
CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC CCCCAAGCTG TTTCAGTGGC   480
CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT TAACAGAAAT CCCCGTCCAG   540
GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCCTGAACAA AATACACCAC   600
ATACCAGACT ATGCCTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAAT   660
AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT   720
TTAAATTACA ATAACCTTGA TGAATTCCCC ACTGCAATTA GGACACTCTC CAACCTTAAA   780
GAACTACATT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA   840
CCTGAACTAA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAATT TCCTGATTTA   900
ACTGGAACTG CAAACCTGGA GAGTCTGACT TTAACTGGAG CACAGATCTC ATCTCTTCCT   960
CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA  1020
GAAGATTTAC CCAGTTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT  1080
GAAATCTACG AAATTAAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGCTGAAT  1140
TTGGCTTGGA ACAAAATTGC TATTATTCAC CCCAATGCAT TTTCCACTTT GCCATCCCTA  1200
ATAAAGCTGG ACCTATCGTC CAACCTCCTG TCGTCTTTTC CTATAACTGG GTTACATGGT  1260
TTAACTCACT TAAAATTAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC  1320
TTTCCAGAAC TCAAGGTTAT AGAAATGCCT TATGCTTACC AGTGCTGTGC ATTTGGAGTG  1380
TGTGAGAATG CCTATAAGAT TTCTAATCAA TGGAATAAAG GTGACAACAG CAGTATGGAC  1440
GACCTTCATA AGAAAGATGC TGGAATGTTT CAGGCTCAAG ATGAACGTGA CCTTGAAGAT  1500
TTCCTGCTTG ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC  1560
CCAGGCCCCT TCAAACCCTG TGAACACCTG CTTGATGGCT GGCTGATCAG AATTGGAGTG  1620
TGGACCATAG CAGTTCTGGC ACTTACTTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA  1680
TCCCCTCTGT ACATTTCCCC CATTAAACTG TTAATTGGGG TCATCGCAGC AGTGAACATG  1740
CTCACGGGAG TCTCCAGTGC CGTGCTGGCT GGTGTGGATG CGTTCACTTT TGGCAGCTTT  1800
GCACGACATG GTGCCTGGTG GGAGAATGGG GTTGGTTGCC ATGTCATTGG TTTTTTGTCC  1860
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AAGTATGGCG CCTCCCCTCT CTGCCTGCCT TTGCCTTTTG GGGAGCCCAG CACCATGGGC  2100
TACATGGTCG CTCTCATCTT GCTCAATTCC CTTTGCTTCC TCATGATGAC CATTGCCTAC  2160
ACCAAGCTCT ACTGCAATTT GGACAAGGGA GACCTGGAGA ATATTTGGGA CTGCTCTATG  2220
GTAAAACACA TTGCCCTGTT GCTCTTCACC AACTGCATCC TAAACTGCCC TGTGGCTTTC  2280
TTGTCCTTCT CCTCTTTAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC  2340
CTTCTGGTGG TAGTCCCACT TCCTGCATGT CTCAATCCCC TTCTCTACAT CTTGTTCAAT  2400
CCTCACTTTA AGGAGGATCT GGTGAGCCTG AGAAAGCAAA CCTACGTCTG GACAAGATCA  2460
AAACACCCAA GCTTGATGTC AATTAACTCT GATGATGTCG AAAAACAGTC CTGTGACTCA  2520
ACTCAAGCCT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCCAGTTCC  2580
GTGCCATCAC CAGCTTATCC AGTGACTGAG AGCTGCCATC TTTCCTCTGT GGCATTTGTC  2640
CCATGTCTTA A
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Seq ID NO: 484 Protein sequence
Protein Accession #: NP_003658.1

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LQNNQLRHVP TEALQNLRSL QSLRLDANHI SYVPPSCFSG LHSLRHLWLD DNALTEIPVQ   180
AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD   240
LNYNNLDEFP TAIRTLSNLK ELHFYDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEFPDL   300
TGTANLESLT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSFSVCQ KLQKIDLRHN   360
EIYEIKVDTF QQLLSLRSLN LAWNKIAIIH PNAFSTLPSL IKLDLSSNLL SSFPITGLHG   420
LTHLKLTGNH ALQSLISSEN FPELKVIEMP YAYQCCAFGV CENAYKISNQ WNKGDNSSMD   480
DLHKKDAGMF QAQDERDLED FLLDFEEDLK ALHSVQCSPS PGPFKPCEHL LDGWLIRIGV   540
WTIAVLALTC NALVTSTVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDAFTFGSF   600
ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSAKFET KAPFSSLKVI   660
ILLCALLALT MAAVPLLGGS KYGASPLCLP LPFGEPSTMG YMVALILLNS LCFLMMTIAY   720
TKLYCNLDKG DLENIWDCSM VKHIALLLFT NCILNCPVAF LSFSSLINLT FISPEVIKFI   780
LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS   840
TQALVTFTSS SITYDLPPSS VPSPAYPVTE SCHLSSVAFV PCL
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Seq ID NO: 485 DNA sequence
Nucleic Acid Accession #: NM_005756.1
Coding sequence: 73..3117

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CTCGCGGTCA GGATGGTTTT CTCTGTCAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA   120
GTTTTACTGA CGTTCAAGAT ATTCCTTGTC ATCATTTGTC TTCATGTCGT TCTGGTAACA   180
TCCCTGGAAG AAGATACTGA TAATTCCAGT TTGTCACCAC CACCTGCTAA ATTATCTGTT   240
GTCAGTTTTG CCCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTTACTTTA   300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAATCA CTATAGTAAA AACCTTCAAT   360
GCTTCAGGCG TCAAACCCCA GAGAAATATC TGCAATTTGT CATCTATTTG CAATGACTCA   420
GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT   480
CAACATATAA CGAATGGCAC CTTAACTGGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA   540
GAGCTCAACA AAACCCTGCA AACCCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA   600
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA   660
TGTGCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTCGAC CAATGGAACA CTGCTGCTGT   720
TCTGTCAGGA TACCCTGCCC TTCCTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG   780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA   840
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CAACCCCTTT CACCCCAGCC TTCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC  1020
CCACAGTCTG AAACGATCTC TTCCCCTATG CCCCAAACCC ATGTCTCCGG CACCCCACCT  1080
CCTGTGAAAG CCTCATTTTC CTCTCCCACC GTGTCTGCCC CTGCGAATGT CAACACTACC  1140
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC  1200
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GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCCCCGC CTGACATGCT GGCCCCTCTG  1320
GCTCAAAGAT TGCTGAAAGT AGTGGATGAC ATTGGCCTAC AGCTGAACTT TTCAAACACG  1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT  1440
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TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATTCTGC  2280
ATTGTCGGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCCTGACTAT ATCCCCAGAT  2340
AACTATGGGC TTGGATCCTA TGGGAAATTC CCCAATGGTT CACCGGATGA CTTCTGCTGG  2400
ATCAACAACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTTG  2460
CTGAACGTCA GCATGTTCAT TGTGGTCCTG GTTCAGCTCT GTCGAATTAA AAAGAAGAAG  2520
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CAACTGGGAG CCCAGCGAAA AACCAGTATT CAAGACCTCA GGAGTATCGC TGGCCTTACA  2580
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CGGCTGGCTG AAAATTCTGA CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT  2820
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CTTTCTTCTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA  3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT  3240
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT  3300
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TTTAAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTTGA CTTCAGCCTG  3480
TTGGTGAGTT TAGTTGTGCA TGCCTTTGTT GTATATAAGC TAAATTCTAG TGACCCATGT  3540
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ACTGCATGGT ACATTGTTGA TTGTTATGAC TGGTACACTC TGGCCCAGCC AGAGCTATAA  4260
TTGTTTTTTA AATGTGTCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA  4320
GGGAACTGTC CTACACTGCT ATTGTTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA  4380
TATACAGGGT CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC  4440
TTATTAGGAA CATTTCAAAC CCCTTTTAGT TAAGTCTTTC ACTAAGGTTC TCTTGCATAT  4500
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG  4560
CTGACTTGTC TTTGCAATAT TTCTTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT  4620
AAAATCAAAA ATGTTAAAAT CAATGAAATA AATTTGCAGT TAAGA
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Seq ID NO: 486 Protein sequence
Protein Accession #: NP_005747.1

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PSSNEVETTS LNDVTLSLLP SNETGVKPQR NICNLSSICN DSAFFRGEIM FQYDKESTVP   120
QNQHITNGTL TGVLSLSELK RSELNKTLQT LSETYFIMCA TAEAQSTLNC TFTIKLNNTM   180
NACAVIAALE RVKIRPMEHC CCSVRIPCPS SPEELEKLQC DLQDPIVCLA DHPRGPPFSS   240
SQSIPVVPRA TVLSQVPKAT SFAEPPDYSP VTHNVPSPIG EIQPLSPQPS APIASSPAID   300
MPPQSETISS PMPQTHVSGT PPPVKASFSS PTVSAPANVN TTSAPPVQTD IVNTSSISDL   360
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Seq ID NO: 487 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2904

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Seq ID NO: 488 Protein sequence
Protein Accession #: Eos sequence

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Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2811

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Seq ID NO: 490 Protein sequence
Protein Accession #: Eos sequence

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Seq ID NO: 491 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3045

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Seq ID NO: 492 Protein sequence
Protein Accession #: Eos sequence

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Seq ID NO: 493 DNA sequence
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Coding sequence: 241..1902

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ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC  720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT  780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC  840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA  900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA  960
GGGTCCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC 1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC 1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACTTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT 1380
CTGGTCCAAA GGAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA 1560
GGTCACAAGA AAGACATTGG CCGATTGAAA CTTCTCCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCGGAGACA AAGTCGGGAA ACTTCGAGTG 1680
TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
TGGAAGACAG GGAAAATTCA GTTGTATCAA GGAACTGATG CTACCAAAAG CATCATTTTT 1800
GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
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TCTTGTATAA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA  2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT  2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA  2220
TAGAAAAAAA AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC  2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT  2340
TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAAAAA AAAAAAAA
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Seq ID NO: 494 Protein sequence
Protein Accession #: NP_056322

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1          11         21         31         41         51
|          |          |          |          |          |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRRNSKGV    60
CEATCEPGCK FGECVGPNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRCV NTHGSYKCFC   120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS   180
GKVICPYNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFNTQ   240
GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKNVT   300
PEPTRTPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER   360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD   420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFDYRL AGDKVGKLRV   480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV   540
SGLCPDSLLS VDD
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Seq ID NO: 495 DNA sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

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1          11         21         31         41         51
|          |          |          |          |          |
GCAGCTCCAG TCCCGGACGC AACCCCGGAG CCGTCTCAGG TCCCTGGGGG GAACGGTGGG    60
TTAGACGGGG ACGGGAAGGG ACAGCGGCCT TCGACCGCCC CCCGAGTAAT TGACCCAGGA   120
CTCATTTTCA GGAAAGCCTG AAAATGAGTA AAATAGTGAA ATGAGGAATT TGAACATTTT   180
ATCTTTGGAT GGGGATCTTC TGAGGATGCA AAGAGTGATT CATCCAAGCC ATGTGGTAAA   240
ATCAGGAATT TGAAGAAAAT GGAGATGTTT ACATTTTTGT TGACGTGTAT TTTTCTACCC   300
CTCCTAAGAG GGCACAGTCT CTTCACCTGT GAACCAATTA CTGTTCCCAG ATGTATGAAA   360
ATGGCCTACA ACATGACGTT TTTCCCTAAT CTGATGGGTC ATTATGACCA GAGTATTGCC   420
GCGGTGGAAA TGGAGCATTT TCTTCCTCTC GCAAATCTGG AATGTTCACC AAACATTGAA   480
ACTTTCCTCT GCAAAGCATT TGTACCAACC TGCATAGAAC AAATTCATGT GGTTCCACCT   540
TGTCGTAAAC TTTGTGAGAA AGTATATTCT GATTGCAAAA AATTAATTGA CACTTTTGGG   600
ATCCGATGGC CTGAGGAGCT TGAATGTGAC AGATTACAAT ACTGTGATGA GACTGTTCCT   660
GTAACTTTTG ATCCACACAC AGAATTTCTT GGTCCTCAGA AGAAAACAGA ACAAGTCCAA   720
AGAGACATTG GATTTTGGTG TCCAAGGCAT CTTAAGACTT CTGGGGGACA AGGATATAAG   780
TTTCTGGGAA TTGACCAGTG TGCGCCTCCA TGCCCCAACA TGTATTTTAA AAGTGATGAG   840
CTAGAGTTTG CAAAAAGTTT TATTGGAACA GTTTCAATAT TTTGTCTTTG TGCAACTCTG   900
TTCACATTCC TTACTTTTTT AATTGATGTT AGAAGATTCA GATACCCAGA GAGACCAATT   960
ATATATTACT CTGTCTGTTA CAGCATTGTA TCTCTTATGT ACTTCATTGG ATTTTTGCTG  1020
GGCGATAGCA CAGCCTGCAA TAAGGCAGAT GAGAAGCTAG AACTTGGTGA CACTGTTGTC  1080
CTAGGCTCTC AAAATAAGGC TTGCACCGTT TTGTTCATGC TTTTGTATTT TTTCACAATG  1140
GCTGGCACTG TGTGGTGGGT GATTCTTACC ATTACTTGGT TCTTAGCTGC AGGAAGAAAA  1200
TGGAGTTGTG AAGCCATCGA GCAAAAAGCA GTGTGGTTTC ATGCTGTTGC ATGGGGAACA  1260
CCAGGTTTCC TGACTGTTAT GCTTCTTGCT CTGAACAAAG TTGAAGGAGA CAACATTAGT  1320
GGAGTTTGCT TTGTTGGCCT TTATGACCTG GATGCTTCTC GCTACTTTGT ACTCTTGCCA  1380
CTGTGCCTTT GTGTGTTTGT TGGGCTCTCT CTTCTTTTAG CTGGCATTAT TTCCTTAAAT  1440
CATGTTCGAC AAGTCATACA ACATGATGGC CGGAACCAAG AAAAACTAAA GAAATTTATG  1500
ATTCGAATTG GAGTCTTCAG CGGCTTGTAT CTTGTGCCAT TAGTGACACT TCTCGGATGT  1560
TACGTCTATG AGCAAGTGAA CAGGATTACC TGGGAGATAA CTTGGGTCTC TGATCATTGT  1620
CGTCAGTACC ATATCCCATG TCCTTATCAG GCAAAAGCAA AAGCTCGACC AGAATTGGCT  1680
TTATTTATGA TAAAATACCT GATGACATTA ATTGTTGGCA TCTCTGCTGT CTTCTGGGTT  1740
GGAAGCAAAA AGACATGCAC AGAATGGGCT GGGTTTTTTA AACGAAATCG CAAGAGAGAT  1800
CCAATCAGTG AAAGTCGAAG AGTACTACAG GAATCATGTG AGTTTTTCTT AAAGCACAAT  1860
TCTAAAGTTA AACACAAAAA GAAGCACTAT AAACCAAGTT CACACAAGCT GAAGGTCATT  1920
TCCAAATCCA TGGGAACCAG CACAGGAGCT ACAGCAAATC ATGGCACTTC TGCAGTAGCA  1980
ATTACTAGCC ATGATTACCT AGGACAAGAA ACTTTGACAG AAATCCAAAC CTCACCAGAA  2040
ACATCAATGA GAGAGGTGAA AGCGGACGGA GCTAGCACCC CCAGGTTAAG AGAACAGGAC  2100
TGTGGTGAAC CTGCCTCGCC AGCAGCATCC ATCTCCAGAC TCTCTGGGGA ACAGGTCGAC  2160
GGGAAGGGCC AGGCAGGCAG TGTATCTGAA AGTGCGCGGA GTGAAGGAAG GATTAGTCCA  2220
AAGAGTGATA TTACTGACAC TGGCCTGGCA CAGAGCAACA ATTTGCAGGT CCCCAGTTCT  2280
TCAGAACCAA GCAGCCTCAA AGGTTCCACA TCTCTGCTTG TTCACCCAGT TTCAGGAGTG  2340
AGAAAAGAGC AGGGAGGTGG TTGTCATTCA GATACTTGAA GAACATTTTC TCTCGTTACT  2400
CAGAAGCAAA TTTGTGTTAC ACTGGAAGTG ACCTATGCAC TGTTTTGTAA GAATCACTGT  2460
TACGTTCTTC TTTTGCACTT AAAGTTGCAT TGCCTACTGT TATACTGGAA AAAATAGAGT  2520
TCAAGAATAA TATGACTCAT TTCACACAAA GGTTAATGAC AACAATATAC CTGAAAACAG  2580
AAATGTGCAG GTTAATAATA TTTTTTTAAT AGTGTGGGAG GACAGAGTTA GAGGAATCTT  2640
CCTTTTCTAT TTATGAAGAT TCTACTCTTG GTAAGAGTAT TTTAAGATGT ACTATGCTAT  2700
TTTACCTTTT TGATATAAAA TCAAGATATT TCTTTGCTGA AGTATTTAAA TCTTATCCTT  2760
GTATCTTTTT ATACATATTT GAAAATAAGC TTATATGTAT TTGAACTTTT TTGAAATCCT  2820
ATTCAAGTAT TTTTATCATG CTATTGTGAT ATTTTAGCAC TTTGGTAGCT TTTACACTGA  2880
ATTTCTAAGA AAATTGTAAA ATAGTCTTCT TTTATACTGT AAAAAAAGAT ATACCAAAAA  2940
GTCTTATAAT AGGAATTTAA CTTTAAAAAC CCACTTATTG ATACCTTACC ATCTAAAATG  3000
TGTGATTTTT ATAGTCTCGT TTTAGGAATT TCACAGATCT AAATTATGTA ACTGAAATAA  3060
GGTGCTTACT CAAAGAGTGT CCACTATTGA TTGTATTATG CTGCTCACTG ATCCTTCTGC  3120
ATATTTAAAA TAAAATGTCC TAAAGGGTTA GTAGACAAAA TGTTAGTCTT TTGTATATTA  3180
GGCCAAGTGC AATTGACTTC CCTTTTTTAA TGTTTCATGA CCACCCATTG ATTGTATTAT  3240
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AACCACTTAC AGTTGCTTAT ATTTTTGTT TTAACTTTTG TTTCTTAACA TTTAGAATAT 3300
TACATTTTGT ATTATACAGT ACCTTTCTCA GACATTTTGT AG

Seq ID NO: 496 Protein sequence
Protein Accession #: NP_003497.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEMFTFLLTC IFLPLLRGHS LFTCEPITVP RCMKMAYNMT FFPNLMGHYD QSIAAVEMEH    60
FLPLANLECS PNIETFLCKA FVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTFGIRWPEE   120
LECDRLQYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGFW CPRHLKTSGG QGYKFLGIDQ   180
CAPPCPNMYF KSDELEFAKS FIGTVSIFCL CATLFTFLTF LIDVRRFRYP ERPIIYYSVC   240
YSIVSLMYFI GFLLGDSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFTMAGTVWW   300
VILTITWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCFVG   360
LYDLDASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKL KKFMIRIGVF   420
SGLYLVPLVT LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMIKY   480
LMTLIVGISA VFWVGSKKTC TEWAGFFKRN RKRDPISESR RVLQESCEFF LKHNSKVKHK   540
KKHYKPSSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLTEIQ TSPETSMREV   600
KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD   660
TGLAQSNNLQ VPSSSEPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT
```

Seq ID NO: 497 DNA sequence
Nucleic Acid Accession #: NM_005046
Coding sequence: 16..777

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1          11         21         31         41         51
|          |          |          |          |          |
GGATTTCCGG GCTCCATGGC AAGATCCCTT CTCCTGCCCC TGCAGATCCT ACTGCTATCC    60
TTAGCCTTGG AAACTGCAGG AGAAGAAGCC CAGGGTGACA AGATTATTGA TGGCGCCCCA   120
TGTGCAAGAG GCTCCCACCC ATGGCAGGTG GCCCTGCTCA GTGGCAATCA GCTCCACTGC   180
GGAGGCGTCC TGGTCAATGA GCGCTGGGTG CTCACTGCCG CCCACTGCAA GATGAATGAG   240
TACACCGTGC ACCTGGGCAG TGATACGCTG GGCGACAGGA GAGCTCAGAG GATCAAGGCC   300
TCGAAGTCAT TCCGCCACCC CGGCTACTCC ACACAGACCC ATGTTAATGA CCTCATGCTC   360
GTGAAGCTCA ATAGCCAGGC CAGGCTGTCA TCCATGGTGA AGAAAGTCAG GCTGCCCTCC   420
CGCTGCGAAC CCCCTGGAAC CACCTGTACT GTCTCCGGCT GGGGCACTAC CACGAGCCCA   480
GATGTGACCT TTCCCTCTGA CCTCATGTGC GTGGATGTCA AGCTCATCTC CCCCCAGGAC   540
TGCACGAAGG TTTACAAGGA CTTACTGGAA AATTCCATGC TGTGCGCTGG CATCCCCGAC   600
TCCAAGAAAA ACGCCTGCAA TGGTGACTCA GGGGGACCGT TGGTGTGCAG AGGTACCCTG   660
CAAGGTCTGG TGTCCTGGGG AACTTTCCCT TGCGGCCAAC CCAATGACCC AGGAGTCTAC   720
ACTCAAGTGT GCAAGTTCAC CAAGTGGATA AATGACACCA TGAAAAAGCA TCGCTAACGC   780
CACACTGAGT TAATTAACTG TGTGCTTCCA ACAGAAAATG CACAGGAGTG AGGACGCCGA   840
TGACCTATGA AGTCAAATTT GACTTTACCT TTCCTCAAAG ATATATTTAA ACCTCATGCC   900
CTGTTGATAA ACCAATCAAA TTGGTAAAGA CCTAAAACCA AAACAAATAA AGAAACACAA   960
AACCCTCAA
```

Seq ID NO: 498 Protein sequence
Protein Accession #: NP_005037

```
1          11         21         31         41         51
|          |          |          |          |          |
MARSLLLPLQ ILLLSLALET AGEEAQGDKI IDGAPCARGS HPWQVALLSG NQLHCGGVLV    60
NERWVLTAAH CKMNEYTVHL GSDTLGDRRA QRIKASKSFR HPGYSTQTHV NDLMLVKLNS   120
QARLSSMVKK VRLPSRCEPP GTTCTVSGWG TTTSPDVTFP SDLMCVDVKL ISPQDCTKVY   180
KDLLENSMLC AGIPDSKKNA CNGDSGGPLV CRGTLQGLVS WGTFPCGQPN DPGVYTQVCK   240
FTKWINDTMK KHR
```

Seq ID NO: 499 DNA sequence
Nucleic Acid Accession #: NM_007196
Coding sequence: 182..962

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1          11         21         31         41         51
|          |          |          |          |          |
GTTCCCAGAA GCTCCCCAGG CTCTAGTGCA GGAGGAGAAG GAGGAGGAGC AGGAGGTGGA    60
GATTCCCAGT TAAAAGGCTC CAGAATCGTG TACCAGGCAG AGAACTGAAG TACTGGGGCC   120
TCCTCCACTG GGTCCGAATC AGTAGGTGAC CCCGCCCCTG GATTCTGGAA GACCTCACCA   180
TGGGACGCCC CCGACCTCGT GCGGCCAAGA CGTGGATGTT CCTGCTCTTG CTGGGGGGAG   240
CCTGGGCAGG ACACTCCAGG GCACAGGAGG ACAAGGTGCT GGGGGGTCAT GAGTGCCAAC   300
CCCATTCGCA GCCTTGGCAG GCGGCCTTGT TCCAGGGCCA GCAACTACTC TGTGGCGGTG   360
TCCTTGTAGG TGGCAACTGG GTCCTTACAG CTGCCCACTG TAAAAAACCG AAATACACAG   420
TACGCCTGGG AGACCACAGC CTACAGAATA AAGATGGCCC AGAGCAAGAA ATACCTGTGG   480
TTCAGTCCAT CCCACACCCC TGCTACAACA GCAGCGATGT GGAGGACCAC AACCATGATC   540
TGATGCTTCT TCAACTGCGT GACCAGGCAT CCCTGGGGTC CAAAGTGAAG CCCATCAGCC   600
TGGCAGATCA TTGCACCCAG CCTGGCCAGA AGTGCACCGT CTCAGGCTGG GGCACTGTCA   660
CCAGTCCCCG AGAGAATTTT CCTGACACTC TCAACTGTGC AGAAGTAAAA ATCTTTCCCC   720
AGAAGAAGTG TGAGGATGCT TACCCGGGGC AGATCACAGA TGGCATGGTC TGTGCAGGCA   780
GCAGCAAAGG GGCTGACACG TGCCAGGGCG ATTCTGGAGG CCCCCTGGTG TGTGATGGTG   840
CACTCCAGGG CATCACATCC TGGGGCTCAG ACCCCTGTGG GAGGTCCGAC AAACCTGGCG   900
TCTATACCAA CATCTGCCGC TACCTGGACT GGATCAAGAA GATCATAGGC AGCAAGGGCT   960
GATTCTAGGA TAAGCACTAG ATCTCCCTTA ATAAACTCAC AACTCTC
```

Seq ID NO: 500 Protein sequence
Protein Accession #: NP_009127

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1          11         21         31         41         51
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|          |          |          |          |          |
MGRPRPRAAK TWMFLLLLGG AWAGHSRAQE DKVLGGHECQ PHSQPWQAAL FQGQQLLCGG    60
VLVGGNWVLT AAHCKKPKYT VRLGDHSLQN KDGPEQEIPV VQSIPHPCYN SSDVEDHNHD   120
LMLLQLRDQA SLGSKVKPIS LADHCTQPGQ KCTVSGWGTV TSPRENFPDT LNCAEVKIFP   180
QKKCEDAYPG QITDGMVCAG SSKGADTCQG DSGGPLVCDG ALQGITSWGS DPCGRSDKPG   240
VYTNICRYLD WIKKIIGSKG
```

Seq ID NO: 501 DNA sequence
Nucleic Acid Accession #: NM_006103
Coding sequence: 29..406

```
1          11         21         31         41         51
|          |          |          |          |          |
CACCTGCACC CCGCCCGGGC ATAGCACCAT GCCTGCTTGT CGCCTAGGCC CGCTAGCCGC    60
CGCCCTCCTC CTCAGCCTGC TGCTGTTCGG CTTCACCCTA GTCTCAGGCA CAGGAGCAGA   120
GAAGACTGGC GTGTGCCCCG AGCTCCAGGC TGACCAGAAC TGCACGCAAG AGTGCGTCTC   180
GGACAGCGAA TGCGCCGACA ACCTCAAGTG CTGCAGCGCG GGCTGTGCCA CCTTCTGCCT   240
TCTCTGCCCA AATGATAAGG AGGGTTCCTG CCCCCAGGTG AACATTAACT TTCCCCAGCT   300
CGGCCTCTGT CGGGACCAGT GCCAGGTGGA CAGCCAGTGT CCTGGCCAGA TGAAATGCTG   360
CCGCAATGGC TGTGGGAAGG TGTCCTGTGT CACTCCCAAT TTCTGAGGTC CAGCCACCAC   420
CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGGTT CCAGCCCACC   480
TGCCCTCCCC TTTTTCGGGA CTCTGTATTC CCTCTTGGGC TGACCACAGC TTCTCCCTTT   540
CCCAACCAAT AAAGTAACCA CTTTCAGCAA AAAAAAAAAA AAAA
```

Seq ID NO: 502 Protein sequence
Protein Accession #: NP_006094

```
1          11         21         31         41         51
|          |          |          |          |          |
MPACRLGPLA AALLLSLLLF GFTLVSGTGA EKTGVCPELQ ADQNCTQECV SDSECADNLK    60
CCSAGCATFC LLCPNDKEGS CPQVNINFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVSC   120
VTPNF
```

Seq ID NO: 503 DNA sequence
Nucleic Acid Accession #: NM_002407
Coding sequence: 65..352

```
1          11         21         31         41         51
|          |          |          |          |          |
CCTCCACAGC AACTTCCTTG ATCCCTGCCA CGCACGACTG AACACAGACA GCAGCCGCCT    60
CGCCATGAAG CTGCTGATGG TCCTCATGCT GGCGGCCCTC CTCCTGCACT GCTATGCAGA   120
TTCTGGCTGC AAACTCCTGG AGGACATGGT TGAAAAGACC ATCAATTCCG ACATATCTAT   180
ACCTGAATAC AAAGAGCTTC TTCAAGAGTT CATAGACAGT GATGCCGCTG CAGAGGCTAT   240
GGGGAAATTC AAGCAGTGTT TCCTCAACCA GTCACATAGA ACTCTGAAAA ACTTTGGACT   300
GATGATGCAT ACAGTGTACG ACAGCATTTG GTGTAATATG AAGAGTAATT AACTTTACCC   360
AAGGCGTTTG GCTCAGAGGG CTACAGACTA TGGCCAGAAC TCATCTGTTG ATTGCTAGAA   420
ACCACTTTTC TTTCTTGTGT TGTCTTTTTA TGTGGAAACT GCTAGACAAC TGTTGAAACC   480
TCAAATTCAT TTCCATTTCA ATAACTAACT GCAAATC
```

Seq ID NO: 504 Protein sequence
Protein Accession #: NP_002398

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1          11         21         31         41         51
|          |          |          |          |          |
MKLLMVLMLA ALLLHCYADS GCKLLEDMVE KTINSDISIP EYKELLQEFI DSDAAAEAMG    60
KFKQCFLNQS HRTLKNFGLM MHTVYDSIWC NMKSN
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Seq ID NO: 505 DNA sequence
Nucleic Acid Accession #: NM_014791.1
Coding sequence: 171..2126

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1          11         21         31         41         51
|          |          |          |          |          |
TTGGCGGGCG GAAGCGGCCA CAACCCGGCG ATCGAAAAGA TTCTTAGGAA CGCCGTACCA    60
GCCGCGTCTC TCAGGACAGC AGGCCCCTGT CCTTCTGTCG GGCGCCGCTC AGCCGTGCCC   120
TCCGCCCCTC AGGTTCTTTT TCTAATTCCA AATAAACTTG CAAGAGGACT ATGAAAGATT   180
ATGATGAACT TCTCAAATAT TATGAATTAC ATGAAACTAT TGGGACAGGT GGCTTTGCAA   240
AGGTCAAACT TGCCTGCCAT ATCCTTACTG GAGAGATGGT AGCTATAAAA ATCATGGATA   300
AAAACACACT AGGGAGTGAT TTGCCCCGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC   360
TGAGACATCA GCATATATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA   420
TGGTTCTTGA GTACTGCCCT GGAGGAGAGC TGTTTGACTA TATAATTTCC CAGGATCGCC   480
TGTCAGAAGA GGAGACCCGG GTTGTCTTCC GTCAGATAGT ATCTGCTGTT GCTTATGTGC   540
ACAGCCAGGG CTATGCTCAC AGGGACCTCA AGCCAGAAAA TTTGCTGTTT GATGAATATC   600
ATAAATTAAA GCTGATTGAC TTTGGTCTCT GTGCAAAACC CAAGGGTAAC AAGGATTACC   660
ATCTACAGAC ATGCTGTGGG AGTCTGGCTT ATGCAGCACC TGAGTTAATA CAAGGCAAAT   720
CATATCTTGG ATCAGAGGCA GATGTTTGGA GCATGGGCAT ACTGTTATAT GTTCTTATGT   780
GTGGATTTCT ACCATTTGAT GATGATAATG TAATGGCTTT ATACAAGAAG ATTATGAGAG   840
GAAAATATGA TGTTCCCAAG TGGCTCTCTC CCAGTAGCAT TCTGCTTCTT CAACAAATGC   900
TGCAGGTGGA CCCAAAGAAA CGGATTTCTA TGAAAAATCT ATTGAACCAT CCCTGGATCA   960
TGCAAGATTA CAACTATCCT GTTGAGTGGC AAAGCAAGAA TCCTTTTATT CACCTCGATG  1020
ATGATTGCGT AACAGAACTT TCTGTACATC ACAGAAACAA CAGGCAAACA ATGGAGGATT  1080
TAATTTCACT GTGGCAGTAT GATCACCTCA CGGCTACCTA TCTTCTGCTT CTAGCCAAGA  1140
AGGCTCGGGG AAAACCAGTT CGTTTAAGGC TTTCTTCTTT CTCCTGTGGA CAAGCCAGTG  1200
CTACCCCATT CACAGACATC AAGTCAAATA ATTGGAGTCT CGAACATGTG ACCGCAAGTG  1260
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ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG  1320
GTGCTGCTAC TCCCCGAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG  1380
AATCTAAATC ATTAACTCCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAAG  1440
AAAATGTATA TACTCCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCCTGAGC  1500
CAAAGACTCC AGTTAATAAG AACCAGCATA AGAGAGAAAT ACTCACTACG CCAAATCGTT  1560
ACACTACACC CTCAAAAGCT AGAAACCAGT GCCTGAAAGA AACTCCAATT AAAATACCAG  1620
TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCAT TAGCCCTGAG AGGCGGTGCC  1680
GCTCAGTGGA ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG  1740
CCAAAGTGTT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA  1800
GCAAAAGGAA GGGTTCTGCC AGAGACGGGC CCAGAAGACT AAAGCTTCAC TATAATGTGA  1860
CTACAACTAG ATTAGTGAAT CCAGATCAAC TGTTGAATGA AATAATGTCT ATTCTTCCAA  1920
AGAAGCATGT TGACTTTGTA CAAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCAGATT  1980
TTGGGAAAGT GACAATGCAA TTTGAATTAG AAGTGTGCCA GCTTCAAAAA CCCGATGTGG  2040
TGGGTATCAG GAGGCAGCGG CTTAAGGGCG ATGCCTGGGT TTACAAAAGA TTAGTGGAAG  2100
ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCCTGCCG GATGAGTGTG  2160
GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGAA  2220
CTACCAACTT GTTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAAACAAAA  2280
GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTTT  2340
TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG  2400
AATGTAAGCT CTTAACTATG TCTCTTTGTA ATGTGTAATT TCTTTCTGAA ATAAAACCAT  2460
TTGTGAATAT
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Seq ID NO: 506 Protein sequence
Protein Accession #: NP_055606.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA    60
LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELFDYIIS QDRLSEEETR VVFRQIVSAV   120
AYVHSQGYAH RDLKPENLLF DEYHKLKLID FGLCAKPKGN KDYHLQTCCG SLAYAAPELI   180
QGKSYLGSEA DVWSMGILLY VLMCGFLPFD DDNVMALYKK IMRGKYDVPK WLSPSSILLL   240
QQMLQVDPKK RISMKNLLNH PWIMQDYNYP VEWQSKNPFI HLDDDCVTEL SVHHRNNRQT   300
MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSFSCG QASATPFTDI KSNNWSLEDV   360
TASDKNYVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTPANKL   420
KNKENVYTPK SAVKNEEYFM FPEPKTPVNK NQHKREILTT PNRYTTPSKA RNQCLKETPI   480
KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV   540
LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLLNEIMS ILPKKHVDFV QKGYTLKCQT   600
QSDFGKVTMQ FELEVCQLQK PDVVGIRRQR LKGDAWVYKR LVEDILSSCK V
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Seq ID NO: 507 DNA sequence
Nucleic Acid Accession #: NM_000582
Coding sequence: 88..990

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1          11         21         31         41         51
|          |          |          |          |          |
GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA    60
AACGCCGACC AAGGAAAACT CACTACCATG AGAATTGCAG TGATTTGCTT TTGCCTCCTA   120
GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAAGCAG   180
CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG   240
CAGAATCTCC TAGCCCCACA GACCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG   300
GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG   360
AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT   420
TCTGATGAAT CTGATGAACT GGTCACTGAT TTTCCCACGG ACCTGCCAGC AACCGAAGTT   480
TTCACTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT   540
GGACTGAGGT CAAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA   600
GACGAGGACA TCACCTCACA CATGGAAAGC GAGGAGTTGA ATGGTGCATA CAAGGCCATC   660
CCCGTTGCCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT   720
GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA   780
TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA   840
CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTTC ACAGCCATGA AGATATGCTG   900
GTTGTAGACC CCAAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA   960
TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATTT CTCACTTTGC  1020
ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT  1080
CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA  1140
ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT  1200
CTATGTTCAT TCTATAGAAG AAATGCAAAC TATCACTGTA TTTTAATATT TGTTATTCTC  1260
TCATGAATAG AAATTTATGT AGAAGCAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT  1320
ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTTAAGTT AGTGTATATT TTGTTGTGAT  1380
TATCTTTTTG TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTC  1440
AATTGCTTAT TTGTTTTCCC ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTTACT  1500
GCCTAAAAAA AAAAAAAAAA AAAA
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Seq ID NO: 508 Protein sequence
Protein Accession #: NP_000573

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1          11         21         31         41         51
|          |          |          |          |          |
MRIAVICFCL LGITCAIPVK QADSGSSEEK QLYNKYPDAV ATWLNPDPSQ KQNLLAPQTL    60
PSKSNESHDH MDDMDDEDDD DHVDSQDSID SNDSDDVDDT DDSHQSDESH HSDESDELVT   120
DFPTDLPATE VFTPVVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYPDA TDEDITSHME   180
SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES   240
NEHSDVIDSQ ELSKVSREFH SHEFHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN
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Seq ID NO: 509 DNA sequence
Nucleic Acid Accession #: AB051390.1
Coding sequence: 34..2457

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1          11         21         31         41         51
|          |          |          |          |          |
AGCGGCCGCG GCACAAAGTT GGGGGCCGCG AAGATGAGGC TGTCCCCGGC GCCCCTGAAG    60
CTGAGCCGGA CTCCGGCACT GCTGGCCCTG GCGCTGCCCC TGGCCGCGGC GCTGGCCTTC   120
TCCGACGAGA CCCTGGACAA AGTGCCCAAG TCAGAGGGCT ACTGCAGCCG TATCCTGCGC   180
GCCCAGGGCA CGCGGCGCGA GGGCTACACC GAGTTCAGCC TCCGCGTGGA GGGCGACCCC   240
GACTTCTACA AGCCGGGAAC CAGCTACCGC GTAACACTTT CAGCTGCTCC TCCCTCCTAC   300
TTCAGAGGAT TCACATTAAT TGCCCTCAGA GAGAACAGAG AGGGTGATAA GGAAGAAGAC   360
CATGCTGGGA CCTTCCAGAT CATAGACGAA GAAGAAACTC AGTTTATGAG CAATTGCCCT   420
GTTGCAGTCA CTGAAAGCAC TCCACGGAGG AGGACCCGGA TCCAGGTGTT TTGGATAGCA   480
CCACCAGCGG GAACAGGCTG CGTGATTCTG AAGGCCAGCA TCGTACAAAA ACGCATTATT   540
TATTTTCAAG ATGAGGGCTC TCTGACCAAG AAACTTTGTG AACAAGATTC CACATTTGAT   600
GGGGTGACTG ACAAACCCAT CTTAGACTGC TGTGCCTGCG GAACTGCCAA GTACAGACTC   660
ACATTTTATG GGAATTGGTC CGAGAAGACA CACCCAAAGG ATTACCCTCG TCGGGCCAAC   720
CACTGGTCTG CGATCATCGG AGGATCCCAC TCCAAGAATT ATGTACTGTG GGAATATGGA   780
GGATATGCCA GCGAAGGCGT CAAACAAGTT GCAGAATTGG GCTCACCCGT GAAAATGGAG   840
GAAGAAATTC GACAACAGAG TGATGAGGTC CTCACCGTCA TCAAAGCCAA AGCCCAATGG   900
CCAGCCTGGC AGCCTCTCAA CGTGAGAGCA GCACCTTCAG CTGAATTTTC CGTGGACAGA   960
ACGCGCCATT TAATGTCCTT CCTGACCATG ATGGGCCCTA GTCCCGACTG GAACGTAGGC  1020
TTATCTGCAG AAGATCTGTG CACCAAGGAA TGTGGCTGGG TCCAGAAGGT GGTGCAAGAC  1080
CTGATTCCCT GGGACGCTGG CACCGACAGC GGGGTGACCT ATGAGTCACC CAACAAACCC  1140
ACCATTCCCC AGGAGAAAAT CCGGCCCCTG ACCAGCCTGG ACCATCCTCA GAGTCCTTTC  1200
TATGACCCAG AGGGTGGGTC CATCACTCAA GTAGCCAGAG TTGTCATCGA GAGAATCGCA  1260
CGGAAGGGTG AACAATGCAA TATTGTACCT GACAATGTCG ATGATATTGT AGCTGACCTG  1320
GCTCCAGAAG AGAAAGATGA AGATGACACC CCTGAAACCT GCATCTACTC CAACTGGTCC  1380
CCATGGTCCG CCTGCAGCTC CTCCACCTGT GACAAAGGCA AGAGGATGCG ACAGCGCATG  1440
CTGAAAGCAC AGCTGGACCT CAGCGTCCCC TGCCCTGACA CCCAGGACTT CCAGCCCTGC  1500
ATGGGCCCTG GCTGCAGTGA CGAAGACGGC TCCACCTGCA CCATGTCCGA GTGGATCACC  1560
TGGTCGCCCT GCAGCATCTC CTGCGGCATG GGCATGAGGT CCCGGGAGAG GTATGTGAAG  1620
CAGTTCCCGG AGGACGGCTC CGTGTGCACG CTGCCCACTG AGGAAACGGA GAAGTGCACG  1680
GTCAACGAGG AGTGCTCTCC CAGCAGCTGC CTGATGACCG AGTGGGGCGA GTGGGACGAG  1740
TGCAGCGCCA CCTGCGGCAT GGGCATGAAG AAGCGGCACC GCATGATCAA GATGAACCCC  1800
GCAGATGGCT CCATGTGCAA AGCCGAGACA TCACAGGCAG AGAAGTGCAT GATGCCAGAG  1860
TGCCACACCA TCCCATGCTT GCTGTCCCCA TGGTCCGAGT GGAGTGACTG CAGCGTGACC  1920
TGCGGGAAGG GCATGCGAAC CCGACAGCGG ATGCTCAAGT CTCTGGCAGA ACTTGGAGAC  1980
TGCAATGAGG ATCTGGAGCA GGTGGAGAAG TGCATGCTCC CTGAATGCCC CATTGACTGT  2040
GAGCTCACCG AGTGGTCCCA GTGGTCGGAA TGTAACAAGT CATGTGGGAA AGGCCACGTG  2100
ATTCGAACCC GGATGATCCA AATGGAGCCT CAGTTTGGAG GTGCACCCTG CCCAGAGACT  2160
GTGCAGCGAA AAAAGTGCCG CATCCGAAAA TGCCTTCGAA ATCCATCCAT CCAAAAGCTA  2220
CGCTGGAGGG AGGCCCCAGA GAGCCGGCGG AGTGAGCAGC TGAAGGAAGA GTCTGAAGGG  2280
GAGCAGTTCC CAGGTTGTAG GATGCGCCCA TGGACGGCCT GGTCAGAATG CACCAAACTG  2340
TGCGGAGGTG GAATTCAGGA ACGTTACATG ACTGTAAAGA AGAGATTCAA AAGCTCCCAG  2400
TTTACCAGCT GCAAAGACAA GAAGGAGATC AGAGCATGCA ATGTTCATCC TTGTTAGCAA  2460
GGGTACGAGT TCCCCAGGGC TGCACTCTAG ATTCCAGAGT CACCAATGGC TGGATTATTT  2520
GCTTGTTTAA GACAATTTAA ATTGTGTACG CTAGTTTTCA TTTTTGCAGT GTGGTTCGCC  2580
CAGTAGTCTT GTGGATGCCA GAGACATCCT TTCTGAATAC TTCTTGATGG GTACAGGCTG  2640
AGTGGGGCGC CCTCACCTCC AGCCAGCCTC TTCCTGCAGA GGAGTAGTGT CAGCCACCTT  2700
GTACTAAGCT GAAACATGTC CCTCTGGAGC TTCCACCTGG CCAGGGAGGA CGGAGACTTT  2760
GACCTACTCC ACATGGAGAG GCAACCATGT CTGGAAGTGA CTATGCCTGA GTCCCAGGGT  2820
GCGGCAGGTA GGAAACATTC ACAGATGAAG ACAGCAGATT CCCCACATTC TCATCTTTGG  2880
CCTGTTCAAT GAAACCATTG TTTGCCCATC TCTTCTTAGT GGAACTTTAG GTCTCTTTTC  2940
AAGTCTCCTC AGTCATCAAT AGTTCCTGGG GAAAAACAGA GCTGGTAGAC TTGAAGAGGA  3000
GCATTGATGT TGGGTGGCTT TTGTTCTTTC ACTGAGAAAT TCGGAATACA TTTGTCTCAC  3060
CCCTGATATT GGTTCCTGAT GCCCCCCCAA CAAAAATAAA TAAATAAATT ATGGCTGCTT  3120
TATTTAAATA TAAGGTAGCT AGTTTTTACA CCTGAGATAA ATAATAAGCT TAGAGTGTAT  3180
TTTTCCCTTG CTTTTGGGGG TTCAGAGGAG TATGTACAAT TCTTCTGGGA AGCCAGCCTT  3240
CTGAACTTTT TGGTACTAAA TCCTTATTGG AACCAAGACA AAGGAAGCAA AATTGGTCTC  3300
TTTAGAGACC AATTTGCCTA AATTTTAAAA TCTTCCTACA CACATCTAGA CGTTCAAGTT  3360
TGCAAATCAG TTTTTAGCAA GAAAACATTT TTGCTATACA AACATTTTGC TAAGTCTGCC  3420
CAAAGCCCCC CCAATGCATT CCTTCAACAA AATACAATCT CTGTACTTTA AAGTTATTTT  3480
AGTCATGAAA TTTTATATGC AGAGAGAAAA AGTTACCGAG ACAGAAAACA AATCTAAGGG  3540
AAAGGAATAT TATGGGATTA AGCTGAGCAA GCAATTCTGG TGGAAAGTCA AACCTGTCAG  3600
TGCTCCACAC CAGGGCTGTG GTCCTCCCAG ACATGCATAG GAATGGCCAC AGGTTTACAC  3660
TGCCTTCCCA GCAATTATAA GCACACCAGA TTCAGGGAGA CTGACCACCA AGGGATAGTG  3720
TAAAAGGACA TTTTCTCAGT TGGGTCCATC AGCAGTTTTT CTTCCTGCAT TTATTGTTGA  3780
AAACTATTGT TTCATTTCTT CTTTTATAGG CCTTATTACT GCTTAATCCA AATGTGTACC  3840
ATTGGTGAGA CACATACAAT GCTCTGAATA CACTACGAAT TTGTATTAAA CACATCAGAA  3900
TATTTCCAAA TACAACATAG TATAGTCCTG AATATGTACT TTTAACACAA GAGAGACTAT  3960
TCAATAAAAA CTCACTGGGT CTTTCATGTC TTTAAGCTAA GTAAGTGTTC AGAAGGTTCT  4020
TTTTTATATT GTCCTCCACC TCCATCATTT TCAATAAAAG ATAGGGCTTT TGCTCCCTTG  4080
TTCTTGGAGG GACCATTATT ACATCTCTGA ACTACCTTTG TATCCAACAT GTTTTAAATC  4140
CTTAAATGAA TTGCTTTCTC CCAAAAAAAG CACAATATAA AGAAACACAA GATTTAATTA  4200
TTTTTCTACT TGGGGGGAAA AAAGTCCTCA TGTAGAAGCA CCCACTTTTG CAATGTTGTT  4260
CTAAGCTATC TATCTAACTC TCAGCCCATG ATAAAGTTCC TTAAGCTGGT GATTCCTAAT  4320
CAAGGACAAG CCACCCTAGT GTCTCATGTT TGTATTTGGT CCCAGTTGGG TACATTTTAA  4380
AATCCTGATT TTCGAGACTT AAAACCAGGT TAATGGCTAA GAATGGGTAA CATGACTCTT  4440
GTTGGATTGT TATTTTTTGT TTGCAATGGG GAATTTATAA GAAGCATCAA GTCTCTTTCT  4500
TACCAAAGTC TTGTTAGGTG GTTTATAGTT CTTTTGGCTA ACAAATCATT TTGGAAATAA  4560
AGATTTTTTA CTACAAAAAT G
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Seq ID NO: 510 Protein sequence
Protein Accession #: BAB18461.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRLSPAPLKL SRTPALLALA LPLAAALAFS DETLDKVPKS EGYCSRILRA QGTRREGYTE    60
FSLRVEGDPD FYKPGTSYRV TLSAAPPSYF RGFTLIALRE NREGDKEEDH AGTFQIIDEE   120
ETQFMSNCPV AVTESTPRRR TRIQVFWIAP PAGTGCVILK ASIVQKRIIY FQDEGSLTKK   180
LCEQDSTFDG VTDKPILDCC ACGTAKYRLT FYGNWSEKTH PKDYPRRANH WSAIIGGSHS   240
KNYVLWEYGG YASEGVKQVA ELGSPVKMEE EIRQQSDEVL TVIKAKAQWP AWQPLNVRAA   300
PSAEFSVDRT RHLMSFLTMM GPSPDWNVGL SAEDLCTKEC GWVQKVVQDL IPWDAGTDSG   360
VTYESPNKPT IPQEKIRPLT SLDHPQSPFY DPEGGSITQV ARVVIERIAR KGEQCNIVPD   420
NVDDIVADLA PEEKDEDDTP ETCIYSNWSP WSACSSSTCD KGKRMRQRML KAQLDLSVPC   480
PDTQDFQPCM GPGCSDEDGS TCTMSEWITW SPCSISCGMG MRSRERYVKQ FPEDGSVCTL   540
PTEETEKCTV NEECSPSSCL MTEWGEWDEC SATCGMGMKK RHRMIKMNPA DGSMCKAETS   600
QAEKCMMPEC HTIPCLLSPW SEWSDCSVTC GKGMRTRQRM LKSLAELGDC NEDLEQVEKC   660
MLPECPIDCE LTEWSQWSEC NKSCGKGHVI RTRMIQMEPQ FGGAPCPETV QRKKCRIRKC   720
LRNPSIQKLR WREARESRRS EQLKEESEGE QFPGCRMRPW TAWSECTKLC GGGIQERYMT   780
VKKRFKSSQF TSCKDKKEIR ACNVHPC
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Seq ID NO: 511 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

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1          11         21         31         41         51
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GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA    60
GCCCTGCAAC GGATCATGGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCC   120
CGGGAGGCGC TGGACACCGA GGAGGCGAA TTCATGGCTT GCAGCCCGGT GGCCCTGGAC   180
GAGAGCGACC CAGACTGGTG CAAGACGGCG TCGGGCCACA TCAAGCGGCC GATGAACGCG   240
TTCATGGTAT GGTCCAAGAT CGAACGCAGG AAGATCATGG AGCAGTCTCC GGACATGCAC   300
AACGCCCAGA TCTCCAACAG GCTGGGCAAG CGCTGGAAAA TGCTGAAGGA CAGCGAGAAG   360
ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC   420
TACAAGTACC GGCCCCGGAA AAAGCCCAAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC   480
CAGAGCCCAG AGAAGAGCGC GGCCGGCGGC GGCGGCGGGA GCGCGGGCGG AGGCGCGGGC   540
GGTGCCAAGA CCTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCCCGCCGCC   600
GCGGGCGCCA AGGCGGGCGC GGGCAAGGCG GCCCAGTCCG GGGACTACGG GGGCGCGGGC   660
GACGACTACG TGCTGGGCAG CCTGCGCGTG AGCGGCTCGG GCGGCGGCGG CGCGGGCAAG   720
ACGGTCAAGT GCGTGTTTCT GGATGAGGAC GACGACCACG ACGACGACGA CGACGAGCTG   780
CAGCTGCAGA TCAAACAGGA GCCGGACGAG GAGGACGAGG AACCACCGCA CCAGCAGCTC   840
CTGCAGCCGC CGGGGCAGCA GCCGTCGCAG CTGCTGAGAC GCTACAACGT CGCCAAAGTG   900
CCCGCCAGCC CTACGCTGAG CAGCTCGGCG GAGTCCCCCG AGGGAGCGAG CCTCTACGAC   960
GAGGTGCGGG CCGGCGCGAC CTCGGGCGCC GGGGGCGGCA GCCGCCTCTA CTACAGCTTC  1020
AAGAACATCA CCAAGCAGCA CCCGCCGCCG CTCGCGCAGC CCGCGCTGTC GCCCGCGTCC  1080
TCGCGCTCGG TGTCCACCTC CTCGTCCAGC AGCAGCGGCA GCAGCAGCGG CAGCAGCGGC  1140
GAGGACGCCG ACGACCTGAT GTTCGACCTG AGCTTGAATT TCTCTCAAAG CGCGCACAGC  1200
GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCCGGGA ACCTGTCCCT GTCGCTGGTG  1260
GATAAGGATT TGGATTCGTT CAGCGAGGGC AGCCTGGGCT CCCACTTCGA GTTCCCCGAC  1320
TACTGCACGC CGGAGCTGAG CGAGATGATC GCGGGGGACT GGCTGGAGGC GAACTTCTCC  1380
GACCTGGTGT TCACATATTG AAAGGCGCCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCAG  1440
AGCTGGGTTC CTTGGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG  1500
ATGATGGTGG TGTTGATGGT GGCGGTGGTA GGGTGGAGGG GAGAGAAGAA GATGCTGATG  1560
ATATTGATAA GATGTCGTGA CGCAAAGAAA TTGGAAAACA TGATGAAAAT TTTGGTGGAG  1620
TTAAAGTGAA ATGAGTAGTT TTTAAACATT TTTCCTGTCC TTTTTTTGTC CCCCCTCCCT  1680
TCCTTTATCG TGTCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA  1740
AAAATGTGTT TTTGTAATTA CTATTTCTTT TTCCTGAAAT TCGTGATTGC AACAAAGGCA  1800
GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT  1860
GTCGGTCTTT GAAGTCTGGA AGACGTCTGC AGAGGACCCT TTTGGCAGCA CAACTGTTAC  1920
TCTAGGGAGT TGGTGGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAAGAAC TGGTGATTTT  1980
TTTTTAACAA AAAAAGGG
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Seq ID NO: 512 Protein sequence
Protein Accession #: NP_003099.1

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1          11         21         31         41         51
|          |          |          |          |          |
MVQQAESLEA ESNLPREALD TEEGEFMACS PVALDESDPD WCKTASGHIK RPMNAFMVWS    60
KIERRKIMEQ SPDMHNAEIS KRLGKRWKML KDSEKIPFIR EAERLRLKHM ADYPDYKYRP   120
RKKPKMDPSA KPSASQSPEK SAAGGGGSA GGGAGGAKTS KGSSKKCGKL KAPAAACAKA   180
GAGKAAQSGD YGGAGDDYVL GSLRVSGSGG GGAGKTVKCV FLDEDDDDDD DDDELQLQIK   240
QEPDEEDEEP PHQQLLQPPG QQPSQLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVRAG   300
ATSGAGGGSR LYYSFKNITK QHPPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD   360
LMFDLSLNFS QSAHSASEQQ LGGGAAAGNL SLSLVDKDLD SFSEGSLGSH FEFPDYCTPE   420
LSEMIAGDWL EANFSDLVFT Y
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Seq ID NO: 513 DNA sequence
Nucleic Acid Accession #: CAT Cluster

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1          11         21         31         41         51
|          |          |          |          |          |
GGTCGACCTA AATCTGATAA CTGGCTTATT ATGTAATTTA TTGGTGTTAT TATAGTAGAG    60
ATTGGTAATC TACAGTAAGA TTTTCAGTTA GGATTTGAGA TTATGATAAT AACTAATAGA   120
ATATTTCTAA ATTGGAATTA GAAGATTGTT GTATGACAGA GAGTCAGGAC TTGCCATTTG   180
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GCAAACATCA AAGTCATTGT TTGGTGTGTA ATAGTACAAA ATCATCTTGC TTAACAGAGA   240
AAGGATATCT GTTGCTCCCG AATGAAACAA TTTTTCTGAA ATAGAGGGCC CAGAATTGGT   300
CTCTGACAAT TAATAAAGAC ATCAAAGATA GCAAAATGAT TTTTATATCT TAGGGCCAAT   360
ACTACCAATT TAATAATTAA AACAAGTTCT GGTGAGCTCT GAACTTGGCA GAATTGGTGG   420
CAACATAGAC TTTGGATTTT CCAAATTCCC CACATAAAAC AAAGGGGATC AACTAGATAG   480
AAAAACCAGA AACCTTTGGA AATATCTGTT TAAAAAAAAA AAAAAGTCGA CGCGGGCC
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Seq ID NO: 514 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1          11         21         31         41         51
|          |          |          |          |          |
GGAGCCACAG TGAAAGTCAA GAATGTCAGT GATTCCACAT TTAATATCTA CATTTTTGCA    60
GGGCAGTTAC TCTTTTGTAG TATAACATTG AGCTGATAGC ACATAGTGTA GACAAGTGAA   120
TACAGGATTC TCTGGGTTGT ATTCCCAGAA GTCTGGAGGT CATTTGGATA TTTGTGGGCC   180
CTTGGCTTCA CTCTGACTTG TGTGACACAT AAAAATTGTG ATGAAATGTC CTATAGATGT   240
CCTGCAGGTC TTAAAAGAAC CTTTCCAAAC TATGAAACAG CCCAGCAGCA CTGAGTTAGA   300
GGTAAATTCT GAACCCTTGA ACACTAAAAC TATTCTAACT GCACATAGAA TTGGCAAGTA   360
GCATTCTATG TCTATGAACA GTATGTCTTT TCTATATAAC AGAGAAAATC TTTTTAAGCA   420
AACTACTCAG TTTAAAACCT AATTCTTCTC ATAATCTCAG TACTTTTGAA TGAAGACATA   480
TCAATGCAAC AGTACACTCT TATTCAGGCA TTTGAAAGAA AGAATTCGAG ATCTAGTTTG   540
TATCAGATAT TATAAATTAG TATGGTTTAG TCTTTGTCAT GAAATTCTAC TTAATTTTTG   600
GACTATAGGT TTAAGAATGT AAGCAGAAGT TCTGCACCAA TCAGAATAAG CTACATTATG   660
CTTGAGTGAC AACTACTGTA ATGACAAAAT ATCAGTGGCT TAATACAATG GTTTTTCTCT   720
CATACTTGTT CATAAAGAGT CAGCAAGGAC CCTGCTCATT ATGGTCCCTC AGGGACCCAG   780
GGTTGTTGGA AGCTCCACCA TTTTAGATAG CTCCCTTCAA AGTCAGCCAT CTTTGGCAGT   840
CCATGTCCCC CAACAGGCTG GCAAAATTTG GCTCTGGATG GCTTCAAGGA TTGAGCATCG   900
GGCAGTTTAA ATGCTTTCAA CATGGAAAGT GGACACCGGC CACTCCCACT CACATCCCTT   960
GGGCCAGAAC TAGGTCACTG GGCCCGGACC TAACTTCGGA GGGTTGGGGA ATTGTAATTC  1020
CTCCATGTAC CCAAAGTGGA GAGAAGCCAG ATACTGAGAA ACATCAATAA TGGCTAACAG  1080
AAATCCATTC TACCATTCCC TTTGCCTAAA GTGAAAAGAT GAGTACTTTC ATCAATTTGT  1140
AAACTGTACT TTTGAAGTAA ATCCTGGTAG CTTGCATGGG GGCTGGATTT CCAGAAAGCC  1200
ATATGTAATT TGGGAATGAC ATTCACTTAA GCTCATAGAA TATCATTATT TGATGTAAAA  1260
TGCCCTCATT TGCAATACAG GACCAAAATG CACTAACCAC AAAACCCCCC TCCCCACGGG  1320
GCCCGGGGTC CCTATTCCCC TCCATCCCTT TAAATGAGGC ATTCTATGAT TTGGAATGGA  1380
AGCCCAGTTG TAGTCGTAAG AATTTTACTT AATTCAAGAA TTATTCTCAC TGAATATGTG  1440
CCAGTTCTGA AAGGAATGCA AAGTCAAATT TTGCATCTTC TTTGCTCAAG GGCCTTTAGA  1500
TGTAACAACA CAGACATGAT ACAAGGCTGA CAATGACATT ATGATTTAAA TATGTTAAAC  1560
AACTTATTAA ATTGTGAATC AACAAAAAAT TATGTTCTTT ATTTTATGGT TTTGCATAGT  1620
CCTGACTCAC TGCCTACATA CCCCTCTTGT TCCTCAGTTC TTATCCCTGA TTTCTTACAG  1680
GATGGCCTAA GACAGCTGTA GATGTTTTTA TTTAGCAAAA AAAAAAAAAA AAAAGTCGAC  1740
GCGGCCGCGA ATTTAGTAG
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Seq ID NO: 515 DNA sequence
Nucleic Acid Accession #: NM_012427
Coding sequence: 43..924

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CCCTGGATGT GGGTGCTCTG TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT   120
GTTCTCGCCA ACAATGATGT TTCCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC   180
AACCAGGACC TGGGAGCTGG GGCCGGGGAA GACGCCCGGT CGGATGACAG CAGCAGCCGC   240
ATCATCAATG GATCCGACTG CGATATGCAC ACCCAGCCGT GGCAGGCCGC GCTGTTGCTA   300
AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGGTGCATC CACAGTGGCT GCTCACGGCC   360
GCCCACTGCA GGAAGAAAGT TTTCAGAGTC CGTCTCGGCC ACTACTCCCT GTCACCAGTT   420
TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAATCCA TCCCCCACCC TGGCTACTCC   480
CACCCTGGCC ACTCTAACGA CCTCATGCTC ATCAAACTGA ACAGAAGAAT TCGTCCCACT   540
AAAGATGTCA GACCCATCAA CGTCTCCTCT CATTGTCCCT CTGCTGGGAC AAAGTGCTTG   600
GTGTCTGGCT GGGGGACAAC CAAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC   660
TTGAATATCA GCGTGCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT   720
GACACCATGT TCTGCGCCCG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTCTGGG   780
GGGCCTGTGG TCTGCAATGG CTCCCTGCAG GGACTCGTGT CCTGGGGAGA TTACCCTTGT   840
GCCCGGCCCA ACAGACCGGG TGTCTACACG AACCTCTGCA AGTTCACCAA GTGGATCCAG   900
GAAACCATCC AGGCCAACTC CTGAGTCATC CCAGGACTCA GCACACCGGC ATCCCCACCT   960
GCTGCAGGGA CAGCCCTGAC ACTCCTTTCA GACCCTCATT CCTTCCCAGA GATGTTGAGA  1020
ATGTTCATCT CTCCAGCCCC TGACCCCATG TCTCCTGGAC TCAGGGTCTG CTTCCCCCAC  1080
ATTGGGCTGA CCGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAAA CTGTCCAGGG  1140
CGGGGGTTGC GTCTCAATCT CCCTGGGGCA CTTTCATCCT CAAGCTCAGG GCCCATCCCT  1200
TCTCTGCAGC TCTGACCCAA ATTTAGTCCC AGAAATAAAC TGAGAAGTGG AAAAAAAAAA
```

Seq ID NO: 516 Protein sequence
Protein Accession #: NP_036559

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1          11         21         31         41         51
|          |          |          |          |          |
MATARPPWMW VLCALITALL LGVTEHVLAN NDVSCDHPSN TVPSGSNQDL GAGAGEDARS    60
DDSSSRIING SDCDMHTQPW QAALLLRPNQ LYCGAVLVHP QWLLTAAHCR KKVFRVRLGH   120
YSLSPVYESG QQMFQGVKSI PHPGYSHPGH SNDLMLIKLN RRIRPTKDVR PINVSSHCPS   180
AGTKCLVSGW GTTKSPQVHF PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS   240
CQGDSGGPVV CNGSLQGLVS WGDYPCARPN RPGVYTNLCK FTKWIQETIQ ANS
```

Seq ID NO: 517 DNA sequence
Nucleic Acid Accession #: NM_001719
Coding sequence: 123..1418

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1          11         21         31         41         51
|          |          |          |          |          |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGCACGGCCG CCTGCCCCCT    60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG   120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC   180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA   240
GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT   300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC   360
CCATGTTCAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG   420
GCCAGGGCTT CTCCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA   480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG   540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC   600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT   660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG   720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG   780
AGGAGGGCTG GCTGGTGTTT GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC   840
GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA   900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT   960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA  1020
GCCAGAACCG CTCCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG  1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC  1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG  1200
AGGGGGAGTG TGCCTTCCCT CTGAACTCCT ACATGAACGC CACCAACCAC GCCATCGTGC  1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCACGC  1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT  1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT  1440
TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA  1500
CTGCCTTTTG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG  1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA  1620
TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAAAA ACAACGCATA AAGAAAAATG  1680
GCCGGGCCAG GTCATTGGCT GGGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA  1740
TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT  1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA  1860
CAATAAAACG AATGAATG
```

Seq ID NO: 518 Protein sequence
Protein Accession #: NP_001710

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1          11         21         31         41         51
|          |          |          |          |          |
MHVRSLRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRLRSQE RREMQREILS    60
ILGLPHRPRP HLQGKHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS   120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY   180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVVNPR   240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS   300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE   360
GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY   420
RNMVVRACGC H
```

Seq ID NO: 519 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 264..782

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1          11         21         31         41         51
|          |          |          |          |          |
CCCTGCTCCA GTCACACCCG GAAGCTGACT GGTCCACGCA CAGCTGAAGC ATGAGGAAAC    60
TCATCGCGGG ACTAATTTTC CTTAAAATTT AGACTTGCAC AGTAAGGACT TCAACTGACC   120
TTCCTCAGAC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC   180
TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC   240
AACTTATCAG CAAGGAGCTC ATCATGCTGA CAGAAGTCAT GGAGGTCTGG CATGGCTTAG   300
TGATCGCGGT GGTGTCCCTC TTCCTGCAGG CCTGCTTCCT CACCGCCATC AACTACCTGC   360
TCAGCAGGCA CATGGCCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCCAGGTTC   420
CCAGGCCCAG CCCTGGCCAC CATCATCCAC CTGCTGTCAA AGAGATGAAG GAGACTCAGA   480
CAGAGAGAGA CATCCCAATG TCTGATTCCC TTTACAGGCA TGACAGCGAC ACACCCTCAG   540
ATAGCTTGGA TAGCTCCTGC AGTTCGCCTC CTGCCTGCCA GGCCACAGAG GATGTGGATT   600
ACACACAAGT CGTCTTTTCT GACCCTGGAG AACTAAAAAA TGACTCCCCG CTGGACTATG   660
AGAACATAAA GGAAATCACA GATTATGTCA ATGTCAATCC AGAAAGACAC AAGCCCAGTT   720
TCTGGTATTT TGTCAACCCT GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGGCCATGT   780
GAATTCCAAA TATTTTTAAT GGGGTCCAGT TCTCTATGGA TTCTTACATT TAATTTGTAG   840
GGAAATGCCA TTTTTCCCCC TTAAACAAGG CATGGGGCTC ACAAGTCTAT GGAGACAGGC   900
CAAAAAGAAT GTGGAGAAGA AAACTGATAA ATACACAGAG GTCCTCAAGA CCCATGGACT   960
CCTGGTCTGT ACCCAAAAAA GCTGTTCGTT CCTCAAAAAC AAAAACAAGG CTTGGCTGGG  1020
AAAACAGGCC AATGCCCCGG CAAGAAAGGT TGAGATCAGA TGTTAGGAAG AACTTTCAGG  1080
TAAAGTATGA GAACTATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCCAGGGA  1140
AAATTTTAAA AAGGTTGAAT CAGCTGTTGT AGAGTTCTAT TTGGCAATCT CATGGTTAAA  1200
TGACTTCCCT TTGAGCTCTT TAATTATTGG CAATAAACAA CTTCTTTAAA AGTTTTAAAT  1260
AAAATAGCAA CCACCACCA
```

Seq ID NO: 520 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MLTEVMEVWH GLVIAVVSLF LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGHH    60
HPPAVKEMKE TQTERDIPMS DSLYRHDSDT PSDSLDSSCS SPPACQATED VDYTQVVFSD   120
PGELKNDSPL DYENIKEITD YVNVNPERHK PSFWYFVNPA LSEPAEYDQV AM
```

Seq ID NO: 521 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 107..328

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1          11         21         31         41         51
|          |          |          |          |          |
CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTCCA AATATTTTTA    60
ATGGGGTCCA GTTCTCTATG GATTCTTACA TTTAATTTGT AGGGAAATGC CATTTTTCCC   120
CCTTAAACAA GGCATGGGGC TCACAAGTCT ATGGAGACAG GCCAAAAAGA ATGTGGAGAA   180
GAAAACTGAT AAATACACAG AGGTCCTCAA GACCCATGGA CTCCTGGTCT GTACCCAAAA   240
AAGCTGTTCG TTCCTCAAAA ACAAAAACAA GGCTTGGCTG GGAAAACAGG CCAATGCCCC   300
GGCAAGAAAG GTTGAGATCA GATGTTAGGA AGAACTTTCA GGTAAAGTAT GAGAACTATG   360
GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCCCAGG GAAAATTTTA AAAAGGTTGA   420
ATCAGCTGTT GTAGAGTTCT ATTTGGCAAT CTCATGGTTA AATGACTTCC CTTTGAGCTC   480
TTTAATTATT GGCAATAAAC AACTTCTTTA AAAGTTTTAA ATAAAATAGC AACCACCACC   540
A
```

Seq ID NO: 522 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPFFPLKQGM GLTSLWRQAK KNVEKKTDKY TEVLKTHGLL VCTQKSCSFL KNKNKAWLGK    60
QANAPARKVE IRC
```

Seq ID NO: 523 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 211..1895

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1          11         21         31         41         51
|          |          |          |          |          |
GGATCTGAGG GGCGCCCAGT CACTTCCTCC ACGTTCTCGT GCTGGGCGGG AGGAGCGGAT    60
GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTCGGA   120
GAGGAATTAT CTGATAAAAT TCCTGGGTTA ATATTTTTAA AAACGGAGAG TTTTTAAAAA   180
TGATTTTTTT CCCTCGAAAA TGACCTTTTT ATGCTTCGAA GCAGTTTGTC AACCAGCATA   240
GTGCTTTTTC TTTTCTCTTC TTTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG   300
CACAGGTTCC TTGAACAGCT GGATTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC   360
CTTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCAACATCA CAGCTCAACT CCAGGAGGGA   420
GAAGGTAATT GTTTCCCTGA ATGGGATGGA CTCATTTGTT GGCCCAGAGG AACAGTGGGG   480
AAAATATCGG CTGTTCCATG CCCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT   540
TTCCGACACT GTAACCCCAA TGGAACATGG GATTTTATGC ACAGCTTAAA TAAAACATGG   600
GCCAATTATT CAGACTGCCT TCGCTTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA   660
TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTC   720
GCTGTGGCTA TTCTCATCAT TGGTTACTTC AGACGATTGC ATTGCACTAG GAACTATATC   780
CACATGCACT TATTTGTGTC TTTCATGCTG AGAGCTACAA GCATCTTTGT CAAAGACAGA   840
GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA   900
CAAAATTCCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT   960
GTTGTGATGT TTATTTACTT CCTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC  1020
TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAAATACCT GTGGGGCTTC  1080
ATCTTGATAG GCTGGGGGTT TCCAGCAGCA TTTGTTGCAG CATGGGCTGT GGCACGAGCA  1140
ACTCTGGCTG ATGCGAGGTG CTGGGAACTT AGTGCTGGAG ACATCAAGTG GATTTATCAA  1200
GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATTCTGT TTCTGAATAC GGTTAGAGTT  1260
CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG  1320
AAACTGGCCA AATCGACACT GGTCCTGGTC CTAGTCTTTG GAGTGCATTA CATCGTGTTC  1380
GTATGCCTGC CTCACTCCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC  1440
TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG  1500
GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAAAGG  1560
ACACCGCCAT GTGGCAGCCG CAGATGCGGC TCAGTGCTCA CCACCGTGAC GCACAGCACC  1620
AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC  1680
AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC  1740
TCAGAGCAGG ACTGCCTGCC ACACTCTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG  1800
CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGGAATCTAA CCCAGACACT  1860
GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA
```

Seq ID NO: 524 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MLRSSLSTSI VLFLFSSFST INESISSRKR HRFLEQLDSD GTITIEEQIV LVLKAKVQCE    60
LNITAQLQEG EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW   120
DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGYSISFGSL AVAILIIGYF   180
RRLHCTRNYI HMHLFVSFML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSVD   240
KSQYIGCKIA VVMFIYFLAT NYYWILVEGL YLHNLIFVAF FSDTKYLWGF ILIGWGFPAA   300
FVAAWAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILFLNTVRV LATKIWETNA   360
VGHDTRKQYR KLAKSTLVLV LVFGVHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFQGFFV   420
SIIYCYCNGE VQAEVKKMWS RWNLSVDWKR TPPCGSRRCG SVLTTVTHST SSQSQVAAST   480
```

RMVLISGKAA KIASRQPDSH ITLPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540
SRPMESNPDT EGCQGETEDV L

Seq ID NO: 525 DNA sequence
Nucleic Acid Accession #: NM_005048
Coding sequence: 143..1795

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1          11         21         31         41         51
|          |          |          |          |          |
GGCCGGTGGC CGGGCCCGA CCACCCCAGC TGCGCGTCGT TACTGGCCAC AAGTTTGCTC    60
TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT   120
TCTTCCTACA GCCGTTCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG   180
GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCCAGCTG GATTCTGATG GCACCATTAC   240
TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC   300
AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTTGTTG   360
GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCCATGC CCTCCTTATA TTTATGACTT   420
CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA   480
CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT   540
CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC   600
CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTTACTTCA GACGATTGCA   660
TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCATGCTGA GAGCTACAAG   720
CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT   780
AATAATGCAG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA   840
TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG   900
GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCGGACAC   960
CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC  1020
ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGCGAGGTGC TGGGAACTTA GTGCTGGAGA  1080
CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT  1140
TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA  1200
CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCTGGTCC TAGTCTTTGG  1260
AGTGCATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT  1320
CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA  1380
CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT  1440
CTCCGTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCCGC AGATCCGGCT CAGTGCTCAC  1500
CACCGTGACG CACAGCACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT  1560
TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC  1620
TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCCTGCCA CACTCTTTCC ACGAGGAGAC  1680
CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT  1740
GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAAACT GAGGATGTTC TCTGAATGGA  1800
CATTTGTGGC TGACTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG  1860
ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT  1920
TTTTAGGCTC CATGAATTGG CTCCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT  1980
GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT  2040
GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG  2100
GCTGTAGCTT TCTCTCATAT ATATCACCCT AAATATAATG AAGATCTTTT AGTGTGTATC  2160
ATTTTCCTTT TAGAAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC  2220
ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA  2280
GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT  2340
TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTCAC  2400
ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC  2460
TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA  2520
TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG  2580
TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAAAAATTT GTTTTAAAAA  2640
T
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Seq ID NO: 526 Protein sequence
Protein Accession #: NP_005039

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1          11         21         31         41         51
|          |          |          |          |          |
MAGLGASLHV WGWLMLGSCL LARAQLDSDG TITIEEQIVL VLKAKVQCEL NITAQLQEGE    60
GNCFPEWDGL ICWPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA   120
NYSDCLRFLQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH   180
MHLFVSFMLR ATSIFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV   240
VMFIYFLATN YYWILVEGLY LHNLIFVAFF SDTKYLWGFI LIGWGFPAAF VAAWAVARAT   300
LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK   360
LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFFVS IIYCYCNGEV   420
QAEVKKMWSR WNLSVDWKRT PPCGSRRCGS VLTTVTHSTS SQSQVAASTR MVLISGKAAK   480
IASRQPDSHI TLPGYVWSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RPMESNPDTE   540
GCQGETEDVL
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Seq ID NO: 527 DNA sequence
Nucleic Acid Accession #: XM_036683
Coding sequence: 38..3655

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1          11         21         31         41         51
|          |          |          |          |          |
GCTTTGCCCA GTAGTTGGAA AGTGAACTCG ACTCGTGATG GTTCTCCTGT CACTTTGGTT    60
GATAGCAGCC GCTCTGGTAG AGGTTAGGAC TTCAGCTGAT GGACAAGCTG GTAATGAAGA   120
AATGGTGCAA ATAGATTTAC CAATAAAGAG ATATAGAGAG TATGAGCTGG TGACTCCAGT   180
CAGCACAAAT CTAGAAGGAC GCTATCTCTC CCATACTCTT TCTGCGAGTC ACAAAAAGAG   240
GTCAGCGAGG GACGTGTCTT CCAACCCTGA GCAGTTGTTC TTTAACATCA CGGCATTTGG   300
AAAAGATTTT CATCTGCGAC TAAAGCCCAA CACTCAACTA GTAGCTCCTG GGGCTGTTGT   360
GGAGTGGCAT GAGACATCTC TGGTGCCTGG GAATATAACC GATCCCATTA ACAACCATCA   420
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ACCAGGAAGT GCTACGTATA GAATCCGCAA AACAGAGCCT TTGCAGACTA ACTGTGCTTA 480
TGTTGGTGAC ATCGTGGACA TTCCAGGAAC CTCTGTTGCC ATCAGCAACT GTGATGGTCT 540
GGCTGGAATG ATAAAAAGTG ATAATGAAGA GTATTTCATT GAACCCTTGG AAAGAGGTAA 600
ACAGATGGAG GAAGAAAAAG GAAGGATTCA TGTTGTCTAC AAGAGATCAG CTGTAGAACA 660
GGCTCCCATA GACATGTCCA AAGACTTCCA CTACAGAGAG TCGGACCTGG AAGGCCTTGA 720
TGATCTAGGT ACTGTTTATG GCAACATCCA CCAGCAGCTG AATGAAACAA TGAGACGCCG 780
CAGACACGCG GGAGAAAACG ATTACAATAT CGAGGTACTG CTGGGAGTGG ATGACTCTGT 840
GGTCCGTTTC CATGGCAAAG AGCACGTCCA AAACTACCTC CTGACCCTAA TGAACATTGT 900
GAATGAAATT TACCATGATG AGTCCCTCGG AGTGCATATA AATGTGGTCC TGGTGCGCAT 960
GATAATGCTG GGATATGCAA AGTCCATCAG CCTCATAGAA AGGGGAAACC CATCCAGAAG 1020
CTTGGAGAAT GTGTGTCGCT GGGCGTCCCA ACAGCAAAGA TCTGATCTCA ACCACTCTGA 1080
ACACCATGAC CATGCAATTT TTTTAACCAG GCAAGACTTT GGACCTGCTG GAATGCAAGG 1140
ATATGCTCCA GTCACCGGCA TGTGTCATCC AGTGAGAAGT TGTACCCTGA ATCATGAGGA 1200
TGGTTTTTCA TCTGCTTTTG TAGTAGCCCA TGAAACGGGC CATGTGTTGG GAATGGAGCA 1260
TGATGGACAA GGCAACAGGT GTGGTGATGA GACTGCTATG GGAAGTGTCA TGGCTCCCTT 1320
GGTACAAGCA GCATTCCATC GTTACCACTG GTCCCGATGC AGTGGTCAAG AACTGAAAAG 1380
ATATATCCAT TCCTATGACT GTCTCCTTGA TGACCCTTTT GATCATGATT GGCCTAAACT 1440
CCCAGAACTT CCTGGAATCA ATTATTCTAT GGATGAGCAA TGTCGTTTTG ATTTTGGTGT 1500
TGGCTATAAA ATGTGCACCG CGTTCCGAAC CTTTGACCCA TGTAAACAGC TGTGGTGTAG 1560
CCATCCTGAT AATCCCTACT TTTGTAAGAC TAAAAAGGGA CCTCCACTTG ATGGGACTGA 1620
ATGTGCTGCT GGAAAATGGT GCTATAAGGG TCATTGCATG TGGAAGAATG CTAATCAGCA 1680
AAAACAAGAT GGCAATTGGG GGTCATGGAC TAAATTTGGC TCCTGTTCTC GGACATGTGG 1740
AACTGGTGTT CGTTTCAGAA CACGCCAGTG CAATAATCCC ATGCCCATCA ATGGTGGTCA 1800
GGATTGTCCT GGTGTTAATT TTGAGTACCA GCTTTGTAAC ACAGAAGAAT GCCAAAAACA 1860
CTTTGAGGAC TTCAGAGCAC AGCAGTGTCA GCAGCGAAAC TCCCACTTTG AATACCAGAA 1920
TACCAAACAC CACTGGTTGC CATATGAACA TCCTGACCCC AAGAAAAGAT GCCACCTTTA 1980
CTGTCAGTCC AAGGAGACTG GAGATGTTGC TTACATGAAA CAACTGGTGC ATGATGGAAC 2040
GCACTGTTCT TACAAAGATC CATATAGCAT ATGTGTGCGA GGAGAGTGTG TGAAAGTGGG 2100
CTGTGATAAA GAAATTGGTT CTAATAAGGT TGAGGATAAG TGTGGTGTCT GTGGAGGAGA 2160
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TCGCACTGTA CGCTGCCTTC AGCCACTCCT TGATGGCACC AACCGCTCTG TGCACAGCAA 2880
ATACTGCATG GGTGACCGTC CCGAGAGCCG CCGGCCCTGT AACAGAGTGC CCTGCCCTGC 2940
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GAGGCAGGTC CTCTGCAGGG CTGGGGACCA CTGTGATGGT GAAAAGCCTG AGTCGGTCAG 3060
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ATAAGTGCAT CATGAATTAC ATGTACATGA GAGGAGATAG TGATATCAGC ATAATGATTT 5340
TGAGGTCAGT ACCTGAGCTG TCTAAAAATA TATTATACAA ACTAAAATGT AGATGAATTA 5400
ACCTCTCAAA GCACAGAATG TGCAAGAACT TTTGCATTTT AATCGTTGTA AACTAACAGC 5460

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CCTAAAAATT CCCATAGAAT AAAATTCTCT CTAGTTTACT TGTGTGTGCA TACATCTCAT  5640
CCACAGGGGA AGATAAAGAT GGTCACACAA ACAGTTTCCA TAAAGATGTA CATATTCATT  5700
ATACTTCTGA CCTTTGGGCT TTCTTTTCTA CTAAGCTAAA AATTCCTTTT TATCAAAGTG  5760
TACACTACTG ATGCTGTTTG TTGTACTGAG AGCACGTACC AATAAAAATG TTAACAAAAT  5820
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Seq ID NO: 528 Protein sequence
Protein Accession #: XP_036683

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LSASHKKRSA RDVSSNPEQL FFNITAFGKD FHLRLKPNTQ LVAPGAVVEW HETSLVPGNI   120
TDPINNHQPG SATYRIRKTE PLQTNCAYVG DIVDIPGTSV AISNCDGLAG MIKSDNEEYF   180
IEPLERGKQM EEEKGRIHVV YKRSAVEQAP IDMSKDFHYR ESDLEGLDDL GTVYGNIHQQ   240
LNETMRRRRH AGENDYNIEV LLGVDDSVVR FHGKEHVQNY LLTLMNIVNE IYHDESLGVH   300
INVVLVRMIM LGYAKSISLI ERGNPSRSLE NVCRWASQQQ RSDLNHSEHH DHAIFLTRQD   360
FGPAGMQGYA PVIGMCHPVR SCTLNHEDGF SSAFVVAHET GHVLGMEHDG QGNRCGDETA   420
MGSVMAPLVQ AAFHRYHWSR CSGQELKRYI HSYDCLLDDP FDHDWPKLPE LPGINYSMDE   480
QCRFDFGVGY KMCTAFRTFD PCKQLWCSHP DNPYFCKTKK GPPLDGTECA AGKWCYKGHC   540
MWKNANQQKQ DGNWGSWTKF GSCSRTCGTG VRFRTRQCNN PMPINGGQDC PGVNFEYQLC   600
NTEECQKHFE DFRAQQCQQR NSHFEYQNTK HHWLPYEHPD PKKRCHLYCQ SKETGDVAYM   660
KQLVHDGTHC SYKDPYSICV RGECVKVGCD KEIGSNKVED KCGVCGGDNS HCRTVKGTFT   720
RTPRKLGYLK MFDIPPGARH VLIQEDEASP HILAIKNQAT GHYILNGKGE EAKSRTFIDL   780
GVEWDYNIED DIESLHTDGP LHDPVIVLII PQENDTRSSL TYKYIIHEDS VPTINSNNVI   840
QEELDTFEWA LKSWSQCSKP CGGGFQYTKY GCRRKSDNKM VHRSFCEANK KPKPIRRMCN   900
IQECTHPLWV AEEWEHCTKT CGSSGYQLRT VRCLQPLLDG TNRSVHSKYC MGDRPESRRP   960
CNRVPCPAQW KTGPWSECSV TCGEGTEVRQ VLCRAGDHCD GEKPESVRAC QLPPCNDEPC  1020
LGDKSIFCQM EVLARYCSIP GYNKLCCESC SKRSSTLPPP YLLEAAETHD DVISNPSDLP  1080
RSLVMPTSLV PYHSETPAKK MSLSSISSVG GPNAYAAFRP NSKPDGANLR QRSAQQAGSK  1140
TVRLVTVPSS PPTKRVHLSS ASQMAAASFF AASDSIGASS QARTSKKDGK IIDNRRPTRS  1200
STLER
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Seq ID NO: 529 DNA sequence
Nucleic Acid Accession #: NM_002774
Coding sequence: 246..980

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AGCCCGGGGC AGGGGCGGGG GCCAGTGTGG TGACACACGC TGTAGCTGTC TCCCCGGCTG   120
GCTGGCTCGC TCTCTCCTGG GGACACAGAG GTCGGCAGGC AGCACACAGA GGGACCTACG   180
GGCAGCTGTT CCTTCCCCCG ACTCAAGAAT CCCCGGAGGC CCGGAGGCCT GCAGCAGGAG   240
CGGCCATGAA GAAGCTGATG GTGGTGCTGA GTCTGATTGC TGCAGCCTGG GCAGAGGAGC   300
AGAATAAGTT GGTGCATGGC GGACCCTGCG ACAAGACATC TCACCCCTAC CAAGCTGCCC   360
TCTACACCTC GGGCCACTTG CTCTGTGGTG GGGTCCTTAT CCATCCACTG TGGGTCCTCA   420
CAGCTGCCCA CTGCAAAAAA CCGAATCTTC AGGTCTTCCT GGGGAAGCAT AACCTTCGGC   480
AAAGGGAGAG TTCCCAGGAG CAGAGTTCTG TTGTCCGGGC TGTGATCCAC CCTGACTATG   540
ATGCCGCCAG CCATGACCAG GACATCATGC TGTTGCGCCT GGCACGCCCA GCCAAACTCT   600
CTGAACTCAT CCAGCCCCTT CCCCTGGAGA GGGACTGCTC AGCCAACACC ACCAGCTGCC   660
ACATCCTGGG CTGGGGCAAG ACAGCAGATG GTGATTTCCC TGACACCATC CAGTGTGCAT   720
ACATCCACCT GGTGTCCCGT GAGGAGTGTG AGCATGCCTA CCCTGGCCAG ATCACCCAGA   780
ACATGTTGTG TGCTGGGGAT GAGAAGTACG GGAAGGATTC CTGCCAGGGT GATTCTGGGG   840
GTCCGCTGGT ATGTGGAGAC CACCTCCGAG GCCTTGTGTC ATGGGGTAAC ATCCCCTGTG   900
GATCAAAGGA GAAGCCAGGA GTCTACACCA ACGTCTGCAG ATACACGAAC TGGATCCAAA   960
AAACCATTCA GGCCAAGTGA CCCTGACATG TGACATCTAC CTCCCGACCT ACCACCCCAC  1020
TGGCTGGTTC CAGAACGTCT CTCACCTAGA CCTTGCCTCC CCTCCTCTCC TGCCCAGCTC  1080
TGACCCTGAT GCTTAATAAA CGCAGCGACG TGAGGGTCCT GATTCTCCCT GGTTTTACCC  1140
CAGCTCCATC CTTGCATCAC TGGGGAGGAC GTGATGAGTG AGGACTTGGG TCCTCGGTCT  1200
TACCCCCACC ACTAAGAGAA TACAGGAAAA TCCCTTCTAG GCATCTCCTC TCCCCAACCC  1260
TTCCACACGT TTGATTTCTT CCTGCAGAGG CCCAGCCACG TGTCTGGAAT CCCAGCTCCG  1320
CTGCTTACTG TCGGTGTCCC CTTGGGATGT ACCTTTCTTC ACTGCAGATT TCTCACCTGT  1380
AAGATGAAGA TAAGGATGAT ACAGTCTCCA TCAGGCAGTG GCTGTTGGAA AGATTTAAGA  1440
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Seq ID NO: 530 Protein sequence
Protein Accession #: NP_002765

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AHCKKPNLQV FLGKHNLRQR ESSQEQSSVV RAVIHPDYDA ASHDQDIMLL RLARPAKLSE   120
LIQPLPLERD CSANTTSCHI LGWGKTADGD FPDTIQCAYI HLVSREECEH AYPGQITQNM   180
LCAGDEKYGK DSCQGDSGGP LVCGDHLRGL VSWGNIPCGS KEKPGVYTNV CRYTNWIQKT   240
IQAK
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Seq ID NO: 531 DNA sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

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GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT   180
TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC   240
TACCTGTTGG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCCTG   300
ATGTTTAACA CAGGCCCAGT TTCAAAAACT TTGACTGTCA ACCGCTGGTT TCTCCGTCAG   360
GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG   420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA   480
CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTTATGG GGGCGGTCCC CACACTGGGC   540
TGGAATTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCCATTTA CAGCAGGAGT   600
TACCTTGTTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC   660
CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG   720
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GCGTTTGTGG TATGCTGGAC CCCGGGCCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC   840
AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC   900
GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG   960
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA  1020
GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA  1080
GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCCACCCA GGTGATGACT  1140
GTCTTAGG
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Seq ID NO: 532 Protein sequence
Protein Accession #: NP_036284

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FHFPFYYLLA NLAAADFFAG IAYVFLMFNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL   120
LVIAVERHMS IMRMRVHSNL TKKRVTLLIL LVWAIAIFMG AVPTLGWNCL CNISACSSLA   180
PIYSRSYLVF WTVSNLMAFL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT   240
VMTVLGAFVV CWTPGLVVLL LDGLNCRQCG VQHVKRWFLL LALLNSVVNP IIYSYKDEDM   300
YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS
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Seq ID NO: 533 DNA sequence
Nucleic Acid Accession #: NM_002821
Coding sequence: 150..3362

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GCGCTCCGGT GCGTCCGCCT CCTGTGCCCG CCGCGGAGCA GTCTGCGGCC CGCCGTGCGC   120
CCTCAGCTCC TTTTCCTGAG CCCGCCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC   180
CCCGCCGGTT GCCTCTGCTC AGCGTCCTGC TGCTGCCGCT GCTGGGCGGT ACCCAGACAG   240
CCATTGTCTT CATCAAGCAG CCGTCCTCCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC   300
TTCGCTGTGA GGTTGAGGCT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC   360
CTGTCCAGGA CACGGAGCGG CGTTTCGCCC AGGGCAGCAG CCTGAGCTTT GCAGCTGTGG   420
ACCGGCTGCA GGACTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG   480
AAGCCCGCAG TGCCAACGCC TCCTTCAACA TCAAATGGAT TGAGGCAGGT CCTGTGGTCC   540
TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGGTCACA CTTCGTTGCC   600
ACATTGATGG GCACCCTCGG CCCACCTACC AATGGTTCCG AGATGGGACC CCCCTTTCTG   660
ATGGTCAGAG CAACCACACA GTCAGCAGCA AGGAGCGGAA CCTGACGCTC CGGCCAGCTG   720
GTCCTGAGCA TAGTGGGCTG TATTCCTGCT GCGCCCACAG TGCTTTTGGC CAGGCTTGCA   780
GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAAGCTT TGCCAGGGTG GTGCTGGCAC   840
CCCAGGACGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC   900
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TCATCCTGGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTGAGCCAC  1140
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TGCCCTCCTG GCTGAAGAAG CCCCAAGACA GCCAGCTGGA GGAGGGCAAA CCCGGCTACT  1440
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GCTTGGGCTC CGGCCCCGCG GCCACCAACA AACGCCACAG CACAAGTGAT AAGATGCACT  2520
TCCCACGGTC TAGCCTGCAG CCCATCACCA CGCTGGGGAA GAGTGAGTTT GGGGAGGTGT  2580
TCCTGGCAAA GGCTCAGGGC TTGGAGGAGG GAGTGGCAGA GACCCTGGTA CTTGTGAAGA  2640
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GCCTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG  2700
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GCACCCAGGT AGCCCTGGGC ATGGAGCACC TGTCCAACAA CCGCTTTGTG CATAAGGACT  2940
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TCAGCAAGGA TGTGTACAAC AGTGAGTACT ACCACTTCCG CCAGGCCTGG GTGCCGCTGC  3060
GCTGGATGTC CCCCGAGGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGTCTGGG  3120
CCTTCGGTGT GCTGATGTGG GAAGTGTTTA CACATGGAGA GATGCCCCAT GGTGGGCAGG  3180
CAGATGATGA AGTACTGGCA GATTTGCAGG CTGGGAAGGC TAGACTTCCT CAGCCCGAGG  3240
GCTGCCCTTC CAAACTCTAT CGGCTGATGC AGCGCTGCTG GGCCCTCAGC CCCAAGGACC  3300
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GAGGAGGGAG CCCGCTCAGG ATGGCCTGGG CAGGGGAGGA CATCTCTAGA GGGAAGCTCA  3420
CAGCATGATG GGCAAGATCC CTGTCCTCCT GGGCCCTGAG GTGCCCTAGT GCAACAGGCA  3480
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TTCTCCCCTT GACCGGGTCC AACTCTGCCA CTCATCTGCC AACTTTGCCT GGGGAGGGCT  3720
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CCCCACCCTT CTCTCCTTTC CTCATCCTAA GTGCCTGGCA GATGAAGGAG TTTTCAGGAG  3960
CTTTTGACAC TATATAAACC GCCCTTTTTG TATGCACCAC GGGCGGCTTT TATATGTAAT  4020
TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG  4080
GCCATCCTTA CCCCACACTT TTATTGTTGT CGTTTTTTGT TTGTTTTGTT TTTTGTTTT  4140
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Seq ID NO: 534 Protein sequence
Protein Accession #: NP_002812

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IKWIEAGPVV LKHPASEAEI QPQTQVTLRC HIDGHPRPTY QWFRDGTPLS DGQSNHTVSS  180
KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SSQNFTLSIA DESFARVVLA PQDVVVARYE  240
EAMPHCQFSA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR  300
CIGQGQRGPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG  360
VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD  420
SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVYDGTWYR  480
CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QQCMEFDKEA TVPCSATGRE KPTIKWERAD  540
GSSLPEWVID NAGTLHFARV TRDDAGNYTC IASNGPQGQI RAHVQLTVAV FITFKVEPER  600
TTVYQGHTAL LQCEAQGDPK PLIQWKGKDR ILDPTKLGPR MHIFQNGSLV IHDVAPEDSG  660
RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPGSPPPYK MIQTIGLSVG AAVAYIIAVL  720
GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN  780
KRHSTSDKMH FPRSSLQPIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ  840
LDFRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ  900
PLSTKQKVAL CTQVALGMEH LSNNRFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY  960
YHFRQAWVPL RWMSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLADLQ 1020
AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP
```

Seq ID NO: 535 DNA sequence
Nucleic Acid Accession #: NM_013952
Coding sequence: 161..1357

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1          11         21         31         41         51
|          |          |          |          |          |
TTCAGAAGGA GGAGAGACAC CGGGCCCAGG GCACCCTCGC GGGCGGGCGG ACCCAAGCAG   60
TGAGGGCCTG CAGCCGGCCG GCCAGGGCAG CGGCAGGCGC GGCCCGGACC TACGGGAGGA  120
AGCCCCGAGC CCTCGGCGGG CTGCGAGCGA CTCCCCGGCG ATGCCTCACA ACTCCATCAG  180
ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG AGGGGCCTTT GTGAATGGCA GACCTCTGCC  240
GGAAGTGGTC CGCCAGCGCA TCGTAGACCT GGCCCACCAG GGTGTAAGGC CCTGCGACAT  300
CTCTCGCCAG CTCCGCGTCA GCCATGGCTG CGTCAGCAAG ATCCTTGGCA GGTACTACGA  360
GACTGGCAGC ATCCGGCCTG GAGTGATAGG GGGCTCCAAG CCCAAGGTGG CCACCCCCAA  420
GGTGGTGGAG AAGATTGGGG ACTACAAACG CCAGAACCCT ACCATGTTTG CCTGGGAGAT  480
CCGAGACCGG CTCCTGGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCCA GTGTCAGCTC  540
CATTAATAGA ATCATCCGGA CCAAAGTGCA GCAACCATTC AACCTCCCTA TGGACAGCTG  600
CGTGGCCACC AAGTCCCTGA GTCCCGGACA CACGCTGATC CCCAGCTCAG CTGTAACTCC  660
CCCGGAGTCA CCCCAGTCGG ATTCCCTGGG CTCCACCTAC TCCATCAATG GGCTCCTGGG  720
CATCGCTCAG CCTGGCAGCG ACAAGAGGAA AATGGATGAC AGTGATCAGG ATAGCTGCCG  780
ACTAAGCATT GACTCACAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGGATGC  840
CTTCAGCCAG CACCACCTCG AGCCGCTCGA GTGCCCATTT GAGCGGCAGC ACTACCCAGA  900
GGCCTATGCC TCCCCCAGCC ACACCAAAGG CGAGCAGGGC CTCTACCCGC TGCCCTTGCT  960
CAACAGCACC CTGGACGACG GGAAGGCCAC CCTGACCCCT TCCAACACGC CACTGGGGCG 1020
CAACCTCTCG ACTCACCAGA CCTACCCCGT GGTGGCAGCT CCGCCCTTTT GGATCTGCAG 1080
CAAGTCGGCT CCGGGGTCCC GCCCTTCAAT GCCTTTCCCC ATGCTGCCTC CGTGTACGGG 1140
CAGTTCACGG GCCAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCCAC GCTGCCCGGA 1200
TACCCACCCC ACATCCCCAC CAGCGGACAG GGCAGCTATG CCTCCTCTGC CATCGCAGGC 1260
ATGGTGGCAG GAAGTGAATA CTCTGGCAAT GCCTATGGCC ACACCCCCTA CTCCTCCTAC 1320
AGCGAGGCCT GGGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATATTA TTACAGTTCC 1380
ACATCAAGGC CGAGTGCACC GCCCACCACT GCCACGGCCT TTGACCATCT GTAGTTGCCA 1440
TGGGGACAGT G
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Seq ID NO: 536 Protein sequence
Protein Accession #: NP_039246

```
1          11         21         31         41         51
|          |          |          |          |          |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK    60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND   120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY   180
SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF   240
ERQHYPEAYA SPSHTKGEQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAA   300
PPFWICSKSA PGSRPSMPFP MLPPCTGSSR ARPSSQGERW WGPRCPDTHP TSPPADRAAM   360
PPLPSQAWWQ EVNTLAMPMA TPPTPPTARP GASPTPAC
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Seq ID NO: 537 DNA sequence
Nucleic Acid Accession #: NM_003466.1
Coding sequence: 11..1363

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1          11         21         31         41         51
|          |          |          |          |          |
GAATTCGGCG ATGCCTCACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG    60
AGGGGCCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT   120
GGCCCACCAG GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCCGCGTCA GCCATGGTTG   180
CGTCAGCAAG ATCCTTGGCA GGTACTACGA GACTGGCAGC ATCCGGCCTG GAGTGATAGG   240
GGGCTCCAAG CCCAAGGTGG CCACCCCCAA GGTGGTGGAG AAGATTGGGG ACTACAAACG   300
CCAGAACCCT ACCATGTTTG CCTGGGAGAT CCGAGACCGG CTCCTGGCTG AGGGCGTCTG   360
TGACAATGAC ACTGTGCCCA GTGTCAGCTC CATTAATAGA ATCATCCGGA CCAAAGTGCA   420
GCAACCATTC AACCTCCCTA TGGACAGCTG CGTGGCCACC AAGTCCCTGA GTCCCGGACA   480
CACGCTGATC CCCAGCTCAG CTGTAACTCC CCCGGAGTCA CCCCAGTCGG ATTCCCTGGG   540
CTCCACCTAC TCCATCAATG GGCTCCTGGG CATCGCTCAG CCTGGCAGCG ACAAGAGGAA   600
AATGGATGAC AGTGATCAGG ATAGCTGCCG ACTAAGCATT GACTCACAGA GCAGCAGCAG   660
CGGACCCCGA AAGCACCTTC GCACGGATGC CTTCAGCCAG CACCACCTCG AGCCGCTCGA   720
GTGCCCATTT GAGCGGCAGC ACTACCCAGA GGCCTATGCC TCCCCCAGCC ACACCAAAGG   780
CGAGCAGGGC CTCTACCCGC TGCCCTTGCT CAACAGCACC CTGGACGACG GGAAGGCCAC   840
CCTGACCCCT TCCAACACGC CACTGGGGCG CAACCTCTCG ACTCACCAGA CCTACCCCGT   900
GGTGGCAGAT CCTCACTCAC CCTTCGCCAT AAAGCAGGAA ACCCCCGAGG TGTCCAGTTC   960
TAGCTCCACC CCTTCCTCTT TATCTAGCTC CGCCTTTTTG GATCTGCAGC AAGTCGGCTC  1020
CGGGGTCCCG CCCTTCAATG CCTTTCCCCA TGCTGCCTCC GTGTACGGGC AGTTCACGGG  1080
CCAGGCCCTC CTCTCAGGGC GAGAGATGGT GGGGCCCACG CTGCCCGGAT ACCCACCCCA  1140
CATCCCCACC AGCGGACAGG GCAGCTATGC CTCCTCTGCC ATCGCAGGCA TGGTGGCAGG  1200
AAGTGAATAC TCTGGCAATG CCTATGGCCA CACCCCCTAC TCCTCCTACA GCGAGGCCTG  1260
GCGCTTCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC  1320
GAGTGCACCG CCCACCACTG CCACGGCCTT TGACCATCTG TAGTTGAAGC TT
```

Seq ID NO: 538 Protein sequence
Protein Accession #: NP_003457

```
1          11         21         31         41         51
|          |          |          |          |          |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK    60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND   120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY   180
SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF   240
ERQHYPEAYA SPSHTKGEQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAD   300
PHSPFAIKQE TPEVSSSSST PSSLSSSAFL DLQQVGSGVP PFNAFPHAAS VYGQFTGQAL   360
LSGREMVGPT LPGYPPHIPT SGQGSYASSA IAGMVAGSEY SGNAYGHTPY SSYSEAWRFP   420
NSSLLSSPYY YSSTSRPSAP PTTATAFDHL
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Seq ID NO: 539 DNA sequence
Nucleic Acid Accession #: NM_006799
Coding sequence: 19..963

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1          11         21         31         41         51
|          |          |          |          |          |
GCCGCGGGAG AGGAGGCCAT GGGCGCGCGC GGGGCGCTGC TGCTGGCGCT GCTGCTGGCT    60
CGGGCTGGAC TCAGGAAGCC GGAGTCGCAG GAGGCGGCGC CGTTATCAGG ACCATGCGGC   120
CGACGGGTCA TCACGTCGCG CATCGTGGGT GGAGAGGACG CCGAACTCGG GCGTTGGCCG   180
TGGCAGGGGA GCCTGCGCCT GTGGGATTCC CACGTATGCG GAGTGAGCCT GCTCAGCCAC   240
CGCTGGGCAC TCACGGCGGC GCACTGCTTT GAAACCTATA GTGACCTTAG TGATCCCTCC   300
GGGTGGATGG TCCAGTTTGG CCAGCTGACT TCCATGCCAT CCTTCTGGAG CCTGCAGGCC   360
TACTACACCC GTTACTTCGT ATCGAATATC TATCTGAGCC CTCGCTACCT GGGGAATTCA   420
CCCTATGACA TTGCCTTGGT GAAGCTGTCT GCACCTGTCA CCTACACTAA ACACATCCAG   480
CCCATCTGTC TCCAGGCCTC CACATTTGAG TTTGAGAACC GGACAGACTG CTGGGTGACT   540
GGCTGGGGGT ACATCAAAGA GGATGAGGCA CTGCCATCTC CCCACACCCT CCAGGAAGTT   600
CAGGTCGCCA TCATAAACAA CTCTATGTGC AACCACCTCT TCCTCAAGTA CAGTTTCCGC   660
AAGGACATCT TTGGAGACAT GGTTTGTGCT GGCAATGCCC AAGGCGGGAA GGATGCCTGC   720
TTCGGTGACT CAGGTGGACC CTTGGCCTGT AACAAGAATG GACTGTGGTA TCAGATTGGA   780
GTCGTGAGCT GGGGAGTGGG CTGTGGTCGG CCCAATCGGC CCGGTGTCTA CACCAATATC   840
AGCCACCACT TTGAGTGGAT CCAGAAGCTG ATGGCCCAGA GTGGCATGTC CCAGCCAGAC   900
CCCTCCTGGC CGCTACTCTT TTTCCCTCTT CTCTGGGCTC TCCCACTCCT GGGGCCGGTC   960
TGAGCCTACC TGAGCCCATG CAGCCTGGGG CCACTGCCAA GTCAGGCCCT GGTTCTCTTC  1020
TGTCTTGTTT GGTAATAAAC ACATTCCAGT TGATGCCTTG CAGGGCATTC TTCAAAA
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Seq ID NO: 540 Protein sequence
Protein Accession #: NP_006790

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1          11         21         31         41         51
|          |          |          |          |          |
MGARGALLLA LLLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWPWQGSLR    60
LWDSHVCGVS LLSHRWALTA AHCFETYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF   120
VSNIYLSPRY LGNSPYDIAL VKLSAPVTYT KHIQPICLQA STFEFENRTD CWVTGWGYIK   180
EDEALPSPHT LQEVQVAIIN NSMCNHLFLK YSFRKDIFGD MVCAGNAQGG KDACFGDSGG   240
PLACNKNGLW YQIGVVSWGV GCGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSWPLL   300
FFPLLWALPL LGPV
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Seq ID NO: 541 DNA sequence
Nucleic Acid Accession #: NM_014344
Coding sequence: 131..1444

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1          11         21         31         41         51
|          |          |          |          |          |
GCGGCCGCGA TGGGGCCGAA GCGCCCGAAG CCCCGGAGCC CACAAACTGC CGGGCCCGCC    60
TCGCCGCCGG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGGCGC ACCGGCACAG   120
CCGCGGGAGC ATGGGCAGGA GGATGCGGGG CGCCGCCGCC ACCGCGGGGC TCTGGCTGCT   180
GGCGCTGGGC TCGCTGCTGG CGCTGTGGGG AGGGCTCCTG CCGCCGCGGA CCGAGCTGCC   240
CGCCTCCCGG CCGCCCGAAG ACCGACTCCC ACGGCGCCCG GCCCGGAGCG GCGGCCCCGC   300
GCCCGCGCCT CGCTTCCCTC TGCCCCCGCC CCTGGCGTGG GACGCCCGCG GCGGCTCCCT   360
GAAAACTTTC CGGGCGCTGC TCACCCTGGC GGCCGGCGCG GACGGCCCGC CCCGGCAGTC   420
CCGGAGCGAG CCCAGGTGGC ACGTGTCAGC CAGGCAGCCC CGGCCGGAGG AGAGCGCCGC   480
GGTGCACGGG GGCGTCTTCT GGAGCCGCGG CCTGGAGGAG CAGGTGCCCC CGGGCTTTTC   540
GGAGGCCCAG GCGGCGGCGT GGCTGGAGGC GGCTCGCGGC GCCCGGATGG TGGCCCTGGA   600
GCGCGGGGGT TGCGGGCGCA GCTCCAACCG ACTGGCCCGT TTTGCCGACG GCACCCGCGC   660
CTGCGTGCGC TACGGCATCA ACCCGGAGCA GATTCAGGGC GAGGCCCTGT CTTACTATCT   720
GGCGCGCCTG CTGGGCCTCC AGCGCCACGT GCCGCCGCTG GCACTGGCTC GGGTGGAGGC   780
TCGGGGCGCG CAGTGGGCGC AGGTGCAGGA GGAGCTGCGC GCTGCGCACT GGACCGAGGG   840
CAGCGTGGTG AGCCTGACAC GCTGGCTGCC CAACCTCACG GACGTGGTGG TGCCCGCGCC   900
CTGGCGCTCG GAGGACGGCC GTCTGCGCCC CCTCCGGGAT GCCGGGGGTG AGCTGGCCAA   960
CCTCAGCCAG GCGGAGCTGG TGGACCTAGT ACAATGGACC GACTTAATCC TTTTCGACTA  1020
CCTGACGGCC AACTTCGACC GGCTCGTAAG CAACCTCTTC AGCCTGCAGT GGGACCCGCG  1080
CGTCATGCAG CGTGCCACCA GCAACCTGCA CCGCGGTCCG GGCGGGGCGC TGGTCTTTCT  1140
GGACAATGAG GCGGGCTTGG TGCACGGCTA CCGGGTAGCA GGCATGTGGG ACAAGTATAA  1200
CGAGCCGCTG TTGCAGTCAG TGTGCGTGTT CCGCGAGCGG ACCGCGCGGC GCGTCCTGGA  1260
GCTGCACCGC GGACAGGACG CCGCGGCCCG GCTGCTGCGC CTCTACCGGC GCCACGAGCC  1320
TCGCTTCCCC GAGCTGGCCG CCCTTGCAGA CCCCCACGCT CAGCTGCTAC AGCGCCGCCT  1380
CGACTTCCTC GCCAAGCACA TTTTGCACTG TAAGGCCAAG TACGGCCGCC GGTCTGGGAC  1440
TTAGTGTCAC CGGGAGGAAA AGAGAGAGAT CTGGGGCTGG GGTATGGATG ATGGGGGGAA  1500
GGGCGGTCGC CTCTGCCACT GTCAGGGACC AGCCGGCCAA CGCCCACCCG CAAAGGTGTC  1560
TAAAAACTTC AGCTTTTCAC CCACCTGCCC CTTTCTTTCA ATCCCACGCT GTTTCCTTTC  1620
AAAGTTCTGG GAGGACGAAC TCACCGAGGC GAGAAGTGTA ACATTCTCTC CACCCAGCTT  1680
ATAAAAGGAT TCTTTACTGT GCCAGCACGG GGATTGGATC CGAAGAAACT GGCTACTGGG  1740
GTTTGGCCCC CGAGTGGCCG TCCCTGTGGG AGATGCACCC CATTCTTGGG CCCCCCTCAT  1800
TCCCTTTCCG AAAAAGGAAA ACTTGCGTTT GAGCCGTTGA GCTAATTCTG CAATTTTCTA  1860
CCAAACAGAG CGCTGGTGGC CCCGGAGCAG GGCTGTGACA TTGGCTGGTG GAGCCCCTTC  1920
CTGTGTTCTC CCTTTGTTCC AGCGCCGCGA TGGTGAGATC ACTGTTCCAA GCAGGGGGAC  1980
GGCTCGCGAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG  2040
ACAATTTGCC TGACTCATTC CTGACCTCTT GTCATTTTGG CCTGAAGGCT ACAAATTCAG  2100
GGTCAGCTGT ATGCACTAAG TCAAATAATG AATTTCTTCC TCCCTCTCGC AACCGACCAA  2160
AATTTTGACA ACGATGATGT TCACCAGAAG GAAAAAAAAA TCAGTTTTAT GCACTTTATT  2220
TTGTTTTGAT TTTCATTTTT TATTAAGAAA AAATTTTATT TTACAGAATT TACCTTCTCT  2280
GTATATATGT GCATAAAGTG TGGTGTAAAT ATACTAAACA AACTTATATT TCAATAAAAG  2340
GGAGTTTAAA ATTTAAAAAA AAAAAAA
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Seq ID NO: 542 Protein sequence
Protein Accession #: NP_055159

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1          11         21         31         41         51
|          |          |          |          |          |
MGRRMRGAAA TAGLWLLALG SLLALWGGLL PPRTELPASR PPEDRLPRRP ARSGGPAPAP    60
RFPLPPPLAW DARGGSLKTF RALLTLAAGA DGPPRQSRSE PRWHVSARQP RPEESAAVHG   120
GVFWSRGLEE QVPPGFSEAQ AAAWLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR   180
YGINPEQIQG EALSYYLARL LGLQRHVPPL ALARVEARGA QWAQVQEELR AAHWTEGSVV   240
SLTRWLPNLT DVVVPAPWRS EDGRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLTA   300
NFDRLVSNLF SLQWDPRVMQ RATSNLHRGP GGALVFLDNE AGLVHGYRVA GMWDKYNEPL   360
LQSVCVFRER TARRVLELHR GQDAAARLLR LYRRHEPRFP ELAALADPHA QLLQRRLDFL   420
AKHILHCKAK YGRRSGT
```

Seq ID NO: 543 DNA sequence
Nucleic Acid Accession #: XM_007652.4
Coding sequence: 1..1290

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGCCGGCT CTGGCGCGTG GAAGCGCCTC AAATCTATGC TAAGGAAGGA TGATGCGCCG    60
CTGTTTTTAA ATGACACCAG CGCCTTTGAC TTCTCGGATG AGGCGGGGGA CGAGGGGCTT   120
TCTCGGTTCA ACAAACTTCG AGTTGTGGTG GCCGATGACG GTTCCGAAGC CCCGGAAAGG   180
CCTGTTAACG GGGCGCACCC GACCCTCCAG GCCGACGATG ATTCCTTACT GGACCAAGAC   240
TTACCTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGGACT CCTGTGACAA CTGCAGCAAA   300
CAGAGAGAGA TACTGAAGCA GAGAAAGGTG AAAGCCAGGT TGACCATTGC TGCCGTTCTG   360
TACTTGCTTT TCATGATTGG AGAACTTGTA GGTGGATACA TTGCAAATAG CCTAGCAATC   420
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ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT   480
TTGTGGCTAT CATCAAAATC ACCAACCAAA AGATTCACCT TTGGATTTCA TCGCTTAGAG   540
GTTTTGTCAG CTATGATTAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTTATAT   600
GAAGCTGTGC AAAGAACTAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC   660
ACCGCAGCTG TTGGAGTTGC AGTTAATGTA ATAATGGGGT TTCTGTTGAA CCAGTCTGGT   720
CACCGTCACT CCCATTCCCA CTCCCTGCCT TCAAATTCCC CTACCAGAGG TTCTGGGTGT   780
GAACGTAACC ATGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTTGTACA TGCTTTGGGA   840
GATTTGGTAC AGAGTGTTGG TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA   900
TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA   960
TTTCGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTTGAAT  1020
GTAGACTATA TCAAAGAAGC CTTGATGAAA ATAGAAGATG TATATTCAGT CGAAGATTTA  1080
AATATCTGGT CTCTCACTTC AGGAAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT  1140
GGAAGTTCAT CTAAATGGGA GGAAGTACAG TCCAAAGCAA ACCATTTATT ATTGAACACA  1200
TTTGGCATGT ATAGATGTAC TATTCAGCTT CAGAGTTACA GGCAAGAAGT CGACAGAACT  1260
TGTGCAAATT GTCAGAGTTC TAGTCCCTGA
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Seq ID NO: 544 Protein sequence
Protein Accession #: XP_007652.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAGSGAWKRL KSMLRKDDAP LFLNDTSAFD FSDEAGDEGL SRFNKLRVVV ADDGSEAPER    60
PVNGAHPTLQ ADDDSLLDQD LPLTNSQLSL KVDSCDNCSK QREILKQRKV KARLTIAAVL   120
YLLFMIGELV GGYIANSLAI MTDALHMLTD LSAIILTLLA LWLSSKSPTK RFTFGFHRLE   180
VLSAMISVLL VYILMGFLLY EAVQRTIHMN YEINGDIMLI TAAVGVAVNV IMGFLLNQSG   240
HRHSHSHSLP SNSPTRGSGC ERNHGQDSLA VRAAFVHALG DLVQSVGVLI AAYIIRFKPE   300
YKIADPICTY VFSLLVAFTT FRIIWDTVVI ILEGVPSHLN VDYIKEALMK IEDVYSVEDL   360
NIWSLTSGKS TAIVHIQLIP GSSSKWEEVQ SKANHLLLNT FGMYRCTIQL QSYRQEVDRT   420
CANCQSSSP
```

Seq ID NO: 545 DNA sequence
Nucleic Acid Accession #: AB037765.1
Coding sequence: 1..2478

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1          11         21         31         41         51
|          |          |          |          |          |
ATGTTTTCCG GCTTCAATGT CTTTAGAGTT GGGATCTCTT TTGTCATAAT GTGCATTTTT    60
TACATGCCAA CAGTAAACTC TTTACCAGAA CTGAGTCCTC AGAAATATTT TAGTACATTG   120
CAACCAGGAA AAGCCTCTTT AGCTTATTTT TGTCAAGCTG ATTCCCCAAG AACATCTGTA   180
TTTCTTGAAG AACTGAATGA GGCTGTTAGA CCTCTGCAGG ACTATGGAAT TTCAGTTGCC   240
AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG GAAAAGAAAA GGATTTGATG   300
AAAGCATATT TATTCAAGGG CAACATATTG CTCAGAGAAT TCCCTACTGA CACCTTGTTT   360
GATGTGAATG CCATTGTCGC CCATGTTCTC TTTGCTCTTC TTTTTAGTGA AGTGAAATAT   420
ATTACCAACC TGGAAGACCT TCAGAACATA GAAAATGCTC TGAAAGGAAA AGCAAATATT   480
ATATTCTCAT ATGTAAGAGC CATTGGAATA CCAGAGCACA GAGCAGTCAT GGAAGCCGCT   540
TTTGTGTATG GGACTACATA CCAATTTGTC TTAACCACAG AAATTGCCCT TTTGGAAAGT   600
ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCATTGTAA ACTAGTCTTG   660
GACTTGACCC AGCAATGTAG AAGAACACTA ATGGAACAGC CATTGACTAC ACTGAACATT   720
CACCTGTTTA TTAAGACAAT GAAAGCACCT CTGTTGACTG AAGTTGCTGA AGATCCTCAA   780
CAAGTTTCAA CTGTCCATCT CCAACTGGGC TTACCACTGG TTTTTATTGT TAGCCAACAG   840
GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTTG CTTGGCGTCT TCTGGGAAAA   900
GCAGGAGTTC TACTCTTGTT AAGGGACTCT TTGGAAGTGA ACATTCCTCA AGATGCTAAT   960
GTGGTCTTCA AAAGAGCAGA AGAGGGAGTT CCAGTGGAAT TTTTGGTATT ACATGATGTT  1020
GATTTAATAA TATCTCATGT GGAAAATAAT ATGCACATTG AGGAAATACA AGAAGATGAA  1080
GACAATGACA TGGAAGGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAAACTGTT  1140
TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACTTACAG TGGAACTAAC AGAAGAAACA  1200
TTTAATGCAA CAGTGATGGC TTCTGACAGC ATAGTACTCT TCTATGCTGG TTGGCAAGCA  1260
GTATCCATGG CATTTTTGCA ATCCTATATT GATGTGGCAG TTAAACTGAA AGGCACATCT  1320
ACTATGCTTC TTACTAGAAT AAACTGTGCA GATTGGTCTG ATGTATGTAC TAAGCAAAAT  1380
GTTACTGAAT TTCCTATCAT AAAGATGTAC AAGAAAGGCG AGAACCCAGT ATCTTATGCT  1440
GGAATGTTAG GAACCGAAGA TCTCCTAAAA TTTATCCAGC TCAACAGGAT TTCATATCCA  1500
GTGAATATAA CATCGATCCA AGAAGCAGAA GAATATTTAA GTGGGGAATT ATATAAAGAC  1560
CTCATCTTGT ATTCTAGTGT GTCAGTATTG GGACTATTTA GTCCAACCAT GAAAACAGCA  1620
AAAGAAGATT TTAGTGAAGC AGGAAACTAC CTAAAAGGAT ATGTTATCAC TGGAATTTAT  1680
TCTGAAGAAG ATGTTTTGCT ACTGTCAACC AAATATGCTG CAAGTCTTCC AGCCCTGCTG  1740
CTTGCCAGAC ACACAGAAGG CAAAATAGAG AGCATCCCAC TAGCTAGCAC ACATGCACAA  1800
GACATAGTTC AAATAATAAC AGATGCACTA CTGGAAATGT TTCCGGAAAT CACTGTGGAA  1860
AATCTTCCCA GTTATTTCAG ACTTCAGAAA CCATTATTGA TTTTGTTCAG TGATGGCACT  1920
GTAAATCCTC AGTATAAAAA AGCAATATTG ACACTGGTAA AGCAGAAATA CTTGGATTCA  1980
TTTACTCCAT GCTGGTTAAA TCTAAAGAAT ACTCCAGTGG GGAGAGGAAT CTTGAGGGCA  2040
TATTTTGATC CTCTGCCTCC CCTTCCTCTT CTTGTTTTGG TGAATCTGCA TTCAGGTGGC  2100
CAAGTATTTG CATTTCCTTC AGACCAGGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG  2160
AAGAAATTAG AAGCAGGACT AGAAAATCAT ATCACAATTT TACCTGCTCA AGAATGGAAA  2220
CCTCCTCTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC  2280
ACTAGGAAAG TTCCCAAGTG TATGAAAGAA ACAGATGTGC AGGAGAATGA TAAGGAACAA  2340
CATGAAGATA AATCGGCAGT CAGAAAAGAA CCGATTGAAA CTCTGAGAAT AAAGCATTGG  2400
AATAGAAGTA ATTGGTTTAA AGAAGCAGAA AAATCATTTA GACGTGATAA AGAGTTAGGA  2460
TGCTCAAAAG TGAACTAA
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Seq ID NO: 546 Protein sequence
Protein Accession #: BAA92582.1

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1          11         21         31         41         51
|          |          |          |          |          |
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MFSGFNVFRV GISFVIMCIF YMPTVNSLPE LSPQKYFSTL QPGKASLAYF CQADSPRTSV   60
FLEELNEAVR PLQDYGISVA KVNCVKEEIS RYCGKEKDLM KAYLFKGNIL LREFPTDTLF  120
DVNAIVAHVL FALLFSEVKY ITNLEDLQNI ENALKGKANI IFSYVRAIGI PEHRAVMEAA  180
FVYGTTYQFV LTTEIALLES IGSEDVEYAH LYFFHCKLVL DLTQQCRRTL MEQPLTTLNI  240
HLFIKTMKAP LLTEVAEDPQ QVSTVHLQLG LPLVFIVSQQ ATYEADRRTA EWVAWRLLGK  300
AGVLLLLRDS LEVNIPQDAN VVFKRAEEGV PVEFLVLHDV DLIISHVENN MHIEEIQEDE  360
DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVELTEET FNATVMASDS IVLFYAGWQA  420
VSMAFLQSYI DVAVKLKGTS TMLLTRINCA DWSDVCTKQN VTEFPIIKMY KKGENPVSYA  480
GMLGTEDLLK FIQLNRISYP VNITSIQEAE EYLSGELYKD LILYSSVSVL GLFSPTMKTA  540
KEDFSEAGNY LKGYVITGIY SEEDVLLLST KYAASLPALL LARHTEGKIE SIPLASTHAQ  600
DIVQIITDAL LEMFPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKKAIL TLVKQKYLDS  660
FTPCWLNLKN TPVGRGILRA YFDPLPPLPL LVLVNLHSGG QVFAFPSDQA IIEENLVLWL  720
KKLEAGLENH ITILPAQEWK PPLPAYDFLS MIDAATSQRG TRKVPKCMKE TDVQENDKEQ  780
HEDKSAVRKE PIETLRIKHW NRSNWFKEAE KSFRRDKELG CSKVN
```

Seq ID NO: 547 DNA sequence
Nucleic Acid Accession #: NM_033102.1
Coding sequence: 1..1662

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGTCCAGA GGCTGTGGGT GAGCCGCCTG CTGCGGCACC GGAAAGCCCA GCTCTTGCTG   60
GTCAACCTGC TAACCTTTGG CCTGGAGGTG TGTTTGGCCG CAGGCATCAC CTATGTGCCG  120
CCTCTGCTGC TGGAAGTGGG GGTAGAGGAG AAGTTCATGA CCATGGTGCT GGGCATTGGT  180
CCAGTGCTGG GCCTGGTCTG TGTCCCGCTC CTAGGCTCAG CCAGTGACCA CTGGCGTGGA  240
CGCTATGGCC GCCGCCGGCC CTTCATCTGG GCACTGTCCT TGGGCATCCT GCTGAGCCTC  300
TTTCTCATCC CAAGGGCCGG CTGGCTAGCA GGGCTGCTGT GCCCGGATCC CAGGCCCCTG  360
GAGCTGGCAC TGCTCATCCT GGGCGTGGGG CTGCTGGACT TCTGTGGCCA GGTGTGCTTC  420
ACTCCACTGG AGGCCCTGCT CTCTGACCTC TTCCGGGACC CGGACCACTG TCGCCAGGCC  480
TACTCTGTCT ATGCCTTCAT GATCAGTCTT GGGGGCTGCC TGGGCTACCT CCTGCCTGCC  540
ATTGACTGGG ACACCAGTGC CCTGGCCCCC TACCTGGGCA CCCAGGAGGA GTGCCTCTTT  600
GGCCTGCTCA CCCTCATCTT CCTCACCTGC GTAGCAGCCA CACTGCTGGT GGCTGAGGAG  660
GCAGCGCTGG GCCCCACCGA GCCAGCAGAA GGGCTGTCGG CCCCCTCCTT GTCGCCCCAC  720
TGCTGTCCAT GCCGGGCCCG CTTGGCTTTC CGGAACCTGG GCGCCCTGCT TCCCCGGCTG  780
CACCAGCTGT GCTGCCGCAT GCCCCGCACC CTGCGCCGGC TCTTCGTGGC TGAGCTGTGC  840
AGCTGGATGG CACTCATGAC CTTCACGCTG TTTTACACGG ATTTCGTGGG CGAGGGGCTG  900
TACCAGGGCG TGCCCAGAGC TGAGCCGGGC ACCGAGGCCC GGAGACACTA TGATGAAGGC  960
GTTCGGATGG GCAGCCTGGG GCTGTTCCTG CAGTGCGCCA TCTCCCTGGT CTTCTCTCTG 1020
GTCATGGACC GGCTGGTGCA GCGATTCGGC ACTCGAGCAG TCTATTTGGC CAGTGTGGCA 1080
GCTTTCCCTG TGGCTGCCGG TGCCACATGC CTGTCCCACA GTGTGGCCGT GGTGACAGCT 1140
TCAGCCGCCC TCACCGGGTT CACCTTCTCA GCCCTGCAGA TCCTGCCCTA CACACTGGCC 1200
TCCCTCTACC ACCGGGAGAA GCAGGTGTTC CTGCCCAAAT ACCGAGGGGA CACTGGAGGT 1260
GCTAGCAGTG AGGACAGCCT GATGACCAGC TTCCTGCCAG GCCCTAAGCC TGGAGCTCCC 1320
TTCCCTAATG GACACGTGGG TGCTGGAGGC AGTGGCCTGC TCCCACCTCC ACCCGCGCTC 1380
TGCGGGGCCT CTGCCTGTGA TGTCTCCGTA CGTGTGGTGG TGGGTGAGCC CACCGAGGCC 1440
AGGGTGGTTC CGGGCCGGGG CATCTGCCTG GACCTCGCCA TCCTGGATAG TGCCTTCCTG 1500
CTGTCCCAGG TGGCCCCATC CCTGTTTATG GGCTCCATTG TCCAGCTCAG CCAGTCTGTC 1560
ACTGCCTATA TGGTGTCTGC CGCAGGCCTG GGTCTGGTCG CCATTTACTT TGCTACACAG 1620
GTAGTATTTG ACAAGAGCGA CTTGGCCAAA TACTCAGCGT GA
```

Seq ID NO: 548 Protein sequence
Protein Accession #: NP_149093.1

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1          11         21         31         41         51
|          |          |          |          |          |
MVQRLWVSRL LRHRKAQLLL VNLLTFGLEV CLAAGITYVP PLLLEVGVEE KFMTMVLGIG   60
PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL  120
ELALLILGVG LLDFCGQVCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA  180
IDWDTSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH  240
CCPCRARLAF RNLGALLPRL HQLCCRMPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL  300
YQGVPRAEPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG TRAVYLASVA  360
AFPVAAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA SLYHREKQVF LPKYRGDTGG  420
ASSEDSLMTS FLPGPKPGAP FPNGHVGAGG SGLLPPPPAL CGASACDVSV RVVVGEPTEA  480
RVVPGRGICL DLAILDSAFL LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIYFATQ  540
VVFDKSDLAK YSA
```

Seq ID NO: 549 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1389

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGATTTAGA TGACAGAGAA   60
ACCCTTGTTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTTAAT  120
GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT  180
GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACGGA CTTTTCCCTT  240
GTTTTATTGA TAAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT  300
AAAACTTTCG GCTTTCCAGG GTATCTGCTC CTCTCTGTTC TTCAGTTTTT GTATCCTTTT  360
ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAGT TTTTCAAAGA  420
ATCCCAGGAG TTGATCCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC  480
ACAGTTACCT TTACTCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC  540
TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT  600
TCACTGGGTC CACACATACC AAAAACAGAA GACGCTTGGG TATTTGCAAA GCCCAATGCC  660
ATTCAAGCGG TCGGGGTTAT GTCTTTTGCA TTTATTTGCC ACCATAACTC CTTCTTAGTT  720
```

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TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC   780
GTGATTTCTG TATTTATCTG TATATTCTTT GCTACATGTG GATACTTGAC ATTTACTGGC   840
TTCACCCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTTGGA   900
AGATTTTGTT ATGGTGTCAC TGTCATTTTG ACATACCCTA TGGAATGCTT TGTGACAAGA   960
GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCA CATTGTTGTA  1020
ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCATTGC TGATTGATTG CCTCGGGATA  1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCCTCA TTTTTATCAT TCCATCAGCC  1140
TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC  1200
ATGCTTCCCA TTGGTGCTGT GGTGATGGTT TTTGGATTCG TCATGGCTAT TACAAATACT  1260
CAAGACTGCA CCCATGGGCA GGAAATGTTC TACTGCTTTC CTGACAATTT CTCTCTCACA  1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC  1380
TTTCAATGA
```

Seq ID NO: 550 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA    60
GFPLGILLLF WVSYVTDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF   120
IAMISYNIIA GDTLSKVFQR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIAKLGKV   180
SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPNA IQAVGVMSFA FICHHNSFLV   240
YSSLEEPTVA KWSRLIHMSI VISVFICIFF ATCGYLTFTG FTQGDLFENY CRNDDLVTFG   300
RFCYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIVV TVMVITVATL VSLLIDCLGI   360
VLELNGVLCA TPLIFIIPSA CYLKLSEEPR THSDKIMSCV MLPIGAVVMV FGFVMAITNT   420
QDCTHGQEMF YCFPDNFSLT NTSESHVQQT TQLSTLNISI FQ
```

Seq ID NO: 551 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1284

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGGATTGCC TTATTCAATG    60
AAGCAAGCTG GGTTTCCTTT GGGAATATTG CTTTTATTCT GGGTTTCATA TGTTACAGAC   120
TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCAGTCT   180
TTGGTCAATA AAACTTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTTTG   240
TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT   300
TTTCAAAGAA TCCCAGGAGT TGATCCTGAA AACGTGTTTA TTGGTCGCCA CTTCATTATT   360
GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT   420
GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAAT TGTAATGGCA   480
AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG   540
CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC   600
TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT   660
ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA   720
TTTACTGGCT TCACCCAAGG GGACTTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA   780
ACATTTGGAA GATTTTGTTA TGGTGTCACT GTCATTTTGA CATACCCTAT GGAATGCTTT   840
GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC   900
ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC   960
CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCCCTCAT TTTTATCATT  1020
CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG  1080
TCTTGTGTCA TGCTTCCCAT TGGTGCTGTG GTGATGGTTT TTGGATTCGT CATGGCTATT  1140
ACAAATACTC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAATTTC  1200
TCTCTCACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACTTTC TACTTTAAAT  1260
ATTAGTATCT TTCAACTCGA GTAA
```

Seq ID NO: 552 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVSYVTD FSLVLLIKGG ALSGTDTYQS    60
LVNKTFGFPG YLLLSVLQFL YPFIAMISYN IIAGDTLSKV FQRIPGVDPE NVFIGRHFII   120
GLSTVTFTLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGPHIP KTEDAWVFAK   180
PNAIQAVGVM SFAFICHHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT   240
FTGFTQGDLF ENYCRNDDLV TFGRFCYGVT VILTYPMECF VTREVIANVF FGGNLSSVFH   300
IVVTVMVITV ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM   360
SCVMLPIGAV VMVFGFVMAI TNTQDCTHGQ EMFYCFPDNF SLTNTSESHV QQTTQLSTLN   420
ISIFQLE
```

Seq ID NO: 553 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1203

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGT TTTCCCTTGT TTTATTGATA    60
AAAGGAGGGG CCCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCGGC   120
TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA   180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT   240
GATCCTGAAA ACGTGTTTAT TGGTCGCCAC TTCATTATTG GACTTTCCAC AGTTACCTTT   300
ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT   360
ACAGGTTTAA CAACTCTGAT TCTTGGAATT GTAATGGCAA GGGCAATTTC ACTGGGTCCA   420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC   480
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GGGGTTATGT CTTTTGCATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA   540
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCATCGT GATTTCTGTA   600
TTTATCTGTA TATTCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG   660
GACTTATTTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTTGGAAG ATTTTGTTAT   720
GGTGTCACTG TCATTTTGAC ATACCCTATG GAATGCTTTG TGACAAGAGA GGTAATTGCC   780
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC   840
ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC   900
AATGGTGTGC TCTGTGCAAC TCCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA   960
CTGTCTGAAG AACCAAGGAC ACACTCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCATT  1020
GGTGCTGTGG TGATGGTTTT TGGATTCGTC ATGGCTATTA CAAATACTCA AGACTGCACC  1080
CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTTCT CTCTCACAAA TACCTCAGAG  1140
TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG  1200
TAA
```

Seq ID NO: 554 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI    60
SYNIIAGDTL SKVFQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLIS   120
TGLTTLILGI VMARAISLGP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL   180
EEPTVAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY   240
GVTVILTYPM ECFVTREVIA NVFFGGNLSS VFHIVVTVMV ITVATLVSLL IDCLGIVLEL   300
NGVLCATPLI FIIPSACYLK LSEEPRTHSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT   360
HGQEMFYCFP DNFSLTNTSE SHVQQTTQLS TLNISIFQLE
```

Seq ID NO: 555 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

```
1          11         21         31         41         51
|          |          |          |          |          |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT    60
CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTTGTATC CTTTTATAGC AATGATAAGT   120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT   180
CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT   240
CTGCCTTTAT CCTTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA   300
GGTTTAACAA CTCTGATTCT TGGAATTGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC   360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCGGG   420
GTTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA   480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT   540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC   600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT   660
GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT   720
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC   780
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT   840
GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG   900
TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGTCTT GTGTCATGCT TCCCATTGGT   960
GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT  1020
GGGCAGGAAA TGTTCTACTG CTTTCCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT  1080
CATGTTCAGC AGACAACACA ACTTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA
```

Seq ID NO: 556 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MGYQRQEPVI PPQVNKTFGF PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPGVD    60
PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLGKVSLIST GLTTLILGIV MARAISLGPH   120
IPKTEDAWVF AKPNAIQAVG VMSFAFICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF   180
ICIFFATCGY LTFTGFTQGD LFENYCRNDD LVTFGRFCYG VTVILTYPME CFVTREVIAN   240
VFFGGNLSSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL   300
SEEPRTHSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES   360
HVQQTTQLST LNISIFQLE
```

Seq ID NO: 557 DNA sequence
Nucleic Acid Accession #: XM_057188.1
Coding sequence: 769..4269

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGGATTGC CTCTCCCTCT CACTCTGGGC TTCTGTCCCA CTCTTATCTT AGTGTCAGTC    60
CTCCCCCAAG TCTGTGTCCC TCTCTCTCCC CTAAATCTCT GGCCCCTCCT TTCTGAGTTC   120
CTGCCCTTCC CCCAATTCTT TGGTTTTTGC ATCCCCCTCT GCCCCTTGCC TCAGTCAAGT   180
CTCCCCTGTG TGTCTCTCTC CCCCCGGCCC GGACCTCTGC ACCCCCCAGG TCGCTGTCCC   240
TCTGTCCCCT TATCGCGGCC TGGGACCCGC CCTCTCCCCG CCTCCCGCTT TGGCGTCTCC   300
AAGACTCCCC GCCCCCCAGA CCTCGCCCCG CCCCAGGCTA GGCTGGAAAG TGGAGGATCC   360
GGTTTGCTCT GGGCGGGTCT GGAAGCAGAG CCGGCGGAGG GAGCGCCGGG GCCCTGGGCT   420
GCAGGAGGTT GCGGCGGCCG CGGCAGCATG GTGGTGCCGG AGAAGGAGCA GAGCTGGATC   480
CCCAAGATCT TCAAGAAGAA GACCTGCACG ACGTTCATAG TTGACTCCAC AGATCCGGGG   540
GATGGGGTCT CGCTCTATTG CCCAGGCTGT TCTCAAACTC CTGGGCTCAA GCAGTCCTTC   600
TGCCTTGACC TCCCAAAGTG CTTGGATTGT GCCCAGCCGT CCTTGAAGTT TTGCTCAGAA   660
GAGCAAACTT TCTGGGAAGT AGCTGCAGGT GTTGGAAGTA GCTGCAGGGG AACTAGGGGA   720
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TTCAAGGATG GAGCTGAAAT GGGTGAACGG ACAAAGTCGG TAAACTGAAT GGAGGATGCC   780
TTCGGGGCAG CCGTCGTGAC CGTGTGGGAC AGCGATGCAC ACACCACGGA GAAGCCCACC   840
GATGCCTACG GAGAGCTGGA CTTCACGGGG GCCGGCCGCA AGCACAGCAA TTTCCTCCGG   900
CTCTCTGACC GAACGGATCC AGCTGCAGTT TATAGTCTGG TCACACGCAC ATGGGGCTTC   960
CGTGCCCCGA ACCTCGTCGT GTCAGTGCTG GGGGGATCGG GGGGCCCCGT CCTCCAGACC  1020
TGGCTGCAGG ACCTGCTGCG TCGTGGGCTG GTGCGGGCTG CCCAGAGCAC AGGAGCCTGG  1080
ATTGTCACTG GGGGTCTGCA CACGGGCATC GGCCGGCATG TTGGTGTGGC TGTACGGGAC  1140
CATCAGATGG CCAGCACTGG GGGCACCAAG GTGGTGGCCA TGGGTGTGGC CCCCTGGGGT  1200
GTGGTCCGGA ATAGAGACAC CCTCATCAAC CCCAAGGGCT CGTTCCCTGC GAGGTACCGG  1260
TGGCGCGGTG ACCCGGAGGA CGGGGTCCAG TTTCCCCTGG ACTACAACTA CTCGGCCTTC  1320
TTCCTGGTGG ACGACGGCAC ACACGGCTGC CTGGGGGGCG AGAACCGCTT CCGCTTGCGC  1380
CTGGAGTCCT ACATCTCACA GCAGAAGACG GGCGTGGGAG GGACTGGAAT TGACATCCCT  1440
GTCCTGCTCC TCCTGATTGA TGGTGATGAG AAGATGTTGA CGCGAATAGA GAACGCCACC  1500
CAGGCTCAGC TCCCATGTCT CCTCGTGGCT GGCTCAGGGG GAGCTGCGGA CTGCCTGGCG  1560
GAGACCCTGG AAGACACTCT GGCCCCAGGG AGTGGGGGAG CCAGGCAAGG CGAAGCCCGA  1620
GATCGAATCA GGCGTTTCTT TCCCAAAGGG GACCTTGAGG TCCTGCAGGC CCAGGTGGAG  1680
AGGATTATGA CCCGGAAGGA GCTCCTGACA GTCTATTCTT CTGAGGATGG GTCTGAGGAA  1740
TTCGAGACCA TAGTTTTGAA GGCCCTTGTG AAGGCCTGTG GGAGCTCGGA GGCCTCAGCC  1800
TACCTGGATG AGCTGCGTTT GGCTGTGGCT TGGAACCGCG TGGACATTGC CCAGAGTGAA  1860
CTCTTTCGGG GGGACATCCA ATGGCGGTCC TTCCATCTCG AAGCTTCCCT CATGGACGCC  1920
CTGCTGAATG ACCGGCCTGA GTTCGTGCGC TTGCTCATTT CCCACGGCCT CAGCCTGGGC  1980
CACTTCCTGA CCCCGATGCG CCTGGCCCAA CTCTACAGCG CGGCGCCCTC CAACTCGCTC  2040
ATCCGCAACC TTTTGGACCA GGCGTCCCAC AGCGCAGGCA CCAAAGCCCC AGCCCTAAAA  2100
GGGGGAGCTG CGGAGCTCCG GCCCCCTGAC GTGGGGCATG TGCTGAGGAT GCTGCTGGGG  2160
AAGATGTGCG CGCCGAGGTA CCCCTCCGGG GGCGCCTGGG ACCCTCACCC AGGCCAGGGC  2220
TTCGGGGAGA GCATGTATCT GCTCTCGGAC AAGGCCACCT CGCCGCTCTC GCTGGATGCT  2280
GGCCTCGGGC AGGCCCCCTG GAGCGACCTG CTTCTTTGGG CACTGTTGCT GAACAGGGCA  2340
CAGATGGCCA TGTACTTCTG GGAGATGGGT TCCAATGCAG TTTCCTCAGC TCTTGGGGCC  2400
TGTTTGCTGC TCCGGGTGAT GGCACGCCTG GAGCCTGACG CTGAGGAGGC AGCACGGAGG  2460
AAAGACCTGG CGTTCAAGTT TGAGGGGATG GGCGTTGACC TCTTTGGCGA GTGCTATCGC  2520
AGCAGTGAGG TGAGGGCTGC CCGCCTCCTC CTCCGTCGCT GCCCGCTCTG GGGGGATGCC  2580
ACTTGCCTCC AGCTGGCCAT GCAAGCTGAC GCCCGTGCCT TCTTTGCCCA GGATGGGGTA  2640
CAGTCTCTGC TGACACAGAA GTGGTGGGGA GATATGGCCA GCACTACACC CATCTGGGCC  2700
CTGGTTCTCG CCTTCTTTTG CCCTCCACTC ATCTACACCC GCCTCATCAC CTTCAGGAAA  2760
TCAGAAGAGG AGCCCACACG GGAGGAGCTA GAGTTTGACA TGGATAGTGT CATTAATGGG  2820
GAAGGGCCTG TCGGGACGGC GGACCCAGCC GAGAAGACGC CGCTGGGGGT CCCGCGCCAG  2880
TCGGGCCGTC CGGGTTGCTG CGGGGGCCGC TGCGGGGGGC GCCGGTGCCT ACGCCGCTGG  2940
TTCCACTTCT GGGGCGCGCC GGTGACCATC TTCATGGGCA ACGTGGTCAG CTACCTGCTG  3000
TTCCTGCTGC TTTTCTCGCG GGTGCTGCTC GTGGATTTCC AGCCGGCGCC GCCCGGCTCC  3060
CTGGAGCTGC TGCTCTATTT CTGGGCTTTC ACGCTGCTGT GCGAGGAACT GCGCCAGGGC  3120
CTGAGCGGAG GCGGGGGCAG CCTCGCCAGC GGGGGCCCCG GGCCTGGCCA TGCCTCACTG  3180
AGCCAGCGCC TGCGCCTCTA CCTCGCCGAC AGCTGGAACC AGTGCGACCT AGTGGCTCTC  3240
ACCTGCTTCC TCCTGGGCGT GGGCTGCCGG CTGACCCCGG GTTTGTACCA CCTGGGCCGC  3300
ACTGTCCTCT GCATCGACTT CATGGTTTTC ACGGTGCGGC TGCTTCACAT CTTCACGGTC  3360
AACAAACAGC TGGGGCCCAA GATCGTCATC GTGAGCAAGA TGATGAAGGA CGTGTTCTTC  3420
TTCCTCTTCT TCCTCGGCGT GTGGCTGGTA GCCTATGGCG TGGCCACGGA GGGGCTCCTG  3480
AGGCCACGGG ACAGTGACTT CCCAAGTATC CTGCGCCGCG TCTTCTACCG TCCCTACCTG  3540
CAGATCTTCG GGCAGATTCC CCAGGAGGAC ATGGACGTGG CCCTCATGGA GCACAGCAAC  3600
TGCTCGTCGG AGCCCGGCTT CTGGGCACAC CCTCCTGGGG CCCAGGCGGG CACCTGCGTC  3660
TCCCAGTATG CCAACTGGCT GGTGGTGCTG CTCCTCGTCA TCTTCCTGCT CGTGGCCAAC  3720
ATCCTGCTGG TCAACTTGCT CATTGCCATG TTCAGTTACA CATTCGGCAA AGTACAGGGC  3780
AACAGCGATC TCTACTGGAA GGCGCAGCGT TACCGCCTCA TCCGGGAATT CCACTCTCGG  3840
CCCGCGCTGG CCCCGCCCTT TATCGTCATC TCCCACTTGC GCCTCCTGCT CAGGCAATTG  3900
TGCAGGCGAC CCCGGAGCCC CCAGCCGTCC TCCCCGGCCC TCGAGCATTT CCGGGTTTAC  3960
CTTTCTAAGG AAGCCGAGCG GAAGCTGCTA ACGTGGGAAT CGGTGCATAA GGAGAACTTT  4020
CTGCTGGCAC GCGCTAGGGA CAAGCGGGAG AGCGACTCCG AGCGTCTGAA GCGCACGTCC  4080
CAGAAGGTGG ACTTGGCACT GAAACAGCTG GGACACATCC GCGAGTACGA ACAGCGCCTG  4140
AAAGTGCTGG AGCGGGAGGT CCAGCAGTGT AGCCGCGTCC TGGGGTGGGT GGCCGAGGCC  4200
CTGAGCCGCT CTGCCTTGCT GCCCCCAGGT GGGCCGCCAC CCCCTGACCT GCCTGGGTCC  4260
AAAGACTGAG CCCTGCTGGC GGACTTCAAG GAGAAGCCCC CACAGGGGAT TTTGCTCCTA  4320
GAGTAAGGCT CATCTGGGCC TCGGCCCCCG CACCTGGTGG CCTTGTCCTT GAGGTGAGCC  4380
CCATGTCCAT CTGGGCCACT GTCAGGACCA CCTTTGGGAG TGTCATCCTT ACAAACCACA  4440
GCATGCCCGG CTCCTCCCAG AACCAGTCCC AGCCTGGGAG GATCAAGGCC TGGATCCCGG  4500
GCCGTTATCC ATCTGGAGGC TGCAGGGTCC TTGGGGTAAC AGGGACCACA GACCCCTCAC  4560
CACTCACAGA TTCCTCACAC TGGGGAAATA AAGCCATTTC AGAGGAAAAA AAAAAAAAAA  4620
AAAAAAAAAA AAAAAAAAAA A
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Seq ID NO: 558 Protein sequence
Protein Accession #: XP_057188.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEDAFGAAVV TVWDSDAHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR    60
TWGFRAPNLV VSVLGGSGGP VLQTWLQDLL RRGLVRAAQS TGAWIVTGGL HTGIGRHVGV   120
AVRDHQMAST GGTKVVAMGV APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVQFPLDYN   180
YSAFFLVDDG THGCLGGENR FRLRLESYIS QQKTGVGGTG IDIPVLLLLI DGDEKMLTRI   240
ENATQAQLPC LLVAGSGGAA DCLAETLEDT LAPGSGGARQ GEARDRIRRF FPKGDLEVLQ   300
AQVERIMTRK ELLTVYSSED GSEEFETIVL KALVKACGSS EASAYLDELR LAVAWNRVDI   360
AQSELFRGDI QWRSFHLEAS LMDALLNDRP EFVRLLISHG LSLGHFLTPM RLAQLYSAAP   420
SNSLIRNLLD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH   480
PGQGFGESMY LLSDKATSPL SLDAGLGQAP WSDLLLWALL LNRAQMAMYF WEMGSNAVSS   540
ALGACLLLRV MARLEPDAEE AARRKDLAFK FEGMGVDLFG ECYRSSEVRA ARLLLRRCPL   600
WGDATCLQLA MQADARAFFA QDGVQSLLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI   660
TFRKSEEEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCGGRRC   720
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WO03042661 [file://E:/WO03042661.pcl]


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LRRWFHFWGA PVTIFMGNVV SYLLFLLLFS RVLLVDFQPA PPGSLELLLY FWAFTLLCEE   780
LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY   840
HLGRTVLCID FMVFTVRLLH IFTVNKQLGP KIVIVSKMMK DVFFFLFFLG VWLVAYGVAT   900
EGLLRPRDSD FPSILRRVFY RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPPGAQA   960
GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQGNSDLYW KAQRYRLIRE  1020
FHSRPALAPP FIVISHLRLL LRQLCRRPRS PQPSSPALEH FRVYLSKEAE RKLLTWESVH  1080
KENFLLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQQCSRVLGW  1140
VAEALSRSAL LPPGGPPPPD LPGSKD
```

Seq ID NO: 559 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

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1          11         21         31         41         51
|          |          |          |          |          |
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC    60
ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCCTCCAGGC   120
CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC   180
CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCCAG CCCTGGCAGG CAGCCCTGTT   240
CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC   300
AGCCCACTGC CTCAAGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAAGGA   360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCCG GCTTCAACAA   420
CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT   480
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC   540
CAGCTGCCTC ATTTCCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC   600
CTTGCGATGC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAACG CCTACCCCGG   660
CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAGGAA GGGGGCAAGG ACTCCTGCCA   720
GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG   780
CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAATATGT   840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC   900
ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCACTCT GTTAATAAGA AACCCTAAGC   960
CAAGACCCTC TACGAACATT CTTTGGGCCT CCTGGACTAC AGGAGATGCT GTCACTTAAT  1020
AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT  1080
GACTCTGGGA ATGACAACAC CTGGTTTGTT CTCTGTTGTA TCCCCAGCCC CAAAGACAGC  1140
TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG
```

Seq ID NO: 560 Protein sequence
Protein Accession #: NP_006844.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA    60
AHCLKPRYIV HLGQHNLQKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV   120
SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIIE HQKCENAYPG   180
NITDTMVCAS VQEGGKDSCQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVYTKVCKYV   240
DWIQETMKNN
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Seq ID NO: 561 DNA sequence
Nucleic Acid Accession #: AY046419.1
Coding sequence: 1..1743

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1          11         21         31         41         51
|          |          |          |          |          |
ATGTTTACCT TCCTGTCATC TGTCACTGCT GCTGTCAGTG GCCTCCTGGT GGGTTATGAA    60
CTTGGGATCA TCTCTGGGGC TCTTCTTCAG ATCAAAACCT TATTAGCCCT GAGCTGCCAT   120
GAGCAGGAAA TGGTTGTGAG CTCCCTCGTC ATTGGAGCCC TCCTTGCCTC ACTCACCGGA   180
GGGGTCCTGA TAGACAGATA TGGAAGAAGG ACAGCAATCA TCTTGTCATC CTGCCTGCTT   240
GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCCTACA CGGTTCTTAT AGTGGGACGC   300
ATTGCCATAG GGGTTTCCAT CTCCCTCTCT TCCATTGCCA CTTGTGTTTA CATCGCAGAG   360
ATTGCTCCTC AACACAGAAG AGGCCTTCTT GTGTCACTGA ATGAGCTGAT GATTGTCATC   420
GGCATTCTTT CTGCCTATAT TTCAAATTAC GCATTTGCCA ATGTTTTCCA TGGCTGGAAG   480
TACATGTTTG GTCTTGTGAT TCCCTTGGGA GTTTTGCAAG CAATTGCAAT GTATTTTCTT   540
CCTCCAAGCC CTCGGTTTCT GGTGATGAAA GGACAAGAGG GAGCTGCTAG CAAGGTTCTT   600
GGAAGGTTAA GAGCACTCTC AGATACAACT GAGGAACTCA CTGTGATCAA ATCCTCCCTG   660
AAAGATGAAT ATCAGTACAG TTTTTGGGAT CTGTTTCGTT CAAAAGACAA CATGCGGACC   720
CGAATAATGA TAGGACTAAC ACTAGTATTT TTTGTACAAA TCACTGGCCA ACCAAACATA   780
TTGTTCTATG CATCAACTGT TTTGAAGTCA GTTGGATTTC AAAGCAATGA GGCAGCTAGC   840
CTCGCCTCCA CTGGGGTTGG AGTCGTCAAG GTCATTAGCA CCATCCCTGC CACTCTTCTT   900
GTAGACCATG TCGGCAGCAA AACATTCCTC TGCATTGGCT CCTCTGTGAT GGCAGCTTCG   960
TTGGTGACCA TGGGCATCGT AAATCTCAAC ATCCACATGA ACTTCACCCA TATCTGCAGA  1020
AGCCACAATT CTATCAACCA GTCCTTGGAT GAGTCTGTGA TTTATCGACC AGGAAACCTG  1080
TCAACCAACA ACAATACTCT CAGAGACCAC TTCAAAGGGA TTTCTTCCCA TAGCAGAAGC  1140
TCACTCATGC CCCTGAGAAA TGATGTGGAT AAGAGAGGGG AGACGACCTC AGCATCCTTG  1200
CTAAATGCTG GATTAAGCCA CACTGAATAC CAGATAGTCA CAGACCCTGG GGACGTCCCA  1260
GCTTTTTTGA AATGGCTGTC CTTAGCCAGC TTGCTTGTTT ATGTTGCTGC TTTTTCAATT  1320
GGTCTAGGAC CAATGCCCTG GCTGGTGCTC AGCGAGATCT TTCCTGGTGG GATCAGAGGA  1380
CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCCTCAT CTCGCTGACA  1440
TTTTTGACTG TAACTGATCT TATTGGCCTG CCATGGGTGT GCTTTATATA TACAATCATG  1500
AGTCTAGCAT CCCTGCTTTT TGTTGTTATG TTTATACCTG AGACAAAGGG ATGCTCTTTG  1560
GAACAAATAT CAATGGAGCT AGCAAAAGTG AACTATGTGA AAAACAACAT TTGTTTTATG  1620
AGTCATCACC AAGAAGAATT AGTGCCAAAA CAGCCTCAAA AAAGAAAACC CCAGGAGCAG  1680
CTCTTGGAGT GTAACAAGCT GTGTGGTAGG GGCCAATCCA GGCAGCTTTC TCCAGAGACC  1740
TAA
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Seq ID NO: 562 Protein sequence
Protein Accession #: AAL02327.1

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1          11         21         31         41         51
|          |          |          |          |          |
MFTFLSSVTA AVSGLLVGYE LGIISGALLQ IKTLLALSCH EQEMVVSSLV IGALLASLTG    60
GVLIDRYGRR TAIILSSCLL GLGSLVLILS LSYTVLIVGR IAIGVSISLS SIATCVYIAE   120
IAPQHRRGLL VSLNELMIVI GILSAYISNY AFANVFHGWK YMFGLVIPLG VLQAIAMYFL   180
PPSPRFLVMK GQEGAASKVL GRLRALSDTT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT   240
RIMIGLTLVF FVQITGQPNI LFYASTVLKS VGFQSNEAAS LASTGVGVVK VISTIPATLL   300
VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMNFTHICR SHNSINQSLD ESVIYGPGNL   360
STNNNTLRDH FKGISSHSRS SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP   420
AFLKWLSLAS LLVYVAAFSI GLGPMPWLVL SEIFPGGIRG RAMALTSSMN WGINLLISLT   480
FLTVTDLIGL PWVCFIYTIM SLASLLFVVM FIPETKGCSL EQISMELAKV NYVKNNICFM   540
SHHQEELVPK QPQKRKPQEQ LLECNKLCGR GQSRQLSPET
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Seq ID NO: 563 DNA sequence
Nucleic Acid Accession #: XM_059466.1
Coding sequence: 1..894

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCCTGGGG    60
CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTACGAGA CCGACCCCCG GCGCCACAAG   120
GAGAGCTGCG AGCGCAGCCG CGCGGGCGCC GACCCCCCGG ACCAGAAGAA CCGCCTGATG   180
CCGCTGTCGC ACCTGCCGCT GCGGGACTCG CCCCCGCTGG GGCGCCGGCT GCTCCCGGGC   240
GGCCCGGGGC GCGCCGACCC CGAGTCCTGG CGCTCGCTCC TGGGGCTCGG CGGGCTGGAC   300
GCCGAGTGCG GCCGGCCCCT CTTCGCCACC TACTCGGGCC TCTGCAGGAA GTGCTACTTC   360
CTGGGCATCG ACCGGGACAT CGACACCCTC ATCCTGAAAG GTATTGCGCA GCGATGCACG   420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCCTTT TAATTTAACC   480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC   540
CTCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC   600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT   660
TGCACCATTT CCCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTTGAA CCGGCTCCCA   720
AAGCTAATTT ATAGCCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC   780
GCCTGGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT   840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA
```

Seq ID NO: 564 Protein sequence
Protein Accession #: XP_059466.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM    60
PLSHLPLRDS PPLGRRLLPG GPGRADPESW RSLLGLGGLD AECGRPLPAT YSGLWRKCYF   120
LGIDRDIDTL ILKGIAQRCT AIKYHFSQPI RLRNIPFNLT KTIQQDEWHL LHLRRITAGF   180
LGMAVAVLLC GCIVATVSFF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP   240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV
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Seq ID NO: 565 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3315

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1          11         21         31         41         51
|          |          |          |          |          |
ATGTCCTTTC GGGCAGCCAG GCTCAGCATG AGGAACAGAA GGAATGACAC TCTGGACAGC    60
ACCCGGACCC TGTACTCCAG CGCGTCTCGG AGCACAGACT TGTCTTACAG TGAAAGCGAC   120
TTGGTGAATT TTATTCAAGC AAATTTTAAG AAACGAGAAT GTGTCTTCTT TACCAAAGAT   180
TCCAAGGCCA CGGAGAATGT GTGCAAGTGT GGCTATGCCC AGAGCCAGCA CATGGAAGGC   240
ACCCAGATCA ACCAAAGTGA GAAATGGAAC TACAAGAAAC ACACCAAGGA ATTTCCTACC   300
GACGCCTTTG GGGATATTCA GTTTGAGACA CTGGGGAAGA AAGGGAAGTA TATACGTCTG   360
TCCTGCGACA CGGACGCGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGAAA   420
ACACCCAACC TGGTCATTTC TGTGACCGGG GGCGCCAAGA ACTTCGCCCT GAAGCCGCGC   480
ATGCGCAAGA TCTTCAGCCG GCTCATCTAC ATCGCGCAGT CCAAAGGTGC TTGGATTCTC   540
ACGGGAGGCA CCCATTATGG CCTGATGAAG TACATCGGGG AGGTGGTGAG AGATAACACC   600
ATCAGCAGGA GTTCAGAGGA GAATATTGTG GCCATTGGCA TAGCAGCTTG GGGCATGGTC   660
TCCAACCGGG ACACCCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTTT AGCCCAGTAC   720
CTTATGGATG ACTTCACAAG AGATCCACTG TATATCCTGG ACAACAACCA CACACATTTG   780
CTGCTCGTGG ACAATGGCTG TCATGGACAT CCCACTGTCG AAGCAAAGCT CCGGAATCAG   840
CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC   900
ATTGTGTGTT TTGCCCAAGG AGGTGGAAAA GAGACTTTGA AAGCCATCAA TACCTCCATC   960
AAAAATAAAA TTCCTTGTGT GGTGGTGGAA GGCTCGGGCC AGATCGCTGA TGTGATCGCT  1020
AGCCTGGTGG AGGTGGAGGA TGCCCTGACA TCTTCTGCCG TCAAGGAGAA GCTGGTGCGC  1080
TTTTTACCCC GCACGGTGTC CCGGCTGCCT GAGGAGGAGA CTGAGAGTTG GATCAAATGG  1140
CTCAAAGAAA TTCTCGAATG TTCTCACCTA TTAACAGTTA TTAAAATGGA AGAAGCTGGG  1200
GATGAAATTG TGAGCAATGC CATCTCCTAC GCTCTATACA AAGCCTTCAG CACCAGTGAG  1260
CAAGACAAGG ATAACTGGAA TGGGCAGCTG AAGCTTCTGC TGGAGTGGAA CCAGCTGGAC  1320
TTAGCCAATG ATGAGATTTT CACCAATGAC CGCCGATGGG AGTCTGCTGA CCTTCAAGAA  1380
GTCATGTTTA CGGCTCTCAT AAAGGACAGA CCCAAGTTTG TCCGCCTCTT TCTGGAGAAT  1440
GGCTTGAACC TACGGAAGTT TCTCACCCAT GATGTCCTCA CTGAACTCTT CTCCAACCAC  1500
TTCAGCACGC TTGTGTACCG GAATCTGCAG ATCGCCAAGA ATTCCTATAA TGATGCCCTC  1560
CTCACGTTTG TCTGGAAACT GGTTGCGAAC TTCCGAAGAG GCTTCCGGAA GGAAGACAGA  1620
AATGGCCGGG ACGAGATGGA CATAGAACTC CACGACGTGT CTCCTATTAC TCGGCACCCC  1680
CTGCAAGCTC TCTTCATCTG GGCCATTCTT CAGAATAAGA AGGAACTCTC CAAAGTCATT  1740
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TGGGAGCAGA CCAGGGGCTG CACTCTGGCA GCCCTGGGAG CCAGCAAGCT TCTGAAGACT  1800
CTGGCCAAAG TGAAGAACGA CATCAATGCT GCTGGGGAGT CCGAGGAGCT CGCTAATGAG  1860
TACGAGACCC GGGCTGTTGA GCTGTTCACT GAGTGTTACA GCAGCGATGA AGACTTGGCA  1920
GAACAGCTGC TGGTCTATTC CTGTGAAGCT TGGGGTGGAA GCAACTGTCT GGAGCTGGCG  1980
GTGGAGGCCA CAGACCAGCA TTTCATCGCC CAGCCTGGGG TCCAGAATTT TCTTTCTAAG  2040
CAATGGTATG GAGAGATTTC CCGAGACACC AAGAACTGGA AGATTATCCT GTGTCTGTTT  2100
ATTATACCCT TGGTGGGCTG TGGCTTTGTA TCATTTAGGA AGAAACCTGT CGACAAGCAC  2160
AAGAAGCTGC TTTGGTACTA TGTGGCGTTC TTCACCTCCC CCTTCGTGGT CTTCTCCTGG  2220
AATGTGGTCT TCTACATCGC CTTCCTCCTG CTGTTTGCCT ACGTGCTGCT CATGGATTTC  2280
CATTCGGTGC CACACCCCCC CGAGCTGGTC CTGTACTCGC TGGTCTTTGT CCTCTTCTGT  2340
GATGAAGTGA GACAGTGGTA CGTAAATGGG GTGAATTATT TTACTGACCT GTGGAATGTG  2400
ATGGACACGC TGGGGCTTTT TTACTTCATA GCAGGAATTG TATTTCGGCT CCACTCTTCT  2460
AATAAAAGCT CTTTGTATTC TGGACGAGTC ATTTTCTGTC TGGACTACAT TATTTTCACT  2520
CTAAGATTGA TCCACATTTT TACTGTAAGC AGAAACTTAG GACCCAAGAT TATAATGCTG  2580
CAGAGGATGC TGATCGATGT GTTCTTCTTC CTGTTCCTCT TTGCGGTGTG GATGGTGGCC  2640
TTTGGCGTGG CCAGGCAAGG GATCCTTAGG CAGAATGAGC AGCGCTGGAG GTGGATATTC  2700
CGTTCGGTCA TCTACGAGCC CTACCTGGCC ATGTTCGGCC AGGTGCCCAG TGACGTGGAT  2760
GGTACCACGT ATGACTTTGC CCACTGCACC TTCACTGGGA ATGAGTCCAA GCCACTGTGT  2820
GTGGAGCTGG ATGAGCACAA CCTGCCCCGG TTCCCCGAGT GGATCACCAT CCCCCTGGTG  2880
TGCATCTACA TGTTATCCAC CAACATCCTG CTGGTCAACC TGCTGGTCGC CATGTTTGGC  2940
TACACGGTGG GCACCGTCCA GGAGAACAAT GACCAGGTCT GGAAGTTCCA GAGGTACTTC  3000
CTGGTGCAGG AGTACTGCAG CCGCCTCAAT ATCCCCTTCC CCTTCATCGT CTTCGCTTAC  3060
TTCTACATGG TGGTGAAGAA GTGCTTCAAG TGTTGCTGCA AGGAGAAAAA CATGGAGTCT  3120
TCTGTCTGCT GTTTCAAAAA TGAAGACAAT GAGACTCTGG CATGGGAGGG TGTCATGAAG  3180
GAAAACTACC TTGTCAAGAT CAACACAAAA GCCAACGACA CCTCAGAGGA AATGAGGCAT  3240
CGATTTAGAC AACTGGATAC AAAGCTTAAT GATCTCAAGG GTCTTCTGAA AGAGATTGCT  3300
AATAAAATCA AATGA
```

Seq ID NO: 566 Protein sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MSFRAARLSM RNRRNDTLDS TRTLYSSASR STDLSYSESD LVNFIQANFK KRECVFFTKD    60
SKATENVCKC GYAQSQHMEG TQINQSEKWN YKKHTKEFPT DAFGDIQFET LGKKGKYIRL   120
SCDTDAEILY ELLTQHWHLK TPNLVISVTG GAKNFALKPR MRKIFSRLIY IAQSKGAWIL   180
TGGTHYGLMK YIGEVVRDNT ISRSSEENIV AIGIAAWGMV SNRDTLIRNC DAEGYFLAQY   240
LMDDFTRDPL YILDNNHTHL LLVDNGCHGH PTVEAKLRNQ LEKYISERTI QDSNYGGKIP   300
IVCFAQGGGK ETLKAINTSI KNKIPCVVVE GSGQIADVIA SLVEVEDALT SSAVKEKLVR   360
FLPRTVSRLP EEETESWIKW LKEILECSHL LTVIKMEEAG DEIVSNAISY ALYKAFSTSE   420
QDKDNWNGQL KLLLEWNQLD LANDEIFTND RRWESADLQE VMFTALIKDR PKFVRLFLEN   480
GLNLRKFLTH DVLTELFSNH FSTLVYRNLQ IAKNSYNDAL LTFVWKLVAN FRRGFRKEDR   540
NGRDEMDIEL HDVSPITRHP LQALFIWAIL QNKKELSKVI WEQTRGCTLA ALGASKLLKT   600
LAKVKNDINA AGESEELANE YETRAVELFT ECYSSDEDLA EQLLVYSCEA WGGSNCLELA   660
VEATDQHFIA QPGVQNFLSK QWYGEISRDT KNWKIILCLF IIPLVGCGFV SFRKKPVDKH   720
KKLLWYYVAF FTSPFVVFSW NVVFYIAFLL LFAYVLLMDF HSVPHPPELV LYSLVFVLFC   780
DEVRQWYVNG VNYFTDLWNV MDTLGLFYFI AGIVFRLHSS NKSSLYSGRV IFCLDYIIFT   840
LRLIHIFTVS RNLGPKIIML QRMLIDVFFF LFLFAVWMVA FGVARQGILR QNEQRWRWIF   900
RSVIYEPYLA MFGQVPSDVD GTTYDFAHCT FTGNESKPLC VELDEHNLPR FPEWITIPLV   960
CIYMLSTNIL LVNLLVAMFG YTVGTVQENN DQVWKFQRYF LVQEYCSRLN IPFPFIVFAY  1020
FYMVVKKCFK CCCKEKNMES SVCCFKNEDN ETLAWEGVMK ENYLVKINTK ANDTSEEMRH  1080
RFRQLDTKLN DLKGLLKEIA NKIK
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Seq ID NO: 567 DNA sequence
Nucleic Acid Accession #: NM_006911.1
Coding sequence: 1..558

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCCTCGCC TGTTCTTGTT CCACCTGCTA GAATTCTGTT TACTACTGAA CCAATTTTCC    60
AGAGCAGTCG CGGCCAAATG GAAGGACGAT GTTATTAAAT TATGCGGCCG CGAATTAGTT   120
CGCGCGCAGA TTGCCATTTG CGGCATGAGC ACCTGGAGCA AAAGGTCTCT GAGCCAGGAA   180
GATGCTCCTC AGACACCTAG ACCAGTGGCA GAAATTGTAC CATCCTTCAT CAACAAAGAT   240
ACAGAAACTA TAATTATCAT GTTGGAATTC ATTGCTAATT TGCCACCGGA GCTGAAGGCA   300
GCCCTATCTG AGAGGCAACC ATCATTACCA GAGCTACAGC AGTATGTACC TGCATTAAAG   360
GATTCCAATC TTAGCTTTGA AGAATTTAAG AAACTTATTC GCAATAGGCA AAGTGAAGCC   420
GCAGACAGCA ATCCTTCAGA ATTAAAATAC TTAGGCTTGG ATACTCATTC TCAAAAAAAG   480
AGACGACCCT ACGTGGCACT GTTTGAGAAA TGTTGCCTAA TTGGTTGTAC CAAAAGGTCT   540
CTTGCTAAAT ATTGCTGA
```

Seq ID NO: 568 Protein sequence
Protein Accession #: NP_008842.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPRLFLFHLL EFCLLLNQFS RAVAAKWKDD VIKLCGRELV RAQIAICGMS TWSKRSLSQE    60
DAPQTPRPVA EIVPSFINKD TETIIIMLEF IANLPPELKA ALSERQPSLP ELQQYVPALK   120
DSNLSFEEFK KLIRNRQSEA ADSNPSELKY LGLDTHSQKK RRPYVALFEK CCLIGCTKRS   180
LAKYC
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Seq ID NO: 569 DNA sequence
Nucleic Acid Accession #: XM_036453.1

Coding sequence: 1..3978

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1          11         21         31         41         51
|          |          |          |          |          |
ATGCTGCCCG TGTACCAGGA GGTGAAGCCC AACCCGCTGC AGCACGCGAA CCTCTGCTCA    60
CGCGTGTTCT TCTGGTGGCT CAATCCCTTG TTTAAAATTG GCCATAAACG GAGATTAGAG   120
GAAGATGATA TGTATTCAGT GCTGCCAGAA GACCGCTCAC AGCACCTTGG AGAGGAGTTG   180
CAAGGGTTCT GGGATAAAGA AGTTTTAAGA GCTGAGAATG ACGCACAGAA GCCTTCTTTA   240
ACAAGAGCAA TCATAAAGTG TTACTGGAAA TCTTATTTAG TTTTGGGAAT TTTTACGTTA   300
ATTGAGGAAA GTGCCAAAGT AATCCAGCCC ATATTTTTGG GAAAAATTAT TAATTATTTT   360
GAAAATTATG ATCCCATGGA TTCTGTGGCT TTGAACACAG CGTACGCCTA TGCCACGGTG   420
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TGTGCTGGGA TGAGGTTACG AGTAGCCATG TGCCATATGA TTTATCGGAA GGCACTTCGT   540
CTTAGTAACA TGGCCATGGG GAAGACAACC ACAGGCCAGA TAGTCAATCT GCTGTCCAAT   600
GATGTGAACA AGTTTGATCA GGTGACAGTG TTCTTACACT TCCTGTGGGC AGGACCACTG   660
CAGGCGATCG CAGTGACTGC CCTACTCTGG ATGGAGATAG GAATATCGTG CCTTGCTGGG   720
ATGGCAGTTC TAATCATTCT CCTGCCCTTG CAAAGCTGTT TTGGGAAGTT GTTCTCATCA   780
CTGAGGAGTA AAACTGCAAC TTTCACGGAT GCCAGGATCA GCACCATGAA TGAAGTTATA   840
ACTGGTATAA GGATAATAAA AATGTACGCC TGGGAAAAGT CATTTTCAAA TCTTATTACC   900
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GTGCGGCTGA CGGTTACCCT CTTCTTCCCC TCAGCCATTG AGAGGGTGTC AGAGGCAATC  1140
GTCAGCATCC GAAGAATCCA GACCTTTTTG CTACTTGATG AGATATCACA GCGCAACCGT  1200
CAGCTGCCGT CAGATGGTAA AAAGATGGTG CATGTGCAGG ATTTTACTGC TTTTTGGGAT  1260
AAGGCATCAG AGACCCCAAC TCTACAAGGC CTTTCCTTTA CTGTCAGACC TGGCGAATTG  1320
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GAATTGGCCC CAAGTCACGG GCTGGTCAGC GTGCATGGAA GAATTGCCTA TGTGTCTCAG  1440
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CCTCTCAGTG CAGTAGATGC GGAAGTTAGC AGACACTTGT TCGAACTGTG TATTTGTCAA  1740
ATTTTGCATG AGAAGATCAC AATTTTAGTG ACTCATCAGT TGCAGTACCT CAAAGCTGCA  1800
AGTCAGATTC TGATATTGAA AGATGGTAAA ATGGTGCAGA AGGGGACTTA CACTGAGTTC  1860
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GCTGAAGTTG AGAATATGAT GATCTCAGTA GAAAGGGTCA TTGAATACAC AGACCTTGAA  3060
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ATAATCTTTG ACAATGTGAA CTTCATGTAC AGTCCAGGTG GGCCTCTGGT ACTGAAGCAT  3180
CTGACAGCAC TCATTAAATC ACAAGAAAAG GTTGGCATTG TGGGAAGAAC CGGAGCTGGA  3240
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GCCGCTGCCC TCACTGAAAC AGCAAAACAG GTATACTTCA AAAGAAATTA TCCACATATT  3900
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Seq ID NO: 570 Protein sequence
Protein Accession #: XP_036453.1

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ENYDPMDSVA LNTAYAYATV LTFCTLILAI LHHLYFYHVQ CAGMRLRVAM CHMIYRKALR   180
LSNMAMGKTT TGQIVNLLSN DVNKFDQVTV FLHFLWAGPL QAIAVTALLW MEIGISCLAG   240
MAVLIILLPL QSCFGKLFSS LRSKTATFTD ARIRTMNEVI TGIRIIKMYA WEKSFSNLIT   300
NLRKKEISKI LRSSCLRGMN LASFFSASKI IVFVTFTTYV LLGSVITASR VFVAVTLYGA   360
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VRLTVTLFFP SAIERVSEAI VSIRRIQTFL LLDEISQRNR QLPSDGKKMV HVQDFTAFWD   420
KASETPTLQG LSFTVRPGEL LAVVGPVGAG KSSLLSAVLG ELAPSHGLVS VHGRIAYVSQ   480
QPWVFSGTLR SNILFGKKYE KERYEKVIKA CALKKDLQLL EDGDLTVIGD RGTTLSGGQK   540
ARVNLARAVY QDADIYLLDD PLSAVDAEVS RHLFELCICQ ILHEKITILV THQLQYLKAA   600
SQILILKDGK MVQKGTYTEF LKSGIDFGSL LKKDNEESEQ PPVPGTPTLR NRTFSESSVW   660
SQQSSRPSLK DGALESQDTE NVPVTLSEEN RSEGKVGFQA YKNYFRAGAH WIVFIFLILL   720
NTAAQVAYVL QDWWLSYWAN KQSMLNVTVN GGGNVTEKLD LNWYLGIYSG LTVATVLFGI   780
ARSLLVFYVL VNSSQTLHNK MFESILKAPV LFFDRNPIGR ILNRFSKDIG HLDDLLPLTF   840
LDFIQTLLQV VGVVSVAVAV IPWIAIPLVP LGIIFIFLRR YFLETSRDVK RLESTTRSPV   900
FSHLSSSLQG LWTIRAYKAE ERCQELFDAH QDLHSEAWFL FLTTSRWFAV RLDAICAMFV   960
IIVAFGSLIL AKTLDAGQVG LALSYALTLM GMFQWCVRQS AEVENMMISV ERVIEYTDLE  1020
KEAPWEYQKR PPPAWPHEGV IIFDNVNFMY SPGGPLVLKH LTALIKSQEK VGIVGRTGAG  1080
KSSLISALFR LSEPEGKIWI DKILTTEIGL HDLRKKMSII PQEPVLFTGT MRKNLDPFNE  1140
HTDEELWNAL QEVQLKETIE DLPGKMDTEL AESGSNFSVG QRQLVCLARA ILRKNQILII  1200
DEATANVDPR TDELIQKKIR EKFAHCTVLT IAHRLNTIID SDKIMVLDSG RLKEYDEPYV  1260
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FETAL
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Seq ID NO: 571 DNA sequence
Nucleic Acid Accession #: AF07120
Coding sequence: 116..4093

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GCCCGTGTAC CAGGAGGTGA AGCCCAACCC GCTGCAGGAC GCGAACATCT GCTCACGCGT   180
GTTCTTCTGG TGGCTCAATC CCTTGTTTAA AATTGGCCAT AAACGGAGAT TAGAGGAAGA   240
TGATATGTAT TCAGTGCTGC CAGAAGACCG CTCACAGCAC CTTGGAGAGG AGTTGCAAGG   300
GTTCTGGGAT AAAGAAGTTT TAAGAGCTGA GAATGACGCA CAGAAGCCTT CTTTAACAAG   360
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GGAAAGTGCC AAAGTAATCC AGCCCATATT TTTGGGAAAA ATTATTAATT ATTTTGAAAA   480
TTATGATCCC ATGGATTCTG TGGCTTTGAA CACAGCGTAC GCCTATGCCA CGGTGCTGAC   540
TTTTTGCACG CTCATTTTGG CTATACTGCA TCACTTATAT TTTTATCACG TTCAGTGTGC   600
TGGGATGAGG TTACGAGTAG CCATGTGCCA TATGATTTAT CGGAAGGCAC TTCGTCTTAG   660
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GAACAAGTTT GATCAGGTGA CAGTGTTCTT ACACTTCCTG TGGGCAGGAC CACTGCAGGC   780
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CGGCAGTGTG ATCACAGCCA GCCGCGTGTT CGTGGCAGTG ACGCTGTATG GGGCTGTGCG  1200
GCTGACGGTT ACCCTCTTCT TCCCCTCAGC CATTGAGAGG GTGTCAGAGG CAATCGTCAG  1260
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ATCAGAGACC CCAACTCTAC AAGGCCTTTC CTTTACTGTC AGACCTGGCG AATTGTTAGC  1440
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CGTTGCCTTT GGGTCCCTGA TTCTGGCAAA AACTCTGGAT GCCGGGCAGG TTGGTTTGGC  3060
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Seq ID NO: 572 Protein sequence
Protein Accession #: AAC27076.1

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LSNMAMGKTT TGQIVNLLSN DVNKFDQVTV FLHFLWAGPL QAIAVTALLW MEIGISCLAG   240
MAVLIILLPL QSCFGKLFSS LRSKTATFTD ARIRTMNEVI TGIRIIKMYA WEKSFSNLIT   300
NLRKKEISKI LRSSCLRGMN LASFFSASKI IVFVTFTTYV LLGSVITASR VFVAVTLYGA   360
VRLTVTLFFP SAIERVSEAI VSIRRIQTFL LLDEISQRNR QLPSDGKKMV HVQDFTAFWD   420
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QPWVFSGTLR SNILFGKKYE KERYEKVIKA CALKKDLQLL EDGDLTVIGD RGTTLSGGQK   540
ARVNLARAVY QDADIYLLDD PLSAVDAEVS RHLFELCICQ ILHEKITILV THQLQYLKAA   600
SQILILKDGK MVQKGTYTEF LKSGIDFGSL LKKDNEESEQ PPVPGTPTLR NRTFSESSVW   660
SQQSSRPSLK DGALESQDTE NVPVTLSEEN RSEGKVGFQA YKNYFRAGAH WIVFIFLILL   720
NTAAQVAYVL QDWWLSYWAN KQSMLNVTVN GGGNVTEKLD LNWYLGIYSG LTVATVLFGI   780
ARSLLVFYVL VNSSQTLHNK MFESILKAPV LFFDRNPIGR ILNRFSKDIG HLDDLLPLTF   840
LDFIQTLLQV VGVVSVAVAV IPWIAIPLVP LGIIFIFLRR YFLETSRDVK RLESTTRSPV   900
FSHLSSSLQG LWTIRAYKAE ERCQELFDAH QDLHSEAWFL FLTTSRWFAV RLDAICAMFV   960
IIVAFGSLIL AKTLDAGQVG LALSYALTLM GMFQWCVRQS AEVENMMISV ERVIEYTDLE  1020
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Seq ID NO: 573 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1365

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AGAAATCCTA AGTTTGCTTC TGAATTTTTT CCTCATGTGG TAGATGTCAC TCATCATGAA   240
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CTGTGGGACC TGAGACATCT GCTTGTGGGT AAAATCCTGA TTGATGTGAG CAATAACATG   360
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GCCAGCCGGC AGGTTTATAT ATGCAGCAAC AATATTCAAG CGCGACAACA GGTTATTGAA   540
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GTCGCTCTGC TCATAAGTAC TTTCCATGTT TTAATTTATG GATGGAAACG AGCTTTTGAG  1260
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Seq ID NO: 574 Protein sequence
Protein Accession #: Eos sequence

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RINQYPESNA EYLASLFPDS LIVKGFNVVS AWALQLGPKD ASRQVYICSN NIQARQQVIE   180
LARQLNFIPI DLGSLSSARE IENLPLRLFT LWRGPVVVAI SLATFFFLYS FVRDVIHPYA   240
RNQQSDFYKI PIEIVNKTLP IVAITLLSLV YLAGLLAAAY QLYYGTKYRR FPPWLETWLQ   300
CRKQLGLLSF FFAMVHVAYS LCLPMRRSER YLFLNMAYQQ VHANIENSWN EEEVWRIEMY   360
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Seq ID NO: 575 DNA sequence
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Coding sequence: 3..1721

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GGTGCGGAAC TTGCCGCCCC CAGCAGCGCC GGCGGGCTAA GCCCAGGGCC GGGCAGACAA   240
AAGAGCCCGC CCGCGTAGGA AGGCACGGCC GGCGGCGGCG GAGCGCAGCG ATGGCCGGGC   300
GAGGGGGCAG CGCGCTGCTG GCTCTGTGCG GGGCACTGGC TGCCTGCGGG TGGCTCCTGG   360
GCGCCGAAGC CCAGGAGCCC GGGGCGCCCG CGGCGGGCAT GAGGCGGCGC CGGCGGCTGC   420
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TGTCCGTGTG GCTGCAGTGC ACCGCCATCA GCAGGATTTA CACGGTGGGG CGCAGCTTCG   540
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AGCCTGAATT TAAATACATT GGGAATATGC ATGGGAATGA GGCTGTTGGA CGAGAACTGC   660
TCATTTTCTT GGCCCAGTAC CTATGCAACG AATACCAGAA GGGGAACGAG ACAATTGTCA   720
ACCTGATCCA CAGTACCCGC ATTCACATCA TGCCTTCCCT GAACCCAGAT GGCTTTGAGA   780
AGGCAGCGTC TCAGCCTGGT GAACTCAAGG ACTGGTTTGT GGGTCGAAGC AATGCCCAGG   840
GAATAGATCT GAACCGGAAC TTTCCAGACC TGGATAGGAT AGTGTACGTG AATGAGAAAG   900
AAGGTGGTCC AAATAATCAT CTGTTGAAAA ATATGAAGAA AATTGTGGAT CAAAACACAA   960
AGCTTGCTCC TGAGACCAAG GCTGTCATTC ATTGGATTAT GGATATTCCT TTTGTGCTTT  1020
CTGCCAATCT CCATGGAGGA GACCTTGTGG CCAATTATCC ATATGATGAG ACGCGGAGTG  1080
GTAGTGCTCA CGAATACAGC TCCTCCCCAG ATGACGCCAT TTTCCAAAGC TTGGCCCGGG  1140
CATACTCTTC TTTCAACCCG GCCATGTCTG ACCCCAATCG GCCACCATGT CGCAAGAATG  1200
ATGATGACAG CAGCTTTGTA GATGGAACCA CCAACGGTGG TGCTTGGTAC AGCGTACCTG  1260
GAGGGATGCA AGACTTCAAT TACCTTAGCA GCAACTGTTT TGAGATCACC GTGGAGCTTA  1320
GCTGTGAGAA GTTCCCACCT GAAGAGACTC TGAAGACCTA CTGGGAGGAT AACAAAAACT  1380
CCCTCATTAG CTACCTTGAG CAGATACACC GAGGAGTTAA AGGATTTGTC CGAGACCTTC  1440
AAGGTAACCC AATTGCGAAT GCCACCATCT CCGTGGAAGG AATAGACCAC GATGTTACAT  1500
CCGCAAAGGA TGGTGATTAC TGGAGATTGC TTATACCTGG AAACTATAAA CTTACAGCCT  1560
CAGCTCCAGG CTATCTGGCA ATAACAAAGA AAGTGGCAGT TCCTTACAGC CCTGCTGCTG  1620
GGGTTGATTT TGAACTGGAG TCATTTTCTG AAAGGAAAGA AGAGGAGAAG GAAGAATTGA  1680
TGGAATGGTG GAAAATGATG TCAGAAACTT TAAATTTTTA AAAAGGCTTC TAGTTAGCTG  1740
CTTTAAATCT ATCTATATAA TGTAGTATGA TGTAATGTGG TCTTTTTTTT AGATTTTGTG  1800
CAGTTAATAC TTAACATTGA TTTATTTTTT AATCATTTAA ATATTAATCA ACTTTCCTTA  1860
AAATAAATAG CCTCTTAGGT AAAAATATAA GAACTTGATA TATTTCATTC TCTTATATAG  1920
TATTCATTTT CCTACCTATA TTACACAAAA AAGTATAGAA AAGATTTAAG TAATTTTGCC  1980
ATCCTAGGCT TAAATGCAAT ATTCCTGGTA TTATTTACAA TGCAGAATTT TTTGAGTAAT  2040
TCTAGCTTTC AAAAATTAGT GAAGTTCTTT TACTGTAATT GGTGACAATG TCACATAATG  2100
AATGCTATTG AAAAGGTTAA CAGATACAGC TCGGAGTTGT GAGCACTCTA CTGCAAGACT  2160
TAAATAGTTC AGTATAAATT GTCGTTTTTT TCTTGTGCTG ACTAACTATA AGCATGATCT  2220
TGTTAATGCA TTTTTGATGG GAAGAAAAGG TACATGTTTA CAAAGAGGTT TTATGAAAAG  2280
AATAAAAATT GACTTCTTGC TTGTACATAT AGGAGCAATA CTATTATATT ATGTAGTCCG  2340
TTAACACTAC TTAAAAGTTT AGGGTTTTCT CTTGGTTGTA GAGTGGCCCA GAATTGCATT  2400
CTGAATGAAT AAACGTTAAA AAAAAATCCC CAGTGAAAAA AAA
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Seq ID NO: 576 Protein sequence
Protein Accession #: NP_001864.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAGRGGSALL ALCGALAACG WLLGAEAQEP GAPAAGMRRR RRLQQEDGIS FEYHRYPELR    60
EALVSVWLQC TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEFKYI GNMHGNEAVG   120
RELLIFLAQY LCNEYQKGNE TIVNLIHSTR IHIMPSLNPD GFEKAASQPG ELKDWFVGRS   180
NAQGIDLNRN FPDLDRIVYV NEKEGGPNNH LLKNMKKIVD QNTKLAPETK AVIHWIMDIP   240
FVLSANLHGG DLVANYPYDE TRSGSAHEYS SSPDDAIFQS LARAYSSFNP AMSDPNRPPC   300
RKNDDDSSFV DGTTNGGAWY SVPGGMQDFN YLSSNCFEIT VELSCEKFPP EETLKTYWED   360
NKNSLISYLE QIHRGVKGFV RDLQGNPIAN ATISVEGIDH DVTSAKDGDY WRLLIPGNYK   420
LTASAPGYLA ITKKVAVPYS PAAGVDFELE SFSERKEEEK EELMEWWKMM SETLNF
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Seq ID NO: 577 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..933

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1          11         21         31         41         51
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ATGTGCAGCA ATGGACGGTG CATCCCGGGC GCCTGGCAGT GTGACGGGCT GCCTGACTGC    60
TTCGACAAGA GTGATGAGAA GGAGTGCCCC AAGGCTAAGT CGAAATGTGG CCCGACCTTC   120
TTCCCCTGTG CCAGCGGCAT CCATTGCATC ATTGGTCGCT TCCGGTGCAA TGGGTTTGAG   180
GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC   240
GCCCGCTACC ACTGCAAGAA CGGCCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG   300
AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAGT   360
GGGCAGGTGT TTGTGACTTC AGAGAACCAA CTTGTGTATT ACCCCAGCAT CACCTATGCC   420
ATCATCGGCA GCTCCGTCAT TTTTGTGCTG GTGGTGGCCC TGCTGGCACT GGTCTTGCAC   480
CACCAGCGGA AGCGGAACAA CCTCATGACG CTGCCCGTGC ACCGGCTGCA GCACCCTGTG   540
CTGCTGTCCC GCCTGGTGGT CCTGGACCAC CCCCACCACT GCAACGTCAC CTACAACGTC   600
AATAATGGCA TCCAGTATGT GGCCAGCCAG GCGGAGCAGA ATGCGTCGGA AGTAGGCTCC   660
CCACCCTCCT ACTCCGAGGC CTTGCTGGAC CAGAGGCCTG CGTGGTATGA CCTTCCTCCA   720
CCGCCCTACT CTTCTGACAC GGAATCTCTG AACCAAGCCG ACCTGCCCCC CTACCGCTCC   780
CGGTCCGGGA GTGCCAACAG TGCCAGCTCC CAGGCAGCCA GCAGCCTCCT GAGCGTGGAA   840
GACACCAGCC ACAGCCCGGG GCAGCCTGGC CCCCAGGAGG GCACTGCTGA GCCCAGGGAC   900
```

TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MCSNGRCIPG AWQCDGLPDC FDKSDEKECP KAKSKCGPTF FPCASGIHCI IGRFRCNGFE    60
DCPDGSDEEN CTANPLLCST ARYHCKNGLC IDKSFICDGQ NNCQDNSDEE SCESSQEPGS   120
GQVFVTSENQ LVYYPSITYA IIGSSVIFVL VVALLALVLH HQRKRNNLMT LPVHRLQHPV   180
LLSRLVVLDH PHHCNVTYNV NNGIQYVASQ AEQNASEVGS PPSYSEALLD QRPAWYDLPP   240
PPYSSDTESL NQADLPPYRS RSGSANSASS QAASSLLSVE DTSHSPGQPG PQEGTAEPRD   300
SEPSQGTEEV
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Seq ID NO: 579 DNA sequence
Nucleic Acid Accession #: AF179274.1
Coding sequence: 1..1125

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1          11         21         31         41         51
|          |          |          |          |          |
ATGGTGCTGT GGGAGTCCCC GCGGCAGTGC AGCAGCTGGA CACTTTGCGA GGGCTTTTGC    60
TGGCTGCTGC TGCTGCCCGT CATGCTACTC ATCGTAGCCC GCCCGGTGAA GCTCGCTGCT   120
TTCCCTACCT CCTTAAGTGA CTGCCAAACG CCCACCGGCT GGAATTGCTC TGGTTATGAT   180
GACAGAGAAA ATGATCTCTT CCTCTGTGAC ACCAACACCT GTAAATTTGA TGGGGAATGT   240
TTAAGAATTG GAGACACTGT GACTTGCGTC TGTCAGTTCA AGTGCAACAA TGACTATGTG   300
CCTGTGTGTG GCTCCAATGG GGAGAGCTAC CAGAATGAGT GTTACCTGCG ACAGGCTGCA   360
TGCAAACAGC AGAGTGAGAT ACTTGTGGTG TCAGAAGGAT CATGTGCCAC AGATGCAGGA   420
TCAGGATCTG GAGATGGAGT CCATGAAGGC TCTGGAGAAA CTAGTCAAAA GGAGACATCC   480
ACCTGTGATA TTTGCCAGTT TGGTGCAGAA TGTGACGAAG ATGCCGAGGA TGTCTGGTGT   540
GTGTGTAATA TTGACTGTTC TCAAACCAAC TTCAATCCCC TCTGCGCTTC TGATGGGAAA   600
TCTTATGATA ATGCATGCCA AATCAAAGAA GCATCGTGTC AGAAACAGGA GAAAATTGAA   660
GTCATGTCTT TGGGTCGATG TCAAGATAAC ACAACTACAA CTACTAAGTC TGAAGATGGG   720
CATTATGCAA GAACAGATTA TGCAGAGAAT GCTAACAAAT TAGAAGAAAG TGCCAGAGAA   780
CACCACATAC CTTGTCCGGA ACATTACAAT GGCTTCTGCA TGCATGGGAA GTGTGAGCAT   840
TCTATCAATA TGCAGGAGCC ATCTTGCAGG TGTGATGCTG GTTATACTGG ACAACACTGT   900
GAAAAAAAGG ACTACAGTGT TCTATACGTT GTTCCCGGTC CTGTACGATT TCAGTATGTC   960
TTAATCGCAG CTGTGATTGG AACAATTCAG ATTGCTGTCA TCTGTGTGGT GGTCCTCTGC  1020
ATCACAAGGA AATGCCCCAG AAGCAACAGA ATTCACAGAC AGAAGCAAAA TACAGGGCAC  1080
TACAGTTCAG ACAATACAAC AAGAGCGTCC ACGAGGTTAA TCTGA
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Seq ID NO: 580 Protein sequence
Protein Accession #: NP_057276.2

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1          11         21         31         41         51
|          |          |          |          |          |
MVLWESPRQC SSWTLCEGFC WLLLLPVMLL IVARPVKLAA FPTSLSDCQT PTGWNCSGYD    60
DRENDLFLCD TNTCKFDGEC LRIGDTVTCV CQFKCNNDYV PVCGSNGESY QNECYLRQAA   120
CKQQSEILVV SEGSCATDAG SGSGDGVHEG SGETSQKETS TCDICQFGAE CDEDAEDVWC   180
VCNIDCSQTN FNPLCASDGK SYDNACQIKE ASCQKQEKIE VMSLGRCQDN TTTTTKSEDG   240
HYARTDYAEN ANKLEESARE HHIPCPEHYN GFCMHGKCEH SINMQEPSCR CDAGYTGQHC   300
EKKDYSVLYV VPGPVRFQYV LIAAVIGTIQ IAVICVVVLC ITRKCPRSNR IHRQKQNTGH   360
YSSDNTTRAS TRLI
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Seq ID NO: 581 DNA sequence
Nucleic Acid Accession #: S78203.1
Coding sequence: 1..2190

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAATCCTT TCCAGAAAAA TGAGTCCAAG GAAACTCTTT TTTCACCTGT CTCCATTGAA    60
GAGGTACCAC CTCGACCACC TAGCCCTCCA AAGAAGCCAT CTCCGACAAT CTGTGGCTCC   120
AACTATCCAC TGAGCATTGC CTTCATTGTG GTGAATGAAT TCTGCGAGCG CTTTTCCTAT   180
TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCCTGTATT TCCTGCACTG GAATGAAGAT   240
ACCTCCACAT CTATATACCA TGCCTTCAGC AGCCTCTGTT ATTTTACTCC CATCCTGGGA   300
GCAGCCATTG CTGACTCGTG GTTGGGAAAA TTCAAGACAA TCATCTATCT CTCCTTGGTG   360
TATGTGCTTG GCCATGTGAT CAAGTCCTTG GGTGCCTTAC CAATACTGGG AGGACAAGTG   420
GTACACACAG TCCTATCATT GATCGGCCTG AGTCTAATAG CTTTGGGGAC AGGAGGCATC   480
AAACCCTGTG TGGCAGCTTT TGGTGGAGAC CAGTTTGAAG AAAAACATGC AGAGGAACGG   540
ACTAGATACT TCTCAGTCTT CTACCTGTCC ATCAATGCAG GGAGCTTGAT TTCTACATTT   600
ATCACACCCA TGCTGAGAGG AGATGTGCAA TGTTTTGGAG AAGACTGCTA TGCATTGGCT   660
TTTGGAGTTC CAGGACTGCT CATGGTAATT GCACTTGTTG TGTTTGCAAT GGGAAGCAAA   720
ATATACAATA AACCACCCCC TGAAGGAAAC ATAGTGGCTC AAGTTTTCAA ATGTATCTGG   780
TTTGCTATTT CCAATCGTTT CAAGAACCGT TCTGGAGACA TTCCAAAGCG ACAGCACTGG   840
CTAGACTGGG CAGCTGAGAA ATATCCAAAG CAGCTCATTA TGGATGTAAA GGCACTGACC   900
AGGGTACTAT TCCTTTATAT CCCATTGCCC ATGTTCTGGG CTCTTTTGGA TCAGCAGGGT   960
TCACGATGGA CTTTGCAAGC CATCAGGATG AATAGGAATT TGGGGTTTTT TGTGCTTCAG  1020
CCGGACCAGA TGCAGGTTCT AAATCCCTTT CTGGTTCTTA TCTTCATCCC GTTGTTTGAC  1080
TTTGTCATTT ATCGTCTGGT CTCCAAGTGT GGAATTAACT TCTCATCACT TAGGAAAATG  1140
GCTGTTGGTA TGATCCTAGC GTGCCTGGCA TTTGCAGTTG CGGCAGCTGT AGAGATAAAA  1200
ATAAATGAAA TGGCCCCAGC CCAGTCAGGT CCCCAGGAGG TTTTCCTACA AGTCTTGAAT  1260
CTGGCAGATG ATGAGGTGAA GGTGACAGTG GTGGGAAATG AAAACAATTC TCTGTTGATA  1320
GAGTCCATCA AATCCTTTCA GAAAACACCA CACTATTCCA AACTGCACCT GAAAACAAAA  1380
AGCCAGGATT TTCACTTCCA CCTGAAATAT CACAATTTGT CTCTCTACAC TGAGCATTCT  1440
GTGCAGGAGA AGAACTGGTA CAGTCTTGTC ATTCGTGAAG ATGGGAACAG TATCTCCAGC  1500
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WO03042661 [file://E:/WO03042661.pcl]


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ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGTT  1560
AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT  1620
GAAGACTATG GTGTGTCTGC TTATAGAACT GTGCAAAGAG GAGAATACCC TGCAGTGCAC  1680
TGTAGAACAG AAGATAAGAA CTTTTCTCTG AATTTGGGTC TTCTAGACTT TGGTGCAGCA  1740
TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGTCTTC AGGCCTGGAA GATTGAAGAC  1800
ATTCCAGCCA ACAAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTTACAGCT  1860
GGGGAGGTCA TGTTCTCTGT CACAGGTCTT GAGTTTTCTT ATTCTCAGGC TCCCTCTAGC  1920
ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG  1980
CTTGTTGTGG CACAGTTCAG TGGCCTGGTA CAGTGGGCCG AATTCATTTT GTTTTCCTGC  2040
CTCCTGCTGG TGATCTGCCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG  2100
ACAGAGGATA TGCGGGGTCC AGCAGATAAG CACATTCCTC ACATCCAGGG GAACATGATC  2160
AAACTAGAGA CCAAGAAGAC AAAACTCTGA
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Seq ID NO: 582 Protein sequence
Protein Accession #: AAB34388.1

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1          11         21         31         41         51
|          |          |          |          |          |
MNPFQKNESK ETLFSPVSIE EVPPRPPSPP KKPSPTICGS NYPLSIAFIV VNEFCERFSY    60
YGMKAVLILY FLYFLHWNED TSTSIYHAFS SLCYFTPILG AAIADSWLGK FKTIIYLSLV   120
YVLGHVIKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFGGD QFEEKHAEER   180
TRYFSVFYLS INAGSLISTF ITPMLRGDVQ CFGEDCYALA FGVPGLLMVI ALVVFAMGSK   240
IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKRQHW LDWAAEKYPK QLIMDVKALT   300
RVLFLYIPLP MFWALLDQQG SRWTLQAIRM NRNLGFFVLQ PDQMQVLNPF LVLIFIPLFD   360
FVIYRLVSKC GINFSSLRKM AVGMILACLA FAVAAAVEIK INEMAPAQSG PQEVFLQVLN   420
LADDEVKVTV VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDFHFHLKY HNLSLYTEHS   480
VQEKNWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG   540
EDYGVSAYRT VQRGEYPAVH CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED   600
IPANKMSIAW QLPQYALVTA GEVMFSVTGL EFSYSQAPSS MKSVLQAAWL LTIAVGNIIV   660
LVVAQFSGLV QWAEFILFSC LLLVICLIFS IMGYYYVPVK TEDMRGPADK HIPHIQGNMI   720
KLETKKTKL
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Seq ID NO: 583 DNA sequence
Nucleic Acid Accession #: NM_032642.1
Coding sequence: 184..1263

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1          11         21         31         41         51
|          |          |          |          |          |
GACCATTAGC AGGCACCCAG GCCTGTCTTT GGCTCGGAAA CGGTGGCCCC CAATGTAGCC    60
TAGTTTGAAC CTAGGAACTG CAGGACCAGA GAGATTCCAC TGGAGCCTGA TGGACGGGTG   120
ACAGAGGGAA CCCTACTCTG GAAACTGTCA GTCCCAGGGC ACTGGGGAGG GCTGAGGCCG   180
ACCATGCCCA GCCTGCTGCT GCTGTTCACG GCTGCTCTGC TGTCCAGCTG GGCTCAGCTT   240
CTGACAGACG CCAACTCCTG GTGGTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG   300
TTTATCATCG GTGCCCAGCC CGTGTGCAGT CAGCTTCCCG GGCTCTCCCC TGGCCAGAGG   360
AAGCTGTGCC AATTGTACCA GGAGCACATG GCCTACATAG GGGAGGGAGC CAAGACTGGC   420
ATCAAGGAAT GCCAGCACCA GTTCCGGCAG CGGCGGTGGA ATTGCAGCAC AGCGGACAAC   480
GCATCTGTCT TTGGGAGAGT CATGCAGATA GGCAGCCGAG AGACCGCCTT CACCCACGCG   540
GTGAGCGCCG CGGGCGTGGT CAACGCCATC AGCCGGGCCT GCCGCGAGGG CGAGCTCTCC   600
ACCTGCGGCT GCAGCCGGAC GGCGCGGCCC AAGGACCTGC CCCGGGACTG GCTGTGGGGC   660
GGCTGTGGGG ACAACGTGGA GTACGGCTAC CGCTTCGCCA AGGAGTTTGT GGATGCCCGG   720
GAGCGAGAGA AGAACTTTGC CAAAGGATCA GAGGAGCAGG GCCGGGTGCT CATGAACCTG   780
CAAAACAACG AGGCCGGTCG CAGGGCTGTG TATAAGATGG CAGACGTAGC CTGCAAATGC   840
CACGGCGTCT CGGGGTCCTG CAGCCTCAAG ACCTGCTGGC TGCAGCTGGC CGAGTTCCGC   900
AAGGTCGGGG ACCGGCTGAA GGAGAAGTAC GACAGCGCGG CCGCCATGCG CGTCACCCGC   960
AAGGGCCGGC TGGAGCTGGT CAACAGCCGC TTCACCCAGC CCACCCCGGA GGACCTGGTC  1020
TATGTGGACC CCAGCCCCGA CTACTGCCTG CGCAACGAGA GCACGGGCTC CCTGGGCACG  1080
CAGGGCCGCC TCTGCAACAA GACCTCGGAG GGCATGGATG GCTGTGAGCT CATGTGCTGC  1140
GGGCGTGGCT ACAACCAGTT CAAGAGCGTG CAGGTGGAGC GCTGCCACTG CAAGTTCCAC  1200
TGGTGCTGCT TCGTCAGGTG TAAGAAGTGC ACGGAGATCG TGGACCAGTA CATCTGTAAA  1260
TAGCCCGGAG GGCCTGCTCC CGGCCCCCCC TGCACTCTGC CTCACAAAGG TCTATATTAT  1320
ATAAATCTAT ATAAATCTAT TTTATATTTG TATAAGTAAA TGGGTGGGTG CTATACAATG  1380
GAAAGATGAA AATGGAAAGG AAGAGCTTAT TTAAGAGACG CTGGAGATCT CTGAGGAGTG  1440
GACTTTGCTG GTTCTCTCCT CTTGGTGGGT GGGAGACAGG GCTTTTTCTC TCCCTCTGGC  1500
GAGGACTCTC AGGATGTAGG GACTTGGAAA TATTTACTGT CTGTCCACCA CGGCCTGGAG  1560
GAGGGAGGTT GTGGTTGGAT GGAGGAGATG ATCTTGTCTG GAAGTCTAGA GTCTTTGTTG  1620
GTTAGAGGAC TGCCTGTGAT CCTGGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA  1680
ACTCAGCTTC AACCTCGATG TCTTCAGGGT CTTGTCCAGA ATGTAGATGG GTTCCGTAAG  1740
AGGCCTGGTG CTCTCTTACT CTTTCATCCA CGTGCACTTG TGCGGCATCT GCAGTTTACA  1800
GGAACGGCTC CTTCCCTAAA ATGAGAAGTC CAAGGTCATC TCTGGCCCAG TGACCACAGA  1860
GAGATCTGCA CCTCCCGGAC TTCAGGCCTG CCTTTCCAGC GAGAATTCTT CATCCTCCAC  1920
GGTTCACTAG CTCCTACCTG AAGAGGAAAG GGGGCCATTT GACCTGACAT GTCAGGAAAG  1980
CCCTAAACTG AATGTTTGCG CCTGGGCTGC AGAAGCCAGG GTGCATGACC AGGCTGCGTG  2040
GACGTTATAC TGTCTTCCCC CACCCCCGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC  2100
CTCCACCGAG GGAGGCCTCA CAAACCACAG GACGCTGCAA CGGGTCAGGC TGGCGGGCCC  2160
GGCGTGCTCA TCATCTCTGC CCCAGGTGTA CGGTTTCTCT CTGACATTAA ATGCCCTTCA  2220
TGGAAAAAAA AAAAAGAAAA AAAAAAAAAA AA
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Seq ID NO: 584 Protein sequence
Protein Accession #: NP_116031.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPSLLLLFTA ALLSSWAQLL TDANSWWSLA LNPVQRPEMF IIGAQPVCSQ LPGLSPGQRK    60
LCQLYQEHMA YIGEGAKTGI KECQHQFRQR RWNCSTADNA SVFGRVMQIG SRETAFTHAV   120
```

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SAAGVVNAIS RACREGELST CGCSRTARPK DLPRDWLWGG CGDNVEYGYR FAKEFVDARE   180
REKNFAKGSE EQGRVLMNLQ NNEAGRRAVY KMADVACKCH GVSGSCSLKT CWLQLAEFRK   240
VGDRLKEKYD SAAAMRVTRK GRLELVNSRF TQPTPEDLVY VDPSPDYCLR NESTGSLGTQ   300
GRLCNKTSEG MDGCELMCCG RGYNQFKSVQ VERCHCKFHW CCFVRCKKCT EIVDQYICK

Seq ID NO:  585 DNA sequence
Nucleic Acid Accession #:  Eos sequence
Coding sequence: 1..1479

1          11         21         31         41         51
|          |          |          |          |          |
ATGGCTTTGA ACTCAGGGTC ACCACCAGCT ATTGGACCTT ACTATGAAAA CCATGGATAC    60
CAACCGGAAA ACCCCTATCC CGCACAGCCC ACTGTGGTCC CCACTGTCTA CGAGGTGCAT   120
CCGGCTCAGT ACTACCCGTC CCCCGTGCCC CAGTACGCCC CGAGGGTCCT GACGCAGGCT   180
TCCAACCCCG TCGTCTGCAC GCAGCCCAAA TCCCCATCCG GGACAGTGTG CACCTCAAAG   240
ACTAAGAAAG CACTGTGCAT CACCTTGACC CTGGGGACCT TCCTCGTGGG AGCTGCGCTG   300
GCCGCTGGCC TACTCTGGAA GTTCATGGGC AGCAAGTGCT CCAACTCTGG GATAGAGTGC   360
GACTCCTCAG GTACCTGCAT CAACCCCTCT AACTGGTGTG ATGGCGTGTC ACACTGCCCC   420
GGCGGGGAGG ACGAGAATCG GTGTGTTCGC CTCTACGGAC CAAACTTCAT CCTTCAGGTG   480
TACTCATCTC AGAGGAAGTC CTGGCACCCT GTGTGCCAAG ACGACTGGAA CGAGAACTAC   540
GGGCGGGCGG CCTGCAGGGA CATGGGCTAT AAGAATAATT TTTACTCTAG CCAAGGAATA   600
GTGGATGACA GCGGATCCAC CAGCTTTATG AAACTGAACA CAAGTGCCGG CAATGTCGAT   660
ATCTATAAAA AACTGTACCA CAGTGATGCC TGTTCTTCAA AAGCAGTGGT TTCTTTACGC   720
TGTATAGCCT GCGGGGTCAA CTTGAACTCA AGCCGCCAGA GCAGGATCGT GGGCGGCGAG   780
AGCGCGCTCC CGGGGGCCTG GCCCTGGCAG GTCAGCCTGC ACGTCCAGAA CGTCCACGTG   840
TGCGGAGGCT CCATCATCAC CCCCGAGTGG ATCGTGACAG CCGCCCACTG CGTGGAAAAA   900
CCTCTTAACA ATCCATGGCA TTGGACGGCA TTTGCGGGGA TTTTGAGACA ATCTTTCATG   960
TTCTATGGAG CCGGATACCA AGTAGAAAAA GTGATTTCTC ATCCAAATTA TGACTCCAAG  1020
ACCAAGAACA ATGACATTGC GCTGATGAAG CTGCAGAAGC CTCTGACTTT CAACGACCTA  1080
GTGAAACCAG TGTGTCTGCC CAACCCAGGC ATGATGCTGC AGCCAGAACA GCTCTGCTGG  1140
ATTTCCGGGT GGGGGGCCAC CGAGGAGAAA GGGAAGACCT CAGAAGTGCT GAACGCTGCC  1200
AAGGTGCTTC TCATTGAGAC ACAGAGATGC AACAGCAGAT ATGTCTATGA CAACCTGATC  1260
ACACCAGCCA TGATCTGTGC CGGCTTCCTG CAGGGGAACG TCGATTCTTG CCAGGGTGAC  1320
AGTGGAGGGC CTCTGGTCAC TTCGAAGAAC AATATCTGGT GGCTGATAGG GGATACAAGC  1380
TGGGGTTCTG GCTGTGCCAA AGCTTACAGA CCAGGAGTGT ACGGGAATGT GATGGTATTC  1440
ACGGACTGGA TTTATCGACA AATGAGGGCA GACGGCTAA

Seq ID NO:  586 Protein sequence
Protein Accession #: Eos sequence

1          11         21         31         41         51
|          |          |          |          |          |
MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA    60
SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC   120
DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGPNFILQV YSSQRKSWHP VCQDDWNENY   180
GRAACRDMGY KNNFYSSQGI VDDSGSTSFM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR   240
CIACGVNLNS SRQSRIVGGE SALPGAWPWQ VSLHVQNVHV CGGSIITPEW IVTAAHCVEK   300
PLNNPWHWTA FAGILRQSFM FYGAGYQVEK VISHPNYDSK TKNNDIALMK LQKPLTFNDL   360
VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNLI   420
TPAMICAGFL QGNVDSCQGD SGGPLVTSKN NIWWLIGDTS WGSGCAKAYR PGVYGNVMVF   480
TDWIYRQMRA DG

Seq ID NO:  587 DNA sequence
Nucleic Acid Accession #:  NM_005656.1
Coding sequence: 57..1535

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|          |          |          |          |          |
GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC AGCAAGATGG    60
CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT GGATACCAAC   120
CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG   180
CTCAGTACTA CCCGTCCCCC GTGCCCCAGT ACGCCCCGAG GGTCCTGACG CAGGCTTCCA   240
ACCCCGTCGT CTGCACGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA   300
AGAAAGCACT GTGCATCACC TTGACCCTGG GGACCTTCCT CGTGGGAGCT GCGCTGGCCG   360
CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGCGACT   420
CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG CGTGTCACAC TGCCCCGGCG   480
GGGAGGACGA GAATCGGTGT GTTCGCCTCT ACGGACCAAA CTTCATCCTT CAGATGTACT   540
CATCTCAGAG GAAGTCCTGG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC   600
GGGCGGCCTG CAGGGACATG GGCTATAAGA ATAATTTTTA CTCTAGCCAA GGAATAGTGG   660
ATGACAGCGG ATCCACCAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT   720
ATAAAAAACT GTACCACAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT   780
TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG   840
CGCTCCCGGG GGCCTGGCCC TGGCAGGTCA GCCTGCACGT CCAGAACGTC CACGTGTGCG   900
GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC   960
TTAACAATCC ATGGCATTGG ACGGCATTTG CGGGGATTTT GAGACAATCT TTCATGTTCT  1020
ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA  1080
AGAACAATGA CATTGCGCTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA  1140
AACCAGTGTG TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT  1200
CCGGGTGGGG GGCCACCGAG GAGAAAGGGA AGACCTCAGA AGTGCTGAAC GCTGCCAAGG  1260
TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC  1320
CAGCCATGAT CTGTGCCGGC TTCCTGCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG  1380
GAGGGCCTCT GGTCACTTCG AACAACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG  1440
GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTCACGG  1500
ACTGGATTTA TCGACAAATG AAGGCAAACG GCTAATCCAC ATGGTCTTCG TCCTTGACGT  1560
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CGTTTTACAA GAAAACAATG GGGCTGGTTT TGCTTCCCCG TGCATGATTT ACTCTTAGAG  1620
ATGATTCAGA GGTCACTTCA TTTTTATTAA ACAGTGAACT TGTCTGGCTT TGGCACTCTC  1680
TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCCAGCC TGCTCTCCCT AACCCCTTGT  1740
CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGCAAGAGG  1800
GTTGGAGGCT GCCCCCATTG AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGGA  1860
TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT  1920
GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTTGGTAGTG  1980
TCCCCAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTC TTAGAGCCTT AGCAGCCCTG  2040
GATGGTGGCC AGAAATAAAG GGACCAGCCC TTCATGGGTG GTGACGTGGT AGTCACTTGT  2100
AAGGGGAACA GAAACATTTT TGTTCTTATG GGGTGAGAAT ATAGACAGTG CCCTTGGTGC  2160
GAGGGAAGCA ATGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA  2220
CATTGGGTGG GGCTCCTGGG AGGGAGACTC AGCCTTCCTC CTCATCCTCC CTGACCCTGC  2280
TCCTAGCACC CTGGAGAGTG AATGCCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC  2340
ATGTCGGCCT CTTCAGGCCT GATAGTCATT GGAAATTGAG GTCCATGGGG GAAATCAAGG  2400
ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC  2460
CTGAGTTCAA AGCCATCTT
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Seq ID NO: 588 Protein sequence
Protein Accession #: NP_005647.1

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1          11         21         31         41         51
|          |          |          |          |          |
MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA    60
SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC   120
DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VCQDDWNENY   180
GRAACRDMGY KNNFYSSQGI VDDSGSTSFM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR   240
CLACGVNLNS SRQSRIVGGE SALPGAWPWQ VSLHVQNVHV CGGSIITPEW IVTAAHCVEK   300
PLNNPWHWTA FAGILRQSFM FYGAGYQVQK VISHPNYDSK TKNNDIALMK LQKPLTFNDL   360
VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNLI   420
TPAMICAGFL QGNVDSCQGD SGGPLVTSNN NIWWLIGDTS WGSGCAKAYR PGVYGNVMVF   480
TDWIYRQMKA NG
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Seq ID NO: 589 DNA sequence
Nucleic Acid Accession #: NM_001935.1
Coding sequence: 1..2301

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAAGACAC CGTGGAAGAT TCTTCTGGGA CTGCTGGGTG CTGCTGCGCT TGTCACCATC    60
ATCACCGTGC CCGTGGTTCT GCTGAACAAA GGCACAGATG ATGCTACAGC TGACAGTCGC   120
AAAACTTACA CTCTAACTGA TTACTTAAAA AATACTTATA GACTGAAGTT ATACTCCTTA   180
AGATGGATTT CAGATCATGA ATATCTCTAC AAACAAGAAA ATAATATCTT GGTATTCAAT   240
GCTGAATATG GAAACAGCTC AGTTTTCTTG GAGAACAGTA CATTTGATGA GTTTGGACAT   300
TCTATCAATG ATTATTCAAT ATCTCCTGAT GGGCAGTTTA TTCTCTTAGA ATACAACTAC   360
GTGAAGCAAT GGAGGCATTC CTACACAGCT TCATATGACA TTTATGATTT AAATAAAAGG   420
CAGCTGATTA CAGAAGAGAG GATTCCAAAC AACACACAGT GGGTCACATG GTCACCAGTG   480
GGTCATAAAT TGGCATATGT TTGGAACAAT GACATTTATG TTAAAATTGA ACCAAATTTA   540
CCAAGTTACA GAATCACATG GACGGGGAAA GAAGATATAA TATATAATGG AATAACTGAC   600
TGGGTTTATG AAGAGGAAGT CTTCAGTGCC TACTCTGCTC TGTGGTGGTC TCCAAACGGC   660
ACTTTTTTAG CATATGCCCA ATTTAACGAC ACAGAAGTCC CACTTATTGA ATACTCCTTC   720
TACTCTGATG AGTCACTGCA GTACCCAAAG ACTGTACGGG TTCCATATCC AAAGGCAGGA   780
GCTGTGAATC CAACTGTAAA GTTCTTTGTT GTAAATACAG ACTCTCTCAG CTCAGTCACC   840
AATGCAACTT CCATACAAAT CACTGCTCCT GCTTCTATGT TGATAGGGGA TCACTACTTG   900
TGTGATGTGA CATGGGCAAC ACAAGAAAGA ATTTCTTTGC AGTGGCTCAG GAGGATTCAG   960
AACTATTCGG TCATGGATAT TTGTGACTAT GATGAATCCA GTGGAAGATG GAACTGCTTA  1020
GTGGCACGGC AACACATTGA AATGAGTACT ACTGGCTGGG TTGGAAGATT TAGGCCTTCA  1080
GAACCTCATT TTACCCTTGA TGGTAATAGC TTCTACAAGA TCATCAGCAA TGAAGAAGGT  1140
TACAGACACA TTTGCTATTT CCAAATAGAT AAAAAAGACT GCACATTTAT TACAAAAGGC  1200
ACCTGGGAAG TCATCGGGAT AGAAGCTCTA ACCAGTGATT ATCTATACTA CATTAGTAAT  1260
GAATATAAAG GAATGCCAGG AGGAAGGAAT CTTTATAAAA TCCAACTTAG TGACTATACA  1320
AAAGTGACAT GCCTCAGTTG TGAGCTGAAT CCGGAAAGGT GTCAGTACTA TTCTGTGTCA  1380
TTCAGTAAAG AGGCGAAGTA TTATCAGCTG AGATGTTCCG GTCCTGGTCT GCCCCTCTAT  1440
ACTCTACACA GCAGCGTGAA TGATAAAGGG CTGAGAGTCC TGGAAGACAA TTCAGCTTTG  1500
GATAAAATGC TGCAGAATGT CCAGATGCCC TCCAAAAAAC TGGACTTCAT TATTTTGAAT  1560
GAAACAAAAT TTTGGTATCA GATGATCTTG CCTCCTCATT TTGATAAATC CAAGAAATAT  1620
CCTCTACTAT TAGATGTGTA TGCAGGCCCA TGTAGTCAAA AAGCAGACAC TGTCTTCAGA  1680
CTGAACTGGG CCACTTACCT TGCAAGCACA GAAAACATTA TAGTAGCTAG CTTTGATGGC  1740
AGAGGAAGTG GTTACCAAGG AGATAAGATC ATGCATGCAA TCAACAGAAG ACTGGGAACA  1800
TTTGAAGTTG AAGATCAAAT TGAAGCAGCC AGACAATTTT CAAAAATGGG ATTTGTGGAC  1860
AACAAACGAA TTGCAATTTG GGGCTGGTCA TATGGAGGGT ACGTAACCTC AATGGTCCTG  1920
GGATCGGGAA GTGGCGTGTT CAAGTGTGGA ATAGCCGTGG CGCCTGTATC CCGGTGGGAG  1980
TACTATGACT CAGTGTACAC AGAACGTTAC ATGGGTCTCC CAACTCCAGA AGACAACCTT  2040
GACCATTACA GAAATTCAAC AGTCATGAGC AGAGCTGAAA ATTTTAAACA AGTTGAGTAC  2100
CTCCTTATTC ATGGAACAGC AGATGATAAC GTTCACTTTC AGCAGTCAGC TCAGATCTCC  2160
AAAGCCCTGG TCGATGTTGG AGTGGATTTC CAGGCAATGT GGTATACTGA TGAAGACCAT  2220
GGAATAGCTA GCAGCACAGC ACACCAACAT ATATATACCC ACATGAGCCA CTTCATAAAA  2280
CAATGTTTCT CTTTACCTTA G
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Seq ID NO: 590 Protein sequence
Protein Accession #: NP_001926.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKTPWKILLG LLGAAALVTI ITVPVVLLNK GTDDATADSR KTYTLTDYLK NTYRLKLYSL    60
```

RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFGH SINDYSISPD GQFILLEYNY 120
VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSPV GHKLAYVWNN DIYVKIEPNL 180
PSYRITWTGK EDIIYNGITD WVYEEEVFSA YSALWWSPNG TFLAYAQFND TEVPLIEYSF 240
YSDESLQYPK TVRVPYPKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
CDVTWATQER ISLQWLRRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360
EPHFTLDGNS FYKIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420
EYKGMPGGRN LYKIQLSDYT KVTCLSCELN PERCQYYSVS FSKEAKYYQL RCSGPGLPLY 480
TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDFIILN ETKFWYQMIL PPHFDKSKKY 540
PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RGSGYQGDKI MHAINRRLGT 600
FEVEDQIEAA RQFSKMGFVD NKRIAIWGWS YGGYVTSMVL GSGSGVFKCG IAVAPVSRWE 660
YYDSVYTERY MGLPTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQQSAQIS 720
KALVDVGVDF QAMWYTDEDH GIASSTAHQH IYTHMSHFIK QCFSLP

Seq ID NO: 591 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

1 11 21 31 41 51

TCGCTTTGTG ATTCTTGATC CGGAACTTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA 60
CGCGATAGAA ACGTGTTCGC TTGCCCAGAA GAAGGGAAGG CGCGAGTGAG GAAAGGAGGT 120
ACTGTAGATG CCCTCCAAAT CCTTGGTTAT GGAATATTTG GCTCATCCCA GTACACTCGG 180
CTTGGCTGTT GGAGTTGCTT GTGGCATGTG CCTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
CTTGGGAGAC AGCGGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG 360
AAAAGGGAAA GTGGCTGCCC AGTGCTCTCA TGCTGCTGTT TCAGCCTACA AGCAGATTCA 420
AAGAAGAAAT CCTGAAATGC TCAAACAATG GGAATACTGT GGCCAGCCCA AGGTGGTGGT 480
CAAAGCTCCT GATGAAGAAA CCCTGATTGC ATTATTGGCC CATGCAAAAA TGCTGGGACT 540
GACTGTAAGT TTAATTCAAG ATGCTGGACG TACTCAGATT GCACCAGGCT CTCAAACTGT 600
CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAAACT 660
TTACTAGGTG GACTTTGATA TGACAACAAC CCCTCCATCA CAAGTGTTTG AAGCCTGTCA 720
GATTCTAACA ACAAAAGCTG AATTTCTTCA CCCAACTTAA ATGTTCTTGA GATGAAAATA 780
AAACCTATTC CCATGTTCTA AAAAAA

Seq ID NO: 592 Protein sequence
Protein Accession #: NP_057161.1

1 11 21 31 41 51

MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60
DSGEYKMILV VRNDLKMGKG KVAAQCSHAA VSAYKQIQRR NPEMLKQWEY CGQPKVVVKA 120
PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPGPADLID KVTGHLKLY

Seq ID NO: 593 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1896

1 11 21 31 41 51

ATGCGCGCCG TGCCGCTGCC CGCCCCGCTC CTGCCGCTGC TGCTGCTCGC GCTCCTGGCC 60
GCTCCCGCCG CCCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
CGCGAGTCGC GGCCACCGCC CGGCCCGGGG CCCGGGAACA CCACCCGGTT TGGGTCTGGG 180
GCGGCGGGCG GCAGCGGCAG CTCCAGCTCC AACAGCAGTG GCGACGCCTT GGTGACCCGC 240
ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGCGTTCGCC 300
TTTACCACCC TCCTCATCGC CTGCCTGCTG CTGCGCGTCT TCAGGTCGGG AAAGAGGTTA 360
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGA AATGGCGCCA 420
CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCCAGCAA GATGCAGTGG AAGGCCTGAT 600
GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAAGTTGG 660
TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCGT CGGAGGTGTT 720
GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC 780
TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC 840
TTTGGGCATC CCTTTAAAGT GCCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900
CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCATCT 960
GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAACCATG 1080
AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TTGTGAAGAC 1140
AGAGCAGTGA CTAAGGTTCT CCAGGGTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
ACCCATCCTG TCAGGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
AGGGTGTTTC GGCGTCCGCG GCAGTCTCTG CATGGCGGAG GGTCAGCGGG TACCGCAACT 1380
TGCCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440
ATCTGTCTCC CCTGCTGTGC CGTGGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
GTCCTTGCGT CATTTGAGCA GAGCCCACAA AAGGCAGCTG CTGCCCACGG GGAGCCTGTC 1560
AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCACGTGA GGATGTCACT 1680
CACCCTGGAG GAGACTTGGA TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG 1740
GATGGCAGAT GCCAGAAGAT GGTCCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
TGTGAGAGGC TCACAGGTTC CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT 1860
TCCCCCCGAC AGCCCCTGTT TCTGTCCAGG CCCTGA

Seq ID NO: 594 Protein sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG    60
AAGGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAFA FTTLLIACLL LRVFRSGKRL   120
KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGCQTLLTVP   180
VPPPFILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV   240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLLPP FGHPFKVPPT STPHGFRQLQ   300
LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLPN PWWHFSATGS PIKTLYTQTM   360
STLGLDVFCG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHHL RLLRECPPLS   420
THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK   480
ICLPCCAVEH LREAKRSSVT VLASFEQSPQ KAAAAHGEPV KRGPSGQLTR HTCPGWGITH   540
ANLQTIPDTQ GQEGPREDVT HPGGDLDGVA NFYLEEEGFQ DGRCQKMVLM SEEGPPSLTG   600
CERLTGSHHF SSHSKSWSFL SPRQPLFLSR P
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Seq ID NO: 595 DNA sequence
Nucleic Acid Accession #: NM_021614.1
Coding sequence: 1..1740

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGGCCGC TCAGCAACTT GAGCGCGTCC    60
CGCCGGAACC TGCACGAGAT GGACTCAGAG GCGCAGCCCC TGCAGCCCCC CGCGTCTGTC   120
GGAGGAGGTG GCGGCGCGTC CTCCCCGTCT GCAGCCGCTG CCGCCGCCGC CGCTGTTTCG   180
TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCCGAGCACA ACAACTCCAA CAACCTGGCG   240
CTCTATGGAA CCGGCGGCGG AGGCAGCACT GGAGGAGGCG GCGGCGGTGG CGGGAGCGGG   300
CACGGCAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG   360
CTGGGCCACC GGCGCGCCCT GTTCCAAAAG CGCAAGCGGC TCAGCGACTA CGCGCTCATC   420
TTCGGCATGT TCGGCATCGT GGTCATGGTC ATCGAGACCG AGCTGTCGTG GGGCGCCTAC   480
GACAAGGCGT CGCTGTATTC CTTAGCTCTG AAATGCCTTA TCAGTCTCTC CACGATCATC   540
CTGCTCGGTC TGATCATCGT GTACCACGCC AGGGAAATAC AGTTGTTCAT GGTGGACAAT   600
GGAGCAGATG ACTGGAGAAT AGCCATGACT TATGAGCGTA TTTTCTTCAT CTGCTTGGAA   660
ATACTGGTGT GTGCTATTCA TCCCATACCT GGGAATTATA CATTCACATG GACGGCCCGG   720
CTTGCCTTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA   780
CCAATGTTCT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC   840
ACTGATGCCT CCTCTAGAAG CATTGGAGCA CTTAATAAGA TAAACTTCAA TACACGTTTT   900
GTTATGAAGA CTTTAATGAC TATATGCCCA GGAACTGTAC TCTTGGTTTT TAGTATCTCA   960
TTATGGATAA TTGCCGCATG GACTGTCCGA GCTTGTGAAA GGTACCATGA TCAACAGGAT  1020
GTTACTAGCA ACTTCCTTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATTGGT  1080
TATGGTGACA TGGTACCTAA CACATACTGT GGAAAAGGAG TCTGCTTACT TACTGGAATT  1140
ATGGGTGCTG GTTGCACAGC CCTGGTGGTA GCTGTAGTGG CAAGGAAGCT AGAACTTACC  1200
AAAGCAGAAA AACACGTGCA CAATTTCATG ATGGATACTC AGCTGACTAA AAGAGTAAAA  1260
AATGCAGCTG CCAATGTACT CAGGGAAACA TGGCTAATTT ACAAAAATAC AAAGCTAGTG  1320
AAAAAGATAG ATCATGCAAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTCAT  1380
CAATTAAGAA GTGTAAAAAT GGAGCAGAGG AAACTGAATG ACCAAGCAAA CACTTTGGTG  1440
GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATTT CTGACTTAAA CGAAAGGAGT  1500
GAAGACTTCG AGAAGAGGAT TGTTACCCTG GAAACAAAAC TAGAGACTTT GATTGGTAGC  1560
ATCCACGCCC TCCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTCATT  1620
GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACTTACA ATGCTGAGCG GTCCCGGTCC  1680
TCGTCCAGGA GGCGGCGGTC CTCTTCCACA GCACCACCAA CTTCATCAGA GAGTAGCTAG
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Seq ID NO: 596 Protein sequence
Protein Accession #: NP_067627.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSSCRYNGGV MRPLSNLSAS RRNLHEMDSE AQPLQPPASV GGGGGASSPS AAAAAAAAVS    60
SSAPEIVVSK PEHNNSNNLA LYGTGGGGST GGGGGGGGSG HGSSSGTKSS KKKNQNIGYK   120
LGHRRALFEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII   180
LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPIP GNYTFTWTAR   240
LAFSYAPSTT TADVDIILSI PMPLRLYLIA RVMLLHSKLF TDASSRSIGA LNKINFNTRF   300
VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQQD VTSNFLGAMW LISITFLSIG   360
YGDMVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNFM MDTQLTKRVK   420
NAAANVLRET WLIYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV   480
DLAKTQNIMY DMISDLNERS EDFEKRIVTL ETKLETLIGS IHALPGLISQ TIRQQQRDFI   540
EAQMESYDKH VTYNAERSRS SSRRRRSSST APPTSSESS
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Seq ID NO: 597 DNA sequence
Nucleic Acid Accession #: NM_016029.1
Coding sequence: 228..1097

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1          11         21         31         41         51
|          |          |          |          |          |
CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGCGGGC CGTCTTCTTC CCCCCGAGCT    60
GGGCGTGCGC GGCCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC   120
TGCTCCTGCT CTTGGTGCAG CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC   180
TATGGGCCGA GTGGCAGGGA CGACGCCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG   240
TGACTGGAGC CTCGAGTGGA ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACTAGGAG   300
TTTCTCTTGT GCTGTCAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC   360
TAGAGAATGG CAATTTAAAA GAAAAAGATA TACTTGTTTT GCCCCTTGAC CTGACCGACA   420
CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC   480
TGGTCAACAA TGGTGGAATG TCCCAGCGTT CTCTGTGCAT GGATACCAGC TTGGATGTCT   540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC   600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA   660
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TATCTGTACC TCTTTCCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTTTTA   720
ATGGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCCAG   780
GACCTGTGCA ATCAAATATT GTGGAGAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG   840
GCAATAATGG AGACCAGTCC CACAAGATGA CAACCAGTCG TTGTGTGCGG CTGATGTTAA   900
TCAGCATGGC CAATGATTTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA   960
CATATTTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA  1020
AAAGGATTGA GAACTTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA  1080
AGACAAAACA TGACTGAAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA  1140
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT  1200
ACTTTTTAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA  1260
AGATTGCCAT GAATCTTGCA AA
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Seq ID NO: 598 Protein sequence
Protein Accession #: NP_057113.1

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1           11          21          31          41          51
|           |           |           |           |           |
MNWELLLWLL VLCALLLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS    60
GIGEELAYQL SKLGVSLVLS ARRVHELERV KRRCLENGNL KEKDILVLPL DLTDTGSHEA   120
ATKAVLQEFG RIDILVNNGG MSQRSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHMIER   180
KQGKIVTVNS ILGIISVPLS IGYCASKHAL RGFFNGLRTE LATYPGIIVS NICPGPVQSN   240
IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISEQP FLLVTYLWQY   300
MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD
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Seq ID NO: 599 DNA sequence
Nucleic Acid Accession #: NM_000793.2
Coding sequence: 401..1222

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AAGCACAGAA AGTGTGTGTA AAACGGAGTA AAGAAAGAAA AAAAAAAAAC TACCCTTAAA   180
GCACATTTAA AAAAAAAAAA CTCTGGCAAT TCAAGAAAGA AACAGGCTAC GTTTAAAGAG   240
CATAGAGACA ATGAAAGGCT AAAGAAAATT TTAAAATCTC TGCCACAGTC TCATAGGTGC   300
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ACCAGAGCGC ACAAGGGAAC TGACTCAGGA GGCAGAGAAG ATGGGCATCC TCAGCGTAGA   420
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GCATGTCTCC AGTACAGAAG GAGGTGACAA CAGTGGCAAT GGTACCCAGG AGAAGATAGC   720
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TGAACGTGTG TGCATTGTGC AGAGACAGAA AATTGCTTAT CTGGGAGGAA AGGGCCCCTT  1140
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CACTACTCAA ATGGCATTGG GCTGAGTAAG TAACCATATC ACCTCTCTTC TTAGTAAAAA  1440
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TGGCTCTATT TGGCATGGAT GGAGCCCAGT TGGAAAATTC CCAAATATTA CAACAAGTCC  1680
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GGTATATTTG TAGATACCGA GAATGATCCC TCAGTCTGAG AGGTTAGAAT GATCATCTGT  1860
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CATTCCATTA ATAACTGAAT AAAAAATAAA TAAAATGGAT AGAAAAAAAC TAAAGTTGAA  3000
AATACATTCT TAAACTAGTT GTCTGAAATG AGAAAAGAGT GAGAACTAGG TGTGCAAGAA  3060
CCAAACGTAT TTTATTTTAT TTTTTAAATG GGAGCAACAT ATCAGTCGTG TCACCAGCTG  3120
GTATATTGTG TAAATATTAA AGCTCCATTG GGACTGATTT TTCATGGCAA CATCAGCTTT  3180
CTAATGTTCT AAATTCTATA AAAACCACCC ACAAAGAAAC AAAGCAAATT TCATTATCTA  3240
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CCTTAAAATT CCCCTTTTTT CTCTATGTAC GATAAAGTAA CAGTATGTCA GATAAGCCGG  3480
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TATGACCATT GAAAAAGGAA AAATGTAGAC TCTGACTTCC GTCCCACTGA AGGATTAATG  5040
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CACTGGTCAG CGTGGTTTTT ATGTGTATTA GGATTGGGGG ATGTGAAGAA ATAAGTATCC  5940
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AAGAGTCATC GACCTCAGTT AGTGGTTGGA TGTAGTCACA TTAGTTTGCC TCTCCCCATC  6180
TTTGTCTCCC TGGCAAGGAG AATATGCGGG ACATGATGCT AAGAGCCCTG GGTAAATGTG  6240
GTGAGAATGC ACGCGTGCAT ATGCTACACA TATGTGCTTC TCAGTTGCAG AAAATGAACT  6300
GCTTTGGGAG ATTATCAGTA GAAAGAGTGT TATCATATTG GTGCTGAGTG CTATGTGTGC  6360
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AAAAAAAAA
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Seq ID NO: 600 Protein sequence
Protein Accession #: NP_000784.2

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RCVWKSFLLD AYKQVKLGED APNSSVVHVS STEGGDNSGN GTQEKIAEGA TCHLLDFASP   120
ERPLVVNFGS ATUPPFTSQL PAFRKLVEEF SSVADFLLVY IDEAHPSDGW AIPGDSSLSF   180
EVKKHQNQED RCAAAQQLLE RFSLPPQCRV VADRMDNNAN IAYGVAFERV CIVQRQKIAY   240
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Seq ID NO: 601 DNA sequence
Nucleic Acid Accession #: NM_005233.1
Coding sequence: 101..3052

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CCTCCTCCTT CTCAGCTGCT CTGTTCTCGA CAGCTTCGGG GAACTGATTC CGCAGCCTTC   180
CAATGAAGTC AATCTACTGG ATTCAAAAAC AATTCAAGGG GAGCTGGGCT GGATCTCTTA   240
TCCATCACAT GGGTGGGAAG AGATCAGTGG TGTGGATGAA CATTACACAC CCATCAGGAC   300
TTACCAGGTG TGCAATGTCA TGGACCACAG TCAAAACAAT TGGCTGAGAA CAAACTGGGT   360
CCCCAGGAAC TCAGCTCAGA AGATTTATGT GGAGCTCAAG TTCACTCTAC GAGACTGCAA   420
TAGCATTCCA TTGGTTTTAG GAACTTGCAA GGAGACATTC AACCTGTACT ACATGGAGTC   480
TGATGATGAT CATGGGGTGA AATTTCGAGA GCATCAGTTT ACAAAGATTG ACACCATTGC   540
AGCTGATGAA AGTTTCACTC AAATGGATCT TGGGGACCGT ATTCTGAAGC TCAACACTGA   600
GATTAGAGAA GTAGGTCCTG TCAACAAGAA GGGATTTTAT TTGGCATTTC AAGATGTTGG   660
TGCTTGTGTT GCCTTGGTGT CTGTGAGAGT ATACTTCAAA AAGTGCCCAT TTACAGTGAA   720
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TGCTAAGTGC CCGCCTCACA GTTCTACTCA GGAAGATGGT TCAATGAACT GCAGGTGTGA  1020
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TAGCATTAAA GCTCTAGAAA CGCAATCAAA GAATGGCCCA GTTCCCGTGT AAAGCACGAC  3060
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CAATAATTCT GGAGATACTG GTGGAAGTT
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Seq ID NO: 602 Protein sequence
Protein Accession #: NP_005224.1

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HYTPIRTYQV CNVMDHSQNN WLRTNWVPRN SAQKIYVELK FTLRDCNSIP LVLGTCKETF   120
NLYYMESDDD HGVKFREHQF TKIDTIAADE SFTQMDLGDR ILKLNTEIRE VGPVNKKGFY   180
LAFQDVGACV ALVSVRVYFK KCPFTVKNLA MFPDTVPMDS QSLVEVRGSC VNNSKEEDPP   240
RMYCSTEGEW LVPIGKCSCN AGYEERGFMC QACRPGFYKA LDGNMKCAKC PPHSSTQEDG   300
SMNCRCENNY FRADKDPPSM ACTRPPSSPR NVISNINETS VILDWSWPLD TGGRKDVTFN   360
IICKKCGWNI KQCEPCSPNV RFLPRQFGLT NTTVTVTDLL AHTNYTFEID AVNGVSELSS   420
PPRQFAAVSI TTNQAAPSPV LTIKKDRTSR NSISLSWQEP EHPNGIILDY EVKYYEKQEQ   480
ETSYTILRAR GTNVTISSLK PDTIYVFQIR ARTAAGYGTN SRKFEFETSP DSFSISGESS   540
QVVMIAISAA VAIILLTVVI YVLIGRFCGY KSKHGADEKR LHFGNGHLKL PGLRTYVDPH   600
TYEDPTQAVH EFAKELDATN ISIDKVVGAG EFGEVCSGRL KLPSKKEISV AIKTLKVGYT   660
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IQLVGMLRGI ASGMKYLSDM GYVHRDLAAR NILINSNLVC KVSDFGLSRV LEDDPEAAYT   780
TRGGKIPIRW TSPEAIAYRK FTSASDVWSY GIVLWEVMSY GERPYWEMSN QDVIKAVDEG   840
YRLPPPMDCP AALYQLMLDC WQKDRNNRPK FEQIVSILDK LIRNPGSLKI ITSAAARPSN   900
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PQKKIISSIK ALETQSKNGP VPV
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Seq ID NO: 603 DNA sequence
Nucleic Acid Accession #: NM_005727.1
Coding sequence: 122..847

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CATGCAGTGC TTCAGCTTCA TTAAGACCAT GATGATCCTC TTCAATTTGC TCATCTTTCT   180
GTGTGGTGCA GCCCTGTTGG CAGTGGGCAT CTGGGTGTCA ATCGATGGGG CATCCTTTCT   240
GAAGATCTTC GGGCCACTGT CGTCCAGTGC CATGCAGTTT GTCAACGTGG GCTACTTCCT   300
CATCGCAGCC GGCGTTGTGG TCTTTGCTCT TGGTTTCCTG GGCTGCTATG GTGCTAAGAC   360
TGAGAGCAAG TGTGCCCTCG TGACGTTCTT CTTCATCCTC CTCCTCATCT TCATTGCTGA   420
GGTTGCAGCT GCTGTGGTCG CCTTGGTGTA CACCACAATG GCTGAGCACT TCCTGACGTT   480
GCTGGTAGTG CCTGCCATCA AGAAAGATTA TGGTTCCCAG GAAGACTTCA CTCAAGTGTG   540
GAACACCACC ATGAAAGGGC TCAAGTGCTG TGGCTTCACC AACTATACGG ATTTTGAGGA   600
CTCACCCTAC TTCAAAGAGA ACAGTGCCTT TCCCCCATTC TGTTGCAATG ACAACGTCAC   660
CAACACAGCC AATGAAACCT GCACCAAGCA AAAGGCTCAC GACCAAAAAG TAGAGGGTTG   720
CTTCAATCAG CTTTTGTATG ACATCCGAAC TAATGCAGTC ACCGTGGGTG GTGTGGCAGC   780
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TGGAATTGGG GGCCTCGAGC TGGCTGCCAT GATTGTGTCC ATGTATCTGT ACTGCAATCT   840
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CCCTGGCAAG CAGCAGTGAT TGGGGGAGGG GACAGGATCT AACAATGTCA CTTGGGCCAG   960
AATGGACCTG CCCTTTCTGC TCCAGACTTG GGGCTAGATA GGGACCACTC CTTTTAGGCG  1020
ATGCCTGACT TTCCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG  1080
GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAAACC CTTGATATGC CCCCTAGGCC  1140
TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT  1200
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Seq ID NO: 604 Protein sequence
Protein Accession #: NP_005718.1

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LVVPAIKKDY GSQEDFTQVW NTTMKGLKCC GFTNYTDFED SPYFKENSAF PPFCCNDNVT   180
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Seq ID NO: 605 DNA sequence
Nucleic Acid Accession #: NM_000729.2
Coding sequence:

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GACGCAGCCG GTGCCTCCCG CAGATCCCGC GGGCTCCGGG CTGCAGCGGG CAGAGGAGGC   180
GCCCCGTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG   240
CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT   300
CGTTAAGAAC CTGCAGAACC TGGACCCCAG CCACAGGATA AGTGACCGGG ACTACATGGG   360
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GCCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACAA   480
TCACACTCAT AACTCATTGT CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC   540
TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACACGCT CACCAGAAGT   600
TGTGCAAACT GAAGACAAAA CTGTTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT   660
TATGCTATTA AAGTGATTTC ATTCTGCC
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Seq ID NO: 606 Protein sequence
Protein Accession #: NP_000720.1

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Seq ID NO: 607 DNA sequence
Nucleic Acid Accession #: NM_001423.1
Coding sequence: 219..692

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Seq ID NO: 608 Protein sequence
Protein Accession #: NP_001414.1

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Seq ID NO: 609 DNA sequence
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Seq ID NO:  610 Protein sequence
Protein Accession #: NP_004952.1

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IFSQTWYDER LCYNDTFESL VLNGNVVSQL WIPDTFFRNS KRTHEHEITM PNQMVRIYKD   180
GKVLYTIRMT IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIYKWENF KLEINEKNSW   240
KLFQFDFTGV SNKTEIITTP VGDFMVMTIF FNVSRRFGYV AFQNYVPSSV TTMLSWVSFW   300
IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIAICFVF CFCALLEFAV   360
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Seq ID NO:  612 Protein sequence
Protein Accession #: NP_068819.1
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ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE   300
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GTGAAATCTG TGTCTGTAAT TTGTTGGGGG GTGGATAGGG TGGGGTCTCC ATCTACTTTT  3180
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Seq ID NO: 614 Protein sequence
Protein Accession #: NP_068822.1

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1           11          21          31          41          51
|           |           |           |           |           |
MEYTIDIIFS QTWNSKRTHE HEITMPNQMV RIYKDGKVLY TIRMTIDAGC SLHMLRFPMD    60
SHSCPLSFSS FSYPENEMIY KWENFKLEIN EKNSWKLFQF DFTGVSNKTE IITTPVGDFM   120
VMTIFFNVSR RFGYVAFQNY VPSSVTTMLS WVSFWIKTES APARTSLGIT SVLTMTTLGT   180
FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFLI YNQTKAHASP KLRHPRINSR   240
AHARTRARSR ACARQHQEAF VCQIVTTEGS DGEERPSCSA QQPPSPGSPE GPRSLCSKLA   300
CCEWCKRFKK YFCMVPDCEG STWQQGRLCI HVYRLDNYSR VVFPVTFFFF NVLYWLVCLN   360
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Seq ID NO: 615 DNA sequence
Nucleic Acid Accession #: NM_021990.1
Coding sequence: 1309..2490

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1          11         21         31         41         51
|          |          |          |          |          |
GCCAGAGCGT GAGCCGCGAC CTCCGCGCAG GTGGTCGCGC CGGTCTCCGC GGAAATGTTG    60
TCCAAAGTTC TTCCAGTCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA   120
CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG   180
GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCCTTTGT   240
CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGT GAGTTTCATA   300
CCTTGGCAGA TGGCCTTTAA CATTTTTGTT TAATTCAATT ATTCTTACTA ATCTTCTTCT   360
TTTTCTTGGC TGTGGTGCAT GGCTGTGGAG CTCAGGGTGG ACTCCTGTTG GGCAGCCAGT   420
TCCTGGATGG CTGTCTGTGG GTGGAGGACT CCTGCCTTTC CTGTTTAGAC ACCCACAAAG   480
GCTGCTCTTT AGCCTCCTTC CCTTCATCCC CTTCCCCTGC CCCCAGTGCA ACGAGTATTA   540
CACAACCAAC AAAACCGCAA AATATTCCCA CAATTTTCTG GTCCTCTCTG GGAGAGGCCG   600
CTCTGGCTTT TCCTCTCAGC CCTGGCCCTC TGCCTGCTCC TCACTCCTGG TTGGTGCTGG   660
TCAGGCTGAC TAGAGGCCAA GGCGACCAAC ACTAGGCAAA CGCGGCCAGC GCTCAGACAT   720
AAATGCCCTC TTCATTTCAC GTGTAACATT CTTTTAAAAT CTAGGTCTTG GTTTTGTTGA   780
TTTTTTCTTA AATAAAAGAG TGATCATAAA AGAGGGACAG CATAGAAAGT CCCCAAAGAG   840
CAGCAAGGTT TTAAAGAAAT TCACAAGCCT AATCTGTCAC TGTCTTATAA TTTGCTATTA   900
CCAGTCACAA TTTAACTAGG TTTTGTGTTG AAAACTTGTT TTGGTTTGCT TCTGTCCCAA   960
GAGGCACTAG CTGGGGCCCC TACAGAGTGC AGGGCAGAGC TTCATTTTTC GTTTGAATGT  1020
TCTAGGGTCG AGGGACCTCA GACTGAATCA AAGAATGAAG CCTCTTCCCG TGATGTTGTC  1080
TATGGCCCCC AGCCCCAGCC TCTGGAAAAT CAGCTCCTCT CTGAGGAAAC AAAGTCAACT  1140
GAGACTGAGA CTGGGAGCAG AGTTGGCAAA CTGCCAGAAG CCTCTCGCAT CCTGAACACT  1200
ATCCTGAGTA ATTATGACCA CAAACTGCGC CCTGGCATTG GAGAGAAGCC CACTGTGGTC  1260
ACTGTTGAGA TCTCCGTCAA CAGCCTTGGT CCTCTCTCTA TCCTAGACAT GGAATACACC  1320
ATTGACATCA TCTTCTCCCA GACCTGGTAC GACGAACGCC TCTGTTACAA CGACACCTTT  1380
GAGTCTCTTG TTCTGAATGG CAATGTGGTG AGCCAGCTAT GGATCCCGGA CACCTTTTTT  1440
AGGAATTCTA AGAGGACCCA CGAGCATGAG ATCACCATGC CCAACCAGAT GGTCCGCATC  1500
TACAAGGATG GCAAGGTGTT GTACACAATT AGGATGACCA TTGATGCCGG ATGCTCACTC  1560
CACATGCTCA GATTTCCAAT GGATTCTCAC TCTTGCCCTC TATCTTTCTC TAGCTTTTCC  1620
TATCCTGAGA ATGAGATGAT CTACAAGTGG GAAAATTTCA AGCTTGAAAT CAATGAGAAG  1680
AACTCCTGGA AGCTCTTCCA GTTTGATTTT ACAGGAGTGA GCAACAAAAC TGAAATAATC  1740
ACAACCCCAG TTGGTGACTT CATGGTCATG ACGATTTTCT TCAATGTGAG CAGGCGGTTT  1800
GGCTATGTTG CCTTTCAAAA CTATGTCCCT TCTTCCGTGA CCACGATGCT CTCCTGGGTT  1860
TCCTTTTGGA TCAAGACAGA GTCTGCTCCA GCCCGGACCT CTCTAGGGAT CACCTCTGTT  1920
CTGACCATGA CCACGTTGGG CACCTTTTCT CGTAAGAATT TCCCGCGTGT CTCCTATATC  1980
ACAGCCTTGG ATTTCTATAT CGCCATCTGC TTCGTCTTCT GCTTCTGCGC TCTGTTGGAG  2040
TTTGCTGTGC TCAACTTCCT GATCTACAAC CAGACAAAAG CCCATGCTTC TCCTAAACTC  2100
CGCCATCCTC GTATCAATAG CCGTGCCCAT GCCCGTACCC GTGCACGTTC CCGAGCCTGT  2160
GCCCGCCAAC ATCAGGAAGC TTTTGTGTGC CAGATTGTCA CCACTGAGGG AAGTGATGGA  2220
GAGGAGCGCC CGTCTTGCTC AGCCCAGCAG CCCCCTAGCC CAGGTAGCCC TGAGGGTCCC  2280
CGCAGCCTCT GCTCCAAGCT GGCCTGCTGT GAGTGGTGCA AGCGTTTTAA GAAGTACTTC  2340
TGCATGGTCC CCGATTGTGA GGGCAGTACC TGGCAGCAGG GCCGCCTCTG CATCCATGTC  2400
TACCGCCTGG ATAACTACTC GAGAGTTGTT TTCCCAGTGA CTTTCTTCTT CTTCAATGTG  2460
CTCTACTGGC TTGTTTGCCT TAACTTGTAG GTACCAGCTG GTACCCTGTG GGGCAACCTC  2520
TCCAGTTCCC CAGGAGGTCC AAGCCCCTTG CCAAGGGAGT TGGGGGAAAG CAGCAGCAGC  2580
AGCAGGAGCG ACTAGAGTTT TTCCTGCCCC ATTCCCCAAA CAGAAGCTTG CAGAGGGTTT  2640
GTCTTTGCTG CCCCTCTCCC CTACCTGGCC CATTCACTGA GTTTTCTCAG CAGACCATTT  2700
CAAATTATTA ATAAATGGGC CACCTCCCTC TTCTTCAAGG AGCATCCGTG ATGCTCAGTG  2760
TTCAAAACCA CAGCCACTTA GTGATCAGCT CCCTAAAACC ATGCCTAAGT ACAGGCGGAT  2820
TAGCTATCTT CCAACAATGC TGACCACCAG ACAATTACTG CATTTTTCCA GAAGCCCACT  2880
ATTGCCTTTG CAGTGCTTTC GGCCCAGTTC TGGCCTCAGC CTCAAAGTGC ACCGACTAGT  2940
TGCTTGCCTA TACCTGGCAC CTCATTAAGA TGCTGGGCAG CAGTATAACA GGAGGAAGAG  3000
ATCCCTCTCC TTTGGTCAGA TTATTATGTT CTCAGTTCTC TCTCCCTGCT ACCCCTTTCT  3060
CTGCAGATAG ATAGACACTG GCATTATCCC TTTAGGAAGA GGGGGGGGCA GCAAGAGAGC  3120
CTATTTGGGA CAGCATTCCT CTCTCTCTGC TGCTGTGACA TCTCCCTCTC CTTGCTGGCT  3180
CCATCTTTCG TCTGCACTAC CAATTCAATG CCCTTCATCC AATGGGTATC TATTTTTGTG  3240
TGTGATTATA GTAACTACTC CCTGCTTTAT ATGCCACCCT CTTCCTTCTC TTTGACCCCT  3300
GTGACTCTTT CTGTAACTTT CCCAGTGACT TCCCCTAGCC CTGACCAGGC ACTAGGCCTT  3360
GGTGACTTCC TGGGGCCAAG AAACTAAGGA AACTCGGCTT TGCAACAGGC ATTACTCGCC  3420
ATTGATTGGT GCCCACCCAG GGCACACTGT CGGAGTTCTA TCACTTGCTT GACCCCTGGA  3480
CCCATAAACC AGTCCACTGT TATACCCGGG GCACTCTAAC CATCACAATC AATCAATCAA  3540
ATTCCCTTAA ATTTGTATGG CACTGGAACT TTGGCAAAGC ACTTTTGACA AGTTGTGTCT  3600
GATTGGAGCT TCATGATAGC CTTGTGACAT CTTTAGGGCA GGATTCTTAT CCCCATTTTG  3660
CAGATGAAAA CCCTGAGTCA CAGATTTCTG TGGGACTGTG GATCTCACTG GAAGCTATCC  3720
AAGAGCCCAC TGTCACCTTC TAGACCACAT GATAGGGCTA GACAGCTCAG TTCACCATGA  3780
TTCTCTTCTG TCACCTCTGC TGGCACACCA GTGGCAAGGC CCAGAATGGC GACCTCTCTT  3840
TAGCTCAATT TCTGGGCCTG AGGTGCTCAG ACTGCCCCCA AGATCAAATC TCTCCTGGCT  3900
GTAGTAACCC AGTGGAATGA ATTTGGACAT GCCCCAATGC TTCTATATGC TAAGTGAAAT  3960
CTGTGTCTGT AATTTGTTGG GGGGTGGATA GGGTGGGGTC TCCATCTACT TTTTGTCACC  4020
ATCATCTGAA ATGGGGAAAT ATGTAAATAA ATATATCAGC AAAGC
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Seq ID NO: 616 Protein sequence
Protein Accession #: NP_068830.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEYTIDIIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ    60
MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWENFKLE   120
INEKNSWKLF QFDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTTM   180
LSWVSFWIKT ESAPARTSLG ITSVLIMTTL GTFSRKNFPR VSYITALDFY IAICFVFCFC   240
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ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE   300
GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPDC EGSTWQQGRL   360
CIHVYRLDNY SRVVFPVTFF FFNVLYWLVC LNL

Seq ID NO:  617 DNA sequence
Nucleic Acid Accession #:  NM_004864.1
Coding sequence: 26..952

1          11         21         31         41         51
|          |          |          |          |          |
CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC    60
TCAGATGCTC CTGGTGTTGC TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT   120
GGCCGAGGCG AGCCGCGCAA GTTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG   180
ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACCAGAG   240
CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCCTGCA GTCCGGATAC TCACGCCAGA   300
AGTGCGGCTG GGATCCGCCG GCCACCTGCA CCTGCGTATC TCTCGGGCCG CCCTTCCCGA   360
GGGGCTCCCC GAGGCCTCCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGGCGTC   420
AAGGTCGTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC   480
GCCCGCGCTG CACCTGCGAC TGTCGCCGCC GCCGTCGCAG TCGGACCAAC TGCTGGCAGA   540
ATCTTCGTCC GCACGGCCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGCGG   600
CCGCAGAGCG CGTGCGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG   660
TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTCGCC   720
ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA   780
CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACGG AGCCAGCGCC   840
CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT   900
GTCGCTCCAG ACCTATGATG ACTTGTTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT   960
GGTCCTTCCA CTGTGCACCT GCGCGGGGGA GGCGACCTCA GTTGTCCTGC CCTGTGGAAT  1020
GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG  1080
TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA  1140
ACTGTGTATT TATTTAAAAC TCTGGTGATA AAAATAAAGC TGTCTGAACT GTTAAAAAAA  1200
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Seq ID NO:  618 Protein sequence
Protein Accession #: NP_004855.1

1          11         21         31         41         51
|          |          |          |          |          |
MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRASF PGPSELHSED SRFRELRKRY    60
EDLLTRLRAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLPEASRL   120
HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSSARPQL   180
ELHLRPQAAR GRRRARARNG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC   240
IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTDT GVSLQTYDDL   300
LAKDCHCI

Seq ID NO:  619 DNA sequence
Nucleic Acid Accession #:  NM_003979.2
Coding sequence: 254..1357

1          11         21         31         41         51
|          |          |          |          |          |
ATAACAGCAT GAAGTGCCGT GGAACTGGAA TAGGCGTGTC CTCTCCCTCG ACCCTCCCCC    60
TCCTTGTCCC TCTGCTCACC CCTCGCTCGT TCCCTCCCTC CGGCGAGGGC CGCCTTTATA   120
ACAACTGCTC AGAGTGCGAG GGCGGGATAG CTGTCCAAGG TCTCCCCCAG CACTGAGGAG   180
CTCGCCTGCT GCCCTCTTGC GCGCGGGAAG CAGCACCAAG TTCACGGCCA ACGCCTTGGC   240
ACTAGGGTCC AGAATGGCTA CAACAGTCCC TGATGGTTGC CGCAATGGCC TGAAATCCAA   300
GTACTACAGA CTTTGTGATA AGGCTGAAGC TTGGGGCATC GTCCTAGAAA CGGTGGCCAC   360
AGCCGGGGTT GTGACCTCGG TGGCCTTCAT GCTCACTCTC CCGATCCTCG TCTGCAAGGT   420
GCAGGACTCC AACAGGCGAA AAATGCTGCC TACTCAGTTT CTCTTCCTCC TGGGTGTGTT   480
GGGCATCTTT GGCCTCACCT TCGCCTTCAT CATCGGACTG GACGGGAGCA CAGGGCCCAC   540
ACGCTTCTTC CTCTTTGGGA TCCTCTTTTC CATCTGCTTC TCCTGCCTGC TGGCTCATGC   600
TGTCAGTCTG ACCAAGCTCG TCCGGGGGAG GAAGCCCCTT TCCCTGTTGG TGATTCTGGG   660
TCTGGCCGTG GGCTTCAGCC TAGTCCAGGA TGTTATCGCT ATTGAATATA TTGTCCTGAC   720
CATGAATAGG ACCAACGTCA ATGTCTTTTC TGAGCTTTCC GCTCCTCGTC GCAATGAAGA   780
CTTTGTCCTC CTGCTCACCT ACGTCCTCTT CTTGATGGCG CTGACCTTCC TCATGTCCTC   840
CTTCACCTTC TGTGGTTCCT TCACGGGCTG GAAGAGACAT GGGGCCCACA TCTACCTCAC   900
GATGCTCCTC TCCATTGCCA TCTGGGTGGC CTGGATCACC CTGCTCATGC TTCCTGACTT   960
TGACCGCAGG TGGGATGACA CCATCCTCAG CTCCGCCTTG GCTGCCAATG GCTGGGTGTT  1020
CCTGTTGGCT TATGTTAGTC CCGAGTTTTG GCTGCTCACA AAGCAACGAA ACCCCATGGA  1080
TTATCCTGTT GAGGATGCTT TCTGTAAACC TCAACTCGTG AAGAAGAGCT ATGGTGTGGA  1140
GAACAGAGCC TACTCTCAAG AGGAAATCAC TCAAGGTTTT GAAGAGACAG GGGACCACGT  1200
CTATGCCCCC TATTCCACAC ATTTTCAGCT GCAGAACCAG CCTCCCCAAA AGGAATTCTC  1260
CATCCCACGG GCCCACGCTT GGCCGAGCCC TTACAAAGAC TATGAAGTAA AGAAAGAGGG  1320
CAGCTAACTC TGTCCTGAAG AGTGGGACAA ATGCAGCCGG GCGGCAGATC TAGCGGGAGC  1380
TCAAAGGGAT GTGGGCGAAA TCTTGAGTCT TCTGAGAAAA CTGTACAAGA CACTACGGGA  1440
ACAGTTTGCC TCCCTCCCAG CCTCAACCAC AATTCTTCCA TGCTGGGGCT GATGTGGGCT  1500
AGTAAGACTC CAGTTCTTAG AGGCGCTGTA GTATTTTTTT TTTTTTGTCT CATCCTTTGG  1560
ATACTTCTTT TAAGTGGGAG TCTCAGGCAA CTCAAGTTTA GACCCTTACT CTTTTTGTTT  1620
GTTTTTTGAA ACAGGATCTT GCTCTGTCAC CCAGGCTTGA GTGCAGTGGT GCGATCACAG  1680
CCCAGTGCAG CCTCGACCAC CTGTGCTCAA GCAATCCTCC CATCTCCATC TCCCAAAGTG  1740
CTGGGATGAC AGGCGTGAGC CACAGCTCCC AGCCTAGGCC CTTAATCTTG CTGTTATTTT  1800
CCATGGACTA AAGGTCTGGT CATCTGAGCT CACGCTGGCT CACACAGCTC TAGGGGCCTG  1860
CTCCTCTAAC TCACAGTGGG TTTTGTGAGG CTCTGTGGCC CAGAGCAGAC CTGCATATCT  1920
GAGCAAAAAT AGCAAAAGCC TCTCTCAGCC CACTGGCCTG AATCTACACT GGAAGCCAAC  1980
TTGCTGGCAC CCCCGCTCCC CAACCCTTCT TGCCTGGGTA GGAGAGGCTA AAGATCACCC  2040
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TAAATTTACT CATCTCTCTA GTGCTGCCTC ACATTGGGCC TCAGCAGCTC CCCAGCACCA  2100
ATTCACAGGT CACCCCTCTC TTCTTGCACT GTCCCCAAAC TTGCTGTCAA TTCCGAGATC  2160
TAATCTCCCC CTACGCTCTG CCAGGAATTC TTTCAGACCT CACTAGCACA AGCCCGGTTG  2220
CTCCTTGTCA GGAGAATTTG TAGATCATTC TCACTTCAAA TTCCTGGGGC TGATACTTCT  2280
CTCATCTTGC ACCCCAACCT CTGTAAATAG ATTTACCGCA TTTACGGCTG CATTCTGTAA  2340
GTGGGCATGG TCTCCTAATG GAGGAGTGTT CATTGTATAA TAAGTTATTC ACCTGAGTAT  2400
GCAATAAAGA TGTGGTGGCC ACTCTTTCAT GGTGGTGGCA GCAAAAAAAA AAAAAA
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Seq ID NO: 620 Protein sequence
Protein Accession #: NP_003970.1

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1          11         21         31         41         51
|          |          |          |          |          |
MATTVPDGCR NGLKSKYYRL CDKAEAWGIV LETVATAGVV TSVAFMLTLP ILVCKVQDSN    60
RRKMLPTQFL FLLGVLGIFG LTFAFIIGLD GSTGPTRFFL FGILFSICFS CLLAHAVSLT   120
KLVRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTMNRT NVNVFSELSA PRRNEDFVLL   180
LTYVLFLMAL TFLMSSFTFC GSFTGWKRHG AHIYLTMLLS IAIWVAWITL LMLPDFDRRW   240
DDTILSSALA ANGWVFLLAY VSPEFWLLTK QRNPMDYPVE DAFCKPQLVK KSYGVENRAY   300
SQEEITQGFE ETGDTLYAPY STHFQLQNQP PQKEFSIPRA HAWPSPYKDY EVKKEGS
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Seq ID NO: 621 DNA sequence
Nucleic Acid Accession #: NM_002423.2
Coding sequence: 48..851

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1          11         21         31         41         51
|          |          |          |          |          |
ACCAAATCAA CCATAGGTCC AAGAACAATT GTCTCTGGAC GGCAGCTATG CGACTCACCG    60
TGCTGTGTGC TGTGTGCCTG CTGCCTGGCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG   120
GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT   180
ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT   240
TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCCGCGT CATAGAAATA ATGCAGAAGC   300
CCAGATGTGG AGTGCCAGAT GTTGCAGAAT ACTCACTATT TCCAAATAGC CCAAAATGGA   360
CTTCCAAAGT GGTCACCTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG   420
TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTCA   480
GGAAAGTTGT ATGGGGAACT GCTGACATCA TGATTGGCTT TGCGCGAGGA GCTCATGGGG   540
ACTCCTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCTGGGACAG   600
GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG   660
GGATTAACTT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT   720
CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA   780
AACTTTCCCA GGATGATATT AAAGGCATTC AGAAACTATA TGGAAAGAGA AGTAATTCAA   840
GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCATTCA TTCATTGGAT TGTATATCAT   900
TGTTGCACAA TCAGAATTGA TAAGCACTGT TCCTCCACTC CATTTAGCAA TTATGTCACC   960
CTTTTTTATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACTCCTTT  1020
ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGCGCGTAG ATGTCAATAA  1080
ATGTTACATA CACAAATAAA TAAAATGTTT ATTCCATGGT AAATTTA
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Seq ID NO: 622 Protein sequence
Protein Accession #: NP_002414.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRLTVLCAVC LLPGSLALPL PQEAGGMSEL QWEQAQDYLK RFYLYDSETK NANSLEAKLK    60
EMQKFFGLPI TGMLNSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL   120
PHITVDRLVS KALNMWGKEI PLHFRKVVWG TADIMIGFAR GAHGDSYPFD GPGNTLAHAF   180
APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYGNGD   240
PQNFKLSQDD IKGIQKLYGK RSNSRKK
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Seq ID NO: 623 DNA sequence
Nucleic Acid Accession #: NM_031457.1
Coding sequence: 204..956

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1          11         21         31         41         51
|          |          |          |          |          |
AAACAGGAAA TAAATACGAA TGAAACTGAG CTCTAAGCAG CATGTAACCT GGCCTGCATC    60
CAGGAAATAG AGGACTTCGG ATCCTTCTAA CCCTACCACC CAACTGGCCC CAGTACATTC   120
ATTCTCTCAG GAAAAAAAAC AAGGTCCCCA CAGCAAAGAA AAGGAATAGG ATCAAGAGAT   180
ACGTGGCTGC TGGCAGAGCA AGCATGAATT CGATGACTTC AGCAGTTCCG GTGGCCAATT   240
CTGTGTTGGT GGTGGCACCC CACAATGGTT ATCCTGTGAC CCCAGGAATT ATGTCTCACG   300
TGCCCCTGTA TCCAAACAGC CAGCCGCAAG TCCACCTAGT TCCTGGGAAC CCACCTAGTT   360
TGGTGTCGAA TGTGAATGGG CAGCCTGTGC AGAAAGCTCT GAAAGAAGGC AAAACCTTGG   420
GGGCCATCCA GATCATCATT GGCCTGGCTC ACATCGGCCT CGGCTCCATC ATGGCGACGG   480
TTCTCGTAGG GGAATACCTG TCTATTTCAT TCTACGGAGG CTTTCCCTTC TGGGGAGGCT   540
TGTGGTTTAT CATTTCAGGA TCTCTCTCCG TGGCAGCAGA AAATCAGCCA TATTCTTATT   600
GCCTGCTGTC TGGCAGTTTG GGCTTGAACA TCGTCAGTGC AATCTGCTCT GCAGTTGGAG   660
TCATACTCTT CATCACAGAT CTAAGTATTC CCCACCCATA TGCCTACCCC GACTATTATC   720
CTTACGCCTG GGGTGTGAAC CCTGGAATGG CGATTTCTGG CGTGCTGCTG GTCTTCTGCC   780
TCCTGGAGTT TGGCATCGCA TGCGCATCTT CCCACTTTGG CTGCCAGTTG GTCTGCTGTC   840
AATCAAGCAA TGTGAGTGTC ATCTATCCAA ACATCTATGC AGCAAACCCA GTGATCACCC   900
CAGAACCGGT GACCTCACCA CCAAGTTATT CCAGTGAGAT CCAAGCAAAT AAGTAAGGCT   960
ACAGATTCTG GAAGCATCTT TCACTGGGAC CAAAAGAAGT CCTCCTCCCT TTCTGGGCTT  1020
CCATAACCCA GGTCGTTCCT GTTCTGACAG CTGAGGAAAC GTCTCTCCCA CTGTTTGTAC  1080
TCTCACCTTC ATTCTTCAAT TCAGTCTAGG AAACCATGCT GTTTCTCTAT CAAGAAGAAG  1140
ACAGAGATTT TAAACAGATG TTAACCAAGA GGGACTCCCT AGGGCACATG CATCAGCACA  1200
TATGTGGGCA TCCAGCCTCT GGGGCCTTGG CACACACACA TTCGTGTGCT CTGCTGCATG  1260
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TGAGCTTGTG GGTTAGAGGA ACAAATATCT AGACATTCAA TCTTCACTCT TTCAATTGTG 1320
CATTCATTTA ATAAATAGAT ACTGAGCATT CAAAAAAAAA AAAAAAAAA

Seq ID NO: 624 Protein sequence
Protein Accession #: NP_113645.1

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1          11         21         31         41         51
|          |          |          |          |          |
MNSMTSAVPV ANSVLVVAPH NGYPVTPGIM SHVPLYPNSQ PQVHLVPGNP PSLVSNVNGQ   60
PVQKALKEGK TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISFYGGFPFW GGLWFIISGS  120
LSVAAENQPY SYCLLSGSLG LNIVSAICSA VGVILFITDL SIPHPYAYPD YYPYAWGVNP  180
GMAISGVLLV FCLLEFGIAC ASSHFGCQLV CCQSSNVSVI YPNIYAANPV ITPEPVTSPP  240
SYSSEIQANK
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Seq ID NO: 625 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

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1          11         21         31         41         51
|          |          |          |          |          |
ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG   60
TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT  120
TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCGCACGG CTACTGCTCT  180
CCTACCTCGG CTTCCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG  240
AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC  300
TACCACCAGT ACGGCGGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA  360
GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC  420
AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG  480
TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCCTCGC TGGGATTGAC ACAAACACAG  540
GTGAAAATCT GGTTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG  600
ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCCGCAGTCT  660
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCCAC  720
CCTCCGACCT CCAACCAGTC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC  780
ACAAGTGCAG CCAGCTCAAT CAATTCCCAC CTGCCGCCGC CGGGCTCCTT ACAGCACCCG  840
CTGGCGCTGG CCTCCGGGAC ACTCTATTAG
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Seq ID NO: 626 Protein sequence
Protein Accession #: NP_005212.1

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1          11         21         31         41         51
|          |          |          |          |          |
MTGVFDRRVP SIRSGDFQAP FQTSAAMHHP SQESPTLPES SATDSDYYSP TGGAPHGYCS   60
PTSASYGKAL NPYQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK  120
EVTEPEVRMV NGKPKKVRKP RTIYSSFQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ  180
VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQGSS RSLSHHPHAH  240
PPTSNQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLY
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Seq ID NO: 627 DNA sequence
Nucleic Acid Accession #: NM_014420
Coding sequence: 118..792

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1          11         21         31         41         51
|          |          |          |          |          |
GCACGAGAGA CGACGTGCTG AGCTGCCAGC TTAGTGGAAG CTCTGCTCTG GGTGGAGAGC   60
AGCCTCGCTT TGGTGACGCA CAGTGCTGGG ACCCTCCAGG AGCCCCGGGA TTGAAGGATG  120
GTGGCGGCCG TCCTGCTGGG GCTGAGCTGG CTCTGCTCTC CCCTGGGAGC TCTGGTCCTG  180
GACTTCAACA ACATCAGGAG CTCTGCTGAC CTGCATGGGG CCCGGAAGGG CTCACAGTGC  240
CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCCTCC AGCCCCGCGA TGAGAAGCCG  300
TTCTGTGCTA CATGTCGTGG GTTGCGGAGG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT  360
GGGACACTCT GTGTGAACGA TGTTTGTACT ACGATGGAAG ATGCAACCCC AATATTAGAA  420
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAACTGGGCA CCCAGTCCAG  480
GAAAACCAAC CCAAAAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG  540
GGAGAAAGTT GTCTGAGAAC TTTTGACTGT GGCCCTGGAC TTTGCTGTGC TCGTCATTTT  600
TGGACGAAAA TTTGTAAGCC AGTCCTTTTG GAGGGACAGG TCTGCTCCAG AAGAGGGCAT  660
AAAGACACTG CTCAAGCTCC AGAAATCTTC CAGCGTTGCG ACTGTGGCCC TGGACTACTG  720
TGTCGAAGCC AATTGACCAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA  780
GAAAAGCTAT AAATATTTCA AAATAAAGAA GAATCCACAT TGCAAAAAAA AAAAAAAAAA  840
A
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Seq ID NO: 628 Protein sequence
Protein Accession #: NP_055235

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1          11         21         31         41         51
|          |          |          |          |          |
MVAAVLLGLS WLCSPLGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR KFCLQPRDEK   60
PFCATCRGLR RRCQRDAMCC PGTLCVNDVC TTMEDATPIL ERQLDEQDGT HAEGTTGHPV  120
QENQPKRKPS IKKSQGRKGQ EGESCLRTFD CGPGLCCARH FWTKICKPVL LEGQVCSRRG  180
HKDTAQAPEI FQRCDCGPGL LCRSQLTSNR QHARLRVCQK IEKL
```

Seq ID NO: 629 DNA sequence
Nucleic Acid Accession #: NM_002448.1
Coding sequence: 241..1134

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1          11         21         31         41         51
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GCGCGAGTGC TCCCGGGAAC TCTGCCTGCG CGGCGGCAGC GACCGGAGGC CAGGCCCAGC    60
ACGCCGGAGC TGGCCTGCTG GGGAGGGGCG GGAGGCGCGC GCGGGAGGGT CCGCCCGGCC   120
AGGCCCCGGG CCCTCGCAGA GGCCGGCCGC GCTCCCAGCC CGCCCGGAGC CCATGCCCGG   180
CGGCTGGCCA GTGCTGCGGC AGAAGGGGGG GCCCGGCTCT GCATGGCCCC GGCTGCTGAC   240
ATGACTTCTT TGCCACTCGG TGTCAAAGTG GAGGACTCCG CCTTCGGCAA GCCGGCGGGG   300
GGAGGCGCGG GCCAGGCCCC CAGCGCCGCC GCGGCCACGG CAGCCGCCAT GGGCGCGGAC   360
GAGGAGGGGG CCAAGCCCAA AGTGTCCCCT TCGCTCCTGC CCTTCAGCGT GGAGGCGCTC   420
ATGGCCGACC ACAGGAAGCC GGGGGCCAAG GAGAGCGCCC TGGCGCCCTC CGAGGGCGTG   480
CAGGCGGCGG GTGGCTCGGC GCAGCCACTG GGCGTCCCGC CGGGGTCGCT GGGAGCCCCG   540
GACGCGCCCT CTTCGCCGCG GCCGCTCGGC CATTTCTCGG TGGGGGGACT CCTCAAGCTG   600
CCAGAAGATG CGCTCGTCAA AGCCGAGAGC CCCGAGAAGC CCGAGAGGAC CCCGTGGATG   660
CAGAGCCCCC GCTTCTCCCC GCCGCCGGCC AGGCGGCTGA GCCCCCCAGC CTGCACCCTC   720
CGCAAACACA AGACGAACCG TAAGCCGCGG ACGCCCTTCA CCACCGCGCA GCTGCTGGCG   780
CTGGAGCGCA AGTTCCGCCA GAAGCAGTAC CTGTCCATCG CCGAGCGCGC GGAGTTCTCC   840
AGCTCGCTCA GCCTCACTGA GACGCAGGTG AAGATATGGT TCCAGAACCG CCGCGCCAAG   900
GCAAAGAGAC TACAAGAGGC AGAGCTGGAG AAGCTGAAGA TGGCCGCCAA GCCCATGCTG   960
CCACCGGCTG CCTTCGGCCT CTCCTTCCCT CTCGGCGGCC CCGCAGCTGT AGCGGCCGCG  1020
GCGGGTGCCT CGCTCTACGG TGCCTCTGGC CCCTTCCAGC GCGCCGCGCT GCCTGTGGCG  1080
CCCGTGGGAC TCTACACGGC CCATGTGGGC TACAGCATGT ACCACCTGAC ATAGAGGGTC  1140
CCAGGTCCCC ACCTGTGGGC CAGCCGATTC CTCCAGCCCT GGTGCTGTAC CCCCGACGTG  1200
CTCCCCTGCT CGGCACCGCC AGCCGCCTTC CCTTTAACCC TCACACTGCT CCAGTTTCAC  1260
CTCTTTGCTC CCTGAGTTCA CTCTCCGAAG TCTGATCCCT GCCAAAAAGT GGCTGGAAGA  1320
GTCCCTTAGT ACTCTTCTAG CATTTAGATC TACACTCTCG AGTTAAAGAT GGGGAAACTG  1380
AGGGCAGAGA GGTTAACAGA TTTATCTAGG GTCCCCAGCA GAATTGACAG TTGAACAGAG  1440
CTAGAGGCCA TGTCTCCTGC ATAGCTTTTC CCTGTCCTGA CACCAGGCAA GAAAAGCGCA  1500
GAGAAATCGG TGTCTGACGA TTTTGGAAAT GAGAACAATC TCAAAAAAAA AAAAAAAAAA  1560
AAAAAAAAAA GAAAAGAGAA AAAAAAGACT AGCCAGCCAG GAAGATGAAT CCTAGCTTCT  1620
TCCATTGGAA AATTTAAGAC AAGTTCAACA ACAAAACATT TGCTCTGGGG GGCAGGGAAA  1680
ACACAGATGT GTTGCAAAGG TAGGTTGAAG GGA
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Seq ID NO: 630 Protein sequence
Protein Accession #: NP_002439.1

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1           11          21          31          41          51
|           |           |           |           |           |
MTSLPLGVKV EDSAFGKPAG GGAGQAPSAA AATAAAMGAD EEGAKPKVSP SLLPFSVEAL    60
MADHRKPGAK ESALAPSEGV QAAGGSAQPL GVPPGSLGAP DAPSSPRPLG HFSVGGLLKL   120
PEDALVKAES PEKPERTPWM QSPRFSPPPA RRLSPPACTL RKHKTNRKPR TPFTTAQLLA   180
LERKFRQKQY LSIAERAEFS SSLSLTETQV KIWFQNRRAK AKRLQEAELE KLKMAAKPML   240
PPAAFGLSFP LGGPAAVAAA AGASLYGASG PFQRAALPVA PVGLYTAHVG YSMYHLT
```

Seq ID NO: 631 DNA sequence
Nucleic Acid Accession #: NM_002557.1
Coding sequence: 13..2049

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1           11          21          31          41          51
|           |           |           |           |           |
CAGACCATTG AGATGTGGAA GCTGTTGCTG TGGGTTGGGC TGGTTCTTGT GCTGAAACAC    60
CACGATGGTG CTGCCCATAA ACTCGTGTGT TATTTCACCA ACTGGGCACA CAGTCGGCCA   120
GGCCCTGCCT CGATCTTGCC CCATGACCTG GACCCCTTTC TCTGCACCCA CCTGATATTT   180
GCCTTTGCCT CAATGAACAA CAATCAGATT GTTGCTAAGG ATCTCCAGGA TGAGAAAATT   240
CTCTACCCAG AGTTCAACAA ACTAAAGGAG AGGAACAGAG AGCTGAAAAC ACTACTGTCC   300
ATCGGCGGGT GGAACTTTGG CACCTCAAGA TTCACCACTA TGTTGTCCAC ATTTGCCAAC   360
CGTGAAAAGT TTATTGCTTC AGTTATATCC CTTCTGAGGA CACATGACTT TGATGGTCTT   420
GACCTTTTCT TCTTATATCC TGGACTAAGA GGCAGCCCCA TGCATGACCG GTGGACTTTT   480
CTCTTCTTAA TTGAAGAGCT CCTGTTTGCC TTCCGGAAGG AGGCACTGCT CACCATGCGC   540
CCGAGGCTGC TGCTGTCTGC TGCTGTTTCT GGGGTCCCAC ACATCGTCCA AACATCCTAT   600
GATGTGCGCT TTCTAGGAAG ACTCCTGGAT TTCATCAATG TCTTGTCTTA TGACTTACAT   660
CGAAGTTGGG AAAGGTTCAC AGGACATAAT AGCCCCCTCT TCTCTCTGCC TGAAGACCCC   720
AAATCTTCGG CATATGCTAT GAATTATTGG AGAAAGCTTG GGGCACCCTC AGAGAAGCTC   780
ATCATGGGGA TCCCCACCTA TGGACGTACC TTTCGCCTCC TCAAAGCCTC TAAGAATGGG   840
TTGCAGGCCA GAGCGATCGG ACCAGCATCT CCAGGGAAGT ACACCAAGCA AGAAGGCTTC   900
TTGGCTTATT TTGAGATTTG TTCCTTTGTC TGGGGAGCGA AGAAGCACTG GATTGATTAC   960
CAGTATGTCC CGTATGCCAA CAAGGGGAAA GAGTGGGTTG GCTATGACAA TGCCATCAGC  1020
TTCAGTTACA AGGCATGGTT TATAAGGCGA GAGCATTTTG GGGGGGCCAT GGTGTGGACA  1080
TTGGACATGG ATGACGTCAG GGGCACGTTC TGTGGCACTG GCCCTTTCCC CCTTGTCTAC  1140
GTATTGAATG ATATCCTGGT GCGGGCTGAG TTCAGTTCAA CTTCTTTACC ACAATTTTGG  1200
CTGTCATCTG CTGTGAATTC TTCAAGCACT GACCCTGAAA GGCTGGCTGT GACCACGGCA  1260
TGGACCACTG ATAGTAAGAT TTTGCCCCCA GGAGGAGAGG CTGGGGTCAC TGAGATCCAC  1320
GGAAAGTGTG AAAATATGAC TATAACCCCT AGAGGTACAA CTGTGACCCC TACAAAGGAA  1380
ACTGTATCCC TTGGAAAGCA CACTGTAGCT CTAGGAGAGA AGACTGAGAT CACTGGGGCA  1440
ATGACCATGA CTTCTGTGGG TCATCAGTCC ATGACCCCTG GAGAGAAGGC CCTGACCCCT  1500
GTGGGTCATC AATCTGTGAC CACTGGACAG AAGACCCTGA CCTCTGTGGG TTATCAGTCT  1560
GTGACCCCTG GGGAAAAGAC CCTGACCCCT GTGGGTCATC AGTCTGTGAC CCCTGTGAGT  1620
CATCAGTCTG TGAGCCCTGG AGGAACGACT ATGACCCCTG TCCATTTTCA GACTGAGACC  1680
CTTAGACAGA ATACAGTGGC CCCTAGAAGG AAGGCTGTGG CCCGTGAAAA GGTGACTGTC  1740
CCCTCCAGAA ACATATCAGT CACCCCTGAA GGGCAGACTA TGCCTTTAAG AGGGGAGAAT  1800
TTGACTTCTG AGGTGGGCAC TCACCCCAGG ATGGGTAACT TGGGTCTTCA GATGGAAGCT  1860
GAAAACAGGA TGATGCTGTC CTCCAGCCCC GTCATCCAGC TCCCGGAACA AACTCCTCTA  1920
GCTTTTGACA ACCGCTTTGT TCCCATCTAT GGAAACCATT CCTCTGTCAA CTCAGTAACC  1980
CCTCAAACAA GTCCTCTTTC TCTAAAAAAA GAAATCCCAG AAAACTCTGC TGTGGATGAA  2040
GAAGCCTAAG CCCCTCTGGT GTCAGAAACC AGGGAAAACC CTTGTCTTTT CTTCTAAGTG  2100
ACATGTTGGA AGCCTTCTCA TCCCGGGGCA AAGCAGGCAT CAAAACCAGA ATAGGCCAAT  2160
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CTCTTTTCCA TTAAATAAAC TGTAAACACA AGAACCCA

Seq ID NO: 632 Protein sequence
Protein Accession #: NP_002548.1

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1          11         21         31         41         51
|          |          |          |          |          |
MWKLLLWVGL VLVLKHHDGA AHKLVCYFTN WAHSRPGPAS ILPHDLDPFL CTHLIFAFAS    60
MNNNQIVAKD LQDEKILYPE FNKLKERNRE LKTLLSIGGW NFGTSRFTTM LSTFANREKF   120
IASVISLLRT HDFDGLDLFP LYPGLRGSPM HDRWTFLFLI EELLFAFRKE ALLTMRPRLL   180
LSAAVSGVPH IVQTSYDVRF LGRLLDFINV LSYDLHGSWE RFTGHNSPLF SLPEDPKSSA   240
YAMNYWRKLG APSEKLIMGI PTYGRTFRLL KASKNGLQAR AIGPASPGKY TKQEGFLAYF   300
EICSFVWGAK KHWIDYQYVP YANKGKEWVG YDNAISPSYK AWFIRREHFG GAMVWTLDMD   360
DVRGTFCGTG PFPLVYVLND ILVRAEFSST SLPQFWLSSA VNSSSTDPER LAVTTAWTTD   420
SKILPPGGEA GVTEIHGKCE NMTITPRGTT VTPTKETVSL GKHTVALGEK TEITGAMTMT   480
SVGHQSMTPG EKALTPVGHQ SVTTGQKTLT SVGYQSVTPG EKTLTPVGHQ SVTPVSHQSV   540
SPGGTTMTPV HFQTETLRQN TVAPRRKAVA REKVTVPSRN ISVTPEGQTM PLRGENLTSE   600
VGTHPRMGNL GLQMEAENRM MLSSSPVIQL PEQTPLAFDN RFVPIYGNHS SVNSVTPQTS   660
PLSLKKEIPE NSAVDEEA
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Seq ID NO: 633 DNA sequence
Nucleic Acid Accession #: NM_003885.1
Coding sequence: 98..1021

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1          11         21         31         41         51
|          |          |          |          |          |
AAACTCAGAA TTTTCGCGGG CTCGGTGAGC GGTTTTATCC CTCCGGCCGG CAGGCTGGGC    60
GCAGGGGGCG AGCCCCCGCC CGGCGCGCAG CAGCACCATG GGCACGGTGC TGTCCCTGTC   120
TCCCAGCTAC CGGAAGGCCA CGCTGTTTGA GGATGGCGCG GCCACCGTGG GCCACTATAC   180
GGCCGTACAG AACAGCAAGA ACGCCAAGGA CAAGAACCTG AAGCGCCACT CCATCATCTC   240
CGTGCTGCCT TGGAAGAGAA TCGTGGCCGT GTCGGCCAAG AAGAAGAACT CCAAGAAGGT   300
GCAGCCTAAC AGCAGCTACC AGAACAACAT CACGCACCTC AACAATGAGA ACCTGAAGAA   360
GTCGCTGTCG TGCGCCAACC TGTCCACATT CGCCCAGCCC CCACCGGCCC AGCCGCCTGC   420
ACCCCCGGCC AGCCAGCTCT CGGGTTCCCA GACCGGGGGC TCCTCCTCAG TCAAGAAAGC   480
CCCTCACCCT GCCGTCACCT CCGCAGGGAC GCCCAAACGG GTCATCGTCC AGGCGTCCAC   540
CAGTGAGCTG CTTCGCTGCC TGGGTGAGTT TCTCTGCCGC CGGTGCTACC GCCTGAAGCA   600
CCTGTCCCCC ACGGACCCCG TGCTCTGGCT GCGCAGCGTG GACCGCTCGC TGCTTCTGCA   660
GGGCTGGCAG GACCAGGGCT TCATCACGCC GGCCAACGTG GTCTTCCTCT ACATGCTCTG   720
CAGGGATGTT ATCTCCTCCG AGGTGGGCTC GGATCACGAG CTCCAGGCCG TCCTGCTGAC   780
ATGCCTGTAC CTCTCCTACT CCTACATGGG CAACGAGATC TCCTACCCGC TCAAGCCCTT   840
CCTGGTGGAG AGCTGCAAGG AGGCCTTTTG GGACCGTTGC CTCTCTGTCA TCAACCTCAT   900
GAGCTCAAAG ATGCTGCAGA TAAATGCCGA CCCACACTAC TTCACACAGG TCTTCTCCGA   960
CCTGAAGAAC GAGAGCGGCC AGGAGGACAA GAAGCGGCTC CTCCTAGGCC TGGATCGGTG  1020
AGCACTGTAG CCTGCGTCAT GGCTCAAGGA TTCAATGCAT TTTTAAGAAT TTATTATTAA  1080
ATCAGTTTTG TGTACAG
```

Seq ID NO: 634 Protein sequence
Protein Accession #: NP_003876.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGTVLSLSPS YRKATLFEDG AATVGHYTAV QNSKNAKDKN LKRHSIISVL PWKRIVAVSA    60
KKKNSKKVQP NSSYQNNITH LNNENLKKSL SCANLSTFAQ PPPAQPPAPP ASQLSGSQTG   120
GSSSVKKAPH PAVTSAGTPK RVIVQASTSE LLRCLGEFLC RRCYRLKHLS PTDPVLWLRS   180
VDRSLLLQGW QDQGFITPAN VVFLYMLCRD VISSEVGSDH ELQAVLLTCL YLSYSYMGNE   240
ISYPLKPFLV ESCKEAFWDR CLSVINLMSS KMLQINADPH YFTQVFSDLK NESGQEDKKR   300
LLLGLDR
```

TABLE 79A:

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
Seq ID No.: Sequence identification number linking information in Table 79A to sequences in Table 80

Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
443646	AI085198	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	Seq ID No. C8 & C224
444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
421582	AI910275	Hs.350470	trefoil factor 1 (breast cancer, estroge	Seq ID No. C10 & C226
411789	AF245505	Hs.72157	Adlican	Seq ID No. C11 & C227
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	Seq ID No. C23 & C238
447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	Seq ID No. C24 & C239
411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No. C26 & C241
423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	Seq ID No. C27 & C242
447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
415214	AI445236	Hs.125124	EphB2	Seq ID No. C30 & C245
443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C38 & C253
420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	Seq ID No. C44 & C259
437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
408243	Y00787	Hs.624	interleukin 8	Seq ID No. C46 & C261
426088	AF036007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	Seq ID No. C48 & C263
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	Seq ID No. C51 & C266
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
416965	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
442275	AW449467	Hs.54795	Homo sapiens secretoglobin, family 3A, m	Seq ID No. C62 & C277
431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C63 & C278
431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C64 & C279
453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
421563	NM_006433	Hs.105806	granulysin	Seq ID No. C68 & C283
430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
414991	C17898		Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-tRNA synthetas	Seq ID No. C71 & C286
424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287

	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
5	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
10	431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. C82 & C297
	431958	X63629	Hs.2677	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No. C84 & C299
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
15	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
20	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	Seq ID No. C106 & C321
35	440659	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
40	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
45	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
	426761	AI015709	Hs.172089	PORIMIN Pro-oncosis receptor inducing me	Seq ID No. C120 & C335
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfami	Seq ID No. C121 & C336
50	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	Seq ID No. C125 & C340
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
55	428513	BE220806	Hs.184697	plexin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
	432874	W94322	Hs.279651	melanoma inhibitory activity	Seq ID No. C131 & C346
60	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
65	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
	432596	AJ224741	Hs.278461	matrilin 3	Seq ID No. C141 & C356
70	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	Seq ID No. C146 & C361
75	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gastrin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	Seq ID No. C150 & C365
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
80	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	Seq ID No. C156 & C371
431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	Seq ID No. C160 & C375
436729	BE621807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	Seq ID No. C172 & C387
439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	Seq ID No. C176 & C391
419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
433336	AF017986	Hs.31386	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No. C184 & C399
416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
425071	NM_013989	Hs.154424	defodinase, iodothyronine, type II	Seq ID No. C191 & C406
421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	Seq ID No. C192 & C407
418576	AW968159	Hs.302740	Epithelial calcium channel 2, CaT-like A	Seq ID No. C193 & C408
419693	AA133749	Hs.301350	FXYD domain-containing ion transport reg	Seq ID No. C194 & C409
419693	AA133749	Hs.301350	FXYD domain-containing ion transport reg	Seq ID No. C195 & C410
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
430144	AI732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
432600	BE391046	Hs.278962	AIM-1 protein	Seq ID No. C207 & C422
452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
434293	NM_004445	Hs.3796	EphB6	Seq ID No. C212 & C427
427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
422424	AI186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
432378	AI493046	Hs.146133	ESTs	Seq ID No. C432 & C433
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

TABLE 79B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

TABLE 79C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position

404682	9797231	Minus	40977-41150
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281

5

WO03042661 [file:///E:/WO03042661.pct] Page 1199 of 1385

Table 80:

Seq ID NO: C1 DNA Sequence
Nucleic Acid Accession #: NM_005814
Coding sequence: 345..1304

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GCCAATCCAG CTGAGGCTGG GCAGAGGTGG GTGAGAAGAG GGAAAATTGC AGGGACCTCC  240
AGTTGGGCCA GGCCAGAAGC TGCTGTAGCT TTAACCAGAC AGCTCAGACC TGTCTGGAGG  300
CTGCCAGTGA CAGGTTAGGT TTAGGGCAGA GAAGAAGCAA GACCATGGTG GGGAAGATGT  360
GGCCTGTGTT GTGGACACTC TGTGCAGTCA GGGTGACCGT CGATGCCATC TCTGTGGAAA  420
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ACAACACTGA AGACAAGGAG GATGCAAGGC CGAACCGGGA AGCCTATGAG GAGCCACCAG 1200
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CAGCTGTGGG GAACATGGCT GGCCTGGTAA GGGGGTCCCT GTGCTGATCC TGCTGACCTC 1500
ACTGTCCTGT GAAGTAACCC CTCCTGGCTG TGACACCTGG TGCGGGCCTG GCCCTCACTC 1560
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GGGGGCTGTC CTGCTCACCT GTGTGCCCAG CACCTGGAGG GGCACCAGGT GGAGGGTTTG 1740
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Seq ID NO: C2 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3150

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GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260
CAGCAGGGAG TAGTGTTTGT ATTTCCTGGG GGCCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320
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ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC   3060
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Seq ID NO: C3 DNA Sequence
Nucleic Acid Accession #: NM_002421.2
Coding sequence: 1..1410

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GTTGAAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAGAT   240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT   300
GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT   360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC   420
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CTTGCTCATG CTTTTCAACC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT   600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC   660
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TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTC   960
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GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT   1260
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTCAT   1320
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Seq ID NO: C4 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1410

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GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCACAAA CCCCAAAAGC ATGTGACAGT   840
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CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT   1140
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GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT   1260
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTCAT   1320
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Seq ID NO: C5 DNA Sequence
Nucleic Acid Accession #: NM_014331.2
Coding sequence: 1..1506

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GGAATCTTCA TCTCTCCTAA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCTCTG   240
ACCATCTGGA CGGTGTGTGG GGTCCTGTCA CTATTTGGAG CTTTGTCTTA TGCTGAATTG   300
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AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA   600
GCAATTCTGA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAAGGTCA AACGCAGAAC   660
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GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG   3060
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Seq ID NO: C6 DNA Sequence
Nucleic Acid Accession #: NM_003246.1
Coding sequence: 112..3624

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TCTGGCGGAG ACAACAGCGT GTTTGACATC TTTGAACTCA CCGGGGCCGC CCGCAAGGGG   240
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GCCAACCTGA TCCCCCCTGT GCCTGATGAC AAGTTCCAAG ACCTGGTGGA TGCTGTGCGG   360
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Seq ID NO: C7 DNA Sequence
Nucleic Acid Accession #: NM_002192
Coding sequence: 86..1366

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Seq ID NO: C8 DNA Sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

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Seq ID NO: C14 DNA Sequence
Nucleic Acid Accession #: NM_003014
Coding sequence: 238..1278

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Seq ID NO: C15 DNA Sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23..1489

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Seq ID NO: C16 DNA Sequence
Nucleic Acid Accession #: NM_024022
Coding sequence: 202..1563

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Seq ID NO: C17 DNA Sequence
Nucleic Acid Accession #: NM_003220
Coding sequence: 63..1376

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CACCCTACCA GCCTATCTAC CCCCAGTCGC AAGATCCTTA CTCCCACGTC AACGACCCCT  300
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CACCCGAGTG TCTCAACGCG TCGCTGCTGG GCGGAGTGCT CCGGAGGGCG AAGTCTAAAA   840
ATGGAGGAAG ATCTTTAAGA GAAAAACTGG ACAAAATAGG ATTAAATCTG CCTGCAGGGA   900
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Seq ID NO: C18 DNA Sequence
Nucleic Acid Accession #: NM_002988
Coding sequence: 71..340

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GCAGATTCCA CAAAAGTTCA TAGTTGACTA TTCTGAAACC AGCCCCCAGT GCCCCAAGCC  240
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GCCCAGTGAA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG  420
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ATTATGAAAT TAGTATTTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTTCCCCT  600
TTCCCTTCAA CTCTTCGTAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTTCTCAG  660
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Seq ID NO: C19 DNA Sequence
Nucleic Acid Accession #: NM_004063
Coding sequence: 121..2619

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TATGGCCAAG AGGGGAAGTT TAGTGGACCC CTGAAACCCA TGACATTTTC TATTTATGAA  240
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ATAGGCACTA AAGTGGGCAA TGTGACTGCC AAGGATCCAG AAGGTCTGGA CATAAGCTAT 1920
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WO03042661 [file:///E:/WO03042661.pdf]


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Seq ID NO: C20 DNA Sequence
Nucleic Acid Accession #: NM_004443
Coding sequence: 28..3024

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CTTCGCACGG GGTTCATCTG GCGGCGGGAT GTGCAGCGGG TCTACGTGGA GCTCAAGTTC   360
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Seq ID NO: C21 DNA Sequence
Nucleic Acid Accession #: NM_001804
Coding sequence: 82..879

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Seq ID NO: C22 DNA Sequence
Nucleic Acid Accession #: NM_021978
Coding sequence: 36..2603

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TTCTACTGAC CCAACTGGGG GCAAAGGTTT GAAGACACAG CCTCCCCCGC CAGCCCCAAG   2880
CTGGGCCGAG GCGCGTTTGT GTATATCTGC CTCCCCTGTC TGTAAGGAGC AGCGGGAACG   2940
GAGCTTCGGA GCCTCCTCAG TGAAGGTGGT GGGGCTGCCG GATCTGGGCT GTGGGGCCCT   3000
TGGGCCACGC TCTTGAGGAA GCCCAGGCTC GGAGGACCCT GGAAAACAGA CGGGTCTGAG   3060
ACTGAAAATG GTTTACCAGC TCCCAGGTGA CTTCAGTGTG TGTATTGTGT AAATGAGTAA   3120
AACATTTTAT TTCTTTTTAA AAAAAAAAA                                     3149
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Seq ID NO: C23 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2268

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AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC   180
AGCGTCGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT   240
CTGGACATCA GCCCCGAGAG GGTCAGAGTG GGAGCATTCC AGTTCAGTTC CACTCCTCAT   300
CTGGAATTCC CCTTGGATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG   360
ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAAATACCT TCTGCACAGA   420
GGGTTGCCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG   480
AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG   540
TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT   600
AGAGGGCAGC ACGTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC   660
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AGGGTCGACC TCCTCTTCCT GCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCCTG   1080
CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC   1140
CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCCTGT GGGGGAGTAC   1200
CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCCGTGG TGGCCCCACC   1260
CTGACGGGCA GTGCCTTGCG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA   1320
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GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT   1440
GAGGCCGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC   1500
TCGGATCCTC AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG   1560
CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC   1620
TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG   1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG   1740
ACTGCCTTCG GGCTGGACAC CAAACCCACC CGGGCTGCGA TGCTGCGGGC CATTAGCCAG   1800
GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA   1860
GTGATGACCG TCCAGAGGGG TGCCCGGCCT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA   1920
GGCGGGAGAG GCGCAGAGGA TGCAGCCGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC   1980
TCTGTCTTGG TCGTGGGCGT GGGGCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT   2040
CCCCGGGATT CCCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG   2100
CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CGGCCAGTCA ACCTCTGCAA ACCCAGCCCG   2160
TGCATGAATG AGGGCAGCTG CGTCCTGCAG AATGGGAGCT ACCGCTGCAA GTGTCGGGAT   2220
GGCTGGGAGG GCCCCCACTG CGAGAACCGA TTCTTGAGAC GCCCCTGA                2268
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Seq ID NO: C24 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..2424

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TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC   120
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CTGGACATCA GCCCCGAGAG GGTCAGAGTG GGAGCATTCC AGTTCAGTTC CACTCCTCAT   300
CTGGAATTCC CCTTGGATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG   360
ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAAATACCT TCTGCACAGA   420
GGGTTGCCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG   480
AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG   540
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AGAGGGCAGC ACGTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC   660
ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC   720
CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTCG CTGGCAATGC CCCATGCTGG   780
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TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAGTGC   960
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GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT  1440
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TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG  1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG  1740
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TCTGTCTTGG TCGTGGGCGT GGGGCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT  2040
CCCCGGGATT CCCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG  2100
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CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC  2340
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AATGTCTGTG CCCCAGGTCC TTAG                                         2424
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Seq ID NO: C25 DNA Sequence
Nucleic Acid Accession #: XM_097386.3
Coding sequence: 142..795

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TCCCGTGCAC CAGGGTCTGC AGCAGCCACT GGGGCCTGGC TGCCTGCTGC ATCTGGCGGC  240
CCTGGACCCC TGGGGCCCCC GTGCACCTGC CCACCTCGGA GCCTGGGGAG GGGCCGTGCA  300
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GTGTCTGTGG GCGATCCGGC CTCCCGGCGG TGGGTGGACC TGGATTCTAA CTCAGAGGAC  420
TTGAGCCTGC TGTTAACTCC GATGATTGTA GGGACAGGCG GGGTGGGTGG GGGGTGGGCG  480
CGAGGCTGGG TCCCGGCCCA GGAGAAGGAA GTCGCTGAAG GCAGTGGCCA TGCTGGCCGT  540
GGAAATGGGA GGCGGTTGCA GAGGGTCTAT GGGGCCCGGT CCTGGATACT CGGCAGGAAG  600
CCGTGTCTGC AGAGGCTCCT CCCTGCCTCA GGTGGCCCCG TTCAACCCCA GCCGTGCCCA  660
TCTCCTGCCA CCGCCTGTCG GTGGGGGTTT AAATTCGGTG TGGCTTTCTG GGGTGCAGCT  720
CAGCACCCCC CCTTATGCAG ACTGGGAGGG GGTCGGGCAG TCCCCTCAGC CACGAGGACC  780
CTGGATGGGT TCTAGTTCAC TTGGGACCGT GGGGCCTGGC TGCGTACTGA GTGGGTGCCC  840
CACAGTCAAG GCCAACGGGG GCTCCCCCTG CTCTGAGATG TTGGGAGAAA GGCGGCTTCT  900
GGAACCTTCC GTGGGACCCG TAAGTGGCTG TCCAGAAAGG CGGGAGGGTG GGCACGGGGC  960
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TCTTATCATG TTTTACCCAC CTTGTCCCTT TTTCCCCCAA TTGTGCTTTT GCATTTTTTT 1080
CCTTGGCAAA TGTAAACTCA GCCTTTCATT CATGACGTGT GAAATTTCAG TTTCTCTGGA 1140
GTTTGTCAGA CGGCGTGGGA ACCACGCCTG AAACTCAGGT AATAGGAGGA AAAAAAAAAA 1200
AACTTAAAAA AATTTTTAAA AAACATAAAA CTACTCTCTA CCTCTGGCTG GGCCCAGCCT 1260
GTCTCGCCCT GGCCGCGGCA GGGTGGCCTG TAACAATTTC AGTTTTCGCA GAACATTCAG 1320
GTATTAAAAG GAAAAAA                                                1337
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Seq ID NO: C26 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 95..2128

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TGCTTCCTGG GAGCTTGTGG TCCGCGTTGA CCATCCCAAT GAAGAGCAGC AGAAAGACGT  180
CACACTGAGA GTATCTGGAG ACCTTCATGT TGGAGGAGTG ATGCTCAAGT TAGTAGAACA  240
GATCAATATA TCCCAAGACT GGTCAGACTT TGCTCTTTGG TGGGAACAGA AGCATTGCTG  300
GCTTCTGAAA ACCCACTGGA CCCTGGACAA ATATGGGGTC CAGGCAGATG CAAAGCTTCT  360
CTTCACCCCT CAGCATAAAA TGCTGCGCCT TCGTCTGCCG AATTTGAAGA TGGTGAGGTT  420
GCGAGTCAGC TTCTCAGCTG TGGTTTTTAA AGCTGTCAGT GATATCTGCA AAATCCTGAA  480
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TATATATGAC CCCATCAATG GAACACCAGC ATCATCCACC ATGACTTGGT TCAGTGACAG   720
CCCTTTGACG GAACAAAACT GCAGCATCCT CGCATTCAGC CAACCCCCCC AGTCCCCAGA   780
AGCACTTGCG GATATGTACC AGCCTCGGTC TCTGGTTGAT AAAGCCAAGC TCAATGCAGG   840
TTGGCTAGAC TCCTCACGCT CCCTTATGGA ACAAGGCATC CAAGAGGATG AGCAGCTGCT   900
CTTACGATTT AAATATTATT CTTTCTTCGA CTTGAATCCT AAATATGATG CTGTCCGAAT   960
AAACCAACTC TATGAGCAAG CCAGGTGGGC CATTCTCTTA GAAGAAATTG ATTGCACAGA  1020
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TGAAACACAG GATTTTGCAG GCGAGTCCGA GGTTGATGAA ATAGAAGCGG CGCTTTCTAA  1140
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CTTTACTGCT TTCACCTGCC TGAGTGCAGA TTGCAAGATT GTGCACGAGT ACATTGGCGG  2040
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GGCAAGCCAA AGGCGCCCCT CCCCAGAGGG ATCCCTAACG TGCCCAGCAT GTAGATTCTG  2220
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Seq ID NO: C27 Protein Sequence
Protein Accession #: NP_005161.1

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NRVKLVNLGF QALRQHVPHG GASKKLSKVE TLRSAVEYIR ALQRLLAEHD AVRNALAGGL  120
RPQAVRPSAP RGPPGTTPVA ASPSRASSSP GRGGSSEPGS PRSAYSSDDS GCEGALSPAE  180
RELLDFSSWL GGY                                                     193
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Seq ID NO: C28 DNA Sequence
Nucleic Acid Accession #: NM_017763
Coding sequence: 169..2520

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WO03042661 [file:///E:/WO03042661.pcp]


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CACCAGCTGC AGCTGGCTGC CCTCTGGCCC TGGCTGCTGA TGGCTACCCT GCAGGCAGGC  240
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TCCCTCAGTT AGTGGGGAGA CTAGCACCTA GGTACCCACA TGGGTATTTA TATCTGAACC 3720
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Seq ID NO: C29 Protein Sequence
Protein Accession #: NP_004280.2

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PDSDSGLSLD SSHNNTSVIK SNSSHSVCDE GAIGYCTDHE SSSHHDLEGA VGGYYPEPSK  180
LCHLDQSDSD FHGDLTFQHV FHNHTYHLQP TAPESTSEPF PWPGKSQKIR SRYLEDTDRN  240
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Seq ID NO: C30 DNA Sequence
Nucleic Acid Accession #: NM_004442
Coding sequence: 19..2982

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WO03042661 [file:///E:/WO03042661.pcc] Page 1217 of 1385


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Seq ID NO: C31 DNA Sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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TCCTCTGATG ACAGTTGTGA CAGCTTTGCT TCTGATAATT TTGCAAACAC GAGGCTGCAG   300
TCAGTTCGGG AAGGCTGTAG GACCCGCAGC CAGTGCAGGC ACTCTGGACC TCTCAGGGTG   360
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Seq ID NO: C32 DNA Sequence
Nucleic Acid Accession #: NM_012445.1
Coding sequence: 276..1271

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GCTGCCGGCC GCGCTCCCGC TGCTCCTGCC GGGTGATGGA AAACCCCAGC CCGGCCGCCG   300
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Seq ID NO: C33 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1314

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Seq ID NO: C34 DNA Sequence
Nucleic Acid Accession #: NM_003045.1
Coding sequence: 148..2037

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TGGAGCGCCA CCTTCGACGA GCTGATAGGC AGACCCATCG GGGAGTTCTC ACGGACACAC   600
ATGACTCTGA ACGCCCCCGG CGTGCTGGCT GAAAACCCCG ACATATTCGC AGTGATCATA   660
ATTCTCATCT TGACAGGACT TTTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA   720
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GGATCGGTTA AAAACTGGCA GCTCACGGAG GAGGATTTTG GGAACACATC AGGCCGTCTC   840
TGTTTGAACA ATGACACAAA AGAAGGGAAG CCCGGTGTTG GTGGATTCAT GCCCTTCGGG   900
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ATCGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCCGT GGGGATCGTG  1020
GCGTCCCTCT TGATCTGCTT CATCGCCTAC TTTGGGGTGT CGGCTGCCCT CACGCTCATG  1080
ATGCCCTACT TCTGCCTGGA CAATAACAGC CCCCTGCCCG ACGCCTTTAA GCACGTGGGC  1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC CGCCAGTCTT  1200
CTAGGTTCCA TGTTTCCCAT GCCTCGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA  1260
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GCAGAGATGT TCTCTTTGAA AACCATACTC TCACCCAAAA ACATGGAGCC TTCCAAAATC  1620
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CTCGCAGGGT CTGCCCTCCT CTGTGCCGTG GTCACGGGCG TCATCTGGAG GCAGCCCGAG   1800
AGCAAGACCA AGCTCTCATT TAAGGTTCCC TTCCTGCCAG TGCTCCCCAT CCTGAGCATC   1860
TTCGTGAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCCG GTTTGCTGTG   1920
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TCCCTGGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAGTG CAAGTGACGC   2040
ACAGCCCCGC CCCCCGGAGG TGGCAGCAGC CCCGAGGGAC GCCCCCAGAG GACCGGGAGG   2100
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Seq ID NO: C35 DNA Sequence
Nucleic Acid Accession #: NM_002776.1
Coding sequence: 82..912

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GCGCTGCTCC CCCAAAACGA CACGCGCTTG GACCCCGAAG CCTATGGCGC CCCGTGCGCG   240
CGCGGCTCGC AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT   300
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GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAGGGCG AGCAGCTCCG CCGGACGACT   420
CGCTCTGTTG TCCATCCCAA GTACCACCAG GGCTCAGGCC CCATCCTGCC AAGGCGAACG   480
GATGAGCACG ATCTCATGTT GCTAAAGCTG GCCAGGCCCG TAGTGCCGGG GCCCCGCGTC   540
CGGGCCCTGC AGCTTCCCTA CCGCTGTGCT CAGCCCGGAG ACCAGTGCCA GGTTGCTGGC   600
TGGGGCACCA CGGCCGCCCG GAGAGTGAAG TACAACAAGG GCCTGACCTG CTCCAGCATC   660
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CAGCATCCAG CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA   900
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CAGATGCCCA GAGGCTCCAT CGTCCATCCT CTTCCTCCCC AGTCGGCTGA ACTCTCCCCT   1020
TGTCTGCACT GTTCAAACCT CTGCCGCCCT CCACACCTCT AAACATCTCC CCTCTCACCT   1080
CATTCCCCCA CCTATCCCCA TTCTCTGCCT GTACTGAAGC TGAAATGCAG GAAGTGGTGG   1140
CAAAGGTTTA TTCCAGAGAA GCCAGGAAGC CGGTCATCAC CCAGCCTCTG AGAGCAGTTA   1200
CTGGGGTCAC CCAACCTGAC TTCCTCTGCC ACTCCCCGCT GTGTGACTTT GGGCAAGCCA   1260
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Seq ID NO: C36 DNA Sequence
Nucleic Acid Accession #: XM_095088
Coding sequence: 1..4074

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GAGCTGCCAA GCGGGGTGCT GGAGGGCCTG AGCCAGCGGC GCGGGCCGCA GCCGGGAGCA   240
GCTGTACGCT CCCGCCGAGG CGGCGCAGTG CCCCGCGGGG CCCGAGCGGT TCCAGAGCGC   300
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GCCGTGGGGA GCCCTCGCCC ACTGGGACGG CTACTGCCCA AGGTACAGGA GGTGGCCCGG   660
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CCATACACAT GTGAAGAATG TGGCAAAGCC TTTAGCTTAT CCTCATCCCT CACTTACCAC   3780
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TGCTCCTCAA CCCTTAAGAA ACATAAGATA ATTCATACTG GAGAGAAACC CTACAAATGT   3900
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Seq ID NO: C37 DNA Sequence
Nucleic Acid Accession #: NM_032044
Coding sequence: 182..658

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CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTTACC ACAAGTCCAA  300
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AGACCCCTTC AGCTTCTACA CCCTTCTGCC CTCTCTCCAT TGCCTGCACC CCACCCCAGC 1080
CACTCAACTC CTGCTTGTTT TTCCTTTGGC CATAGGAAGG TTTACCAGTA GAATCCTTGC 1140
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Seq ID NO: C38 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 52..3042

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CCCAAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTTGGAGGAT  240
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ACGCTCCTCT GAAATGCTTG TCTTTTTTCT GTTGCCGAAA TAGCTGGTCC TTTTTCGGGA   5640
GTTAGATGTA TAGAGTGTTT GTATGTAAAC ATTTCTTGTA GGCATCACCA TGAACAAAGA   5700
TATATTTTCT ATTTATTTAT TATATGTGCA CTTCAAGAAG TCACTGTCAG AGAAATAAAG   5760
AATTGTCTTA AATGTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA                5808
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Seq ID NO: C39 DNA Sequence
Nucleic Acid Accession #: NM_014373
Coding sequence: 322.1338

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ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA  180
AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA  240
GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATTT CAGCAGGTCT  300
TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAACTGCTC TTTTCAGTAC  360
CAGTTACGTC AAACAAACCA GCCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT  420
GGGAAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAAACAC CTGTCAAAAT  480
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ATCTGCCTAT TTACTCAAAT TATTTCCTTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC  660
CTGACAGCTT GTATAGATTA TTGCCTGAAT TTCTCTAAAA CAACCAAGCT TTCATTTAAG  720
TGTCAAAAAT TATTTTATTT CTTTACAGTA ATTTTAATTT GGATTTCAGT CCTTGCTTAT  780
GTTTTGGGAG ACCCAGCCAT CTACCAAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC  840
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TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA  960
ACTTCCTATA TGAATGAAAC TATCTTATAT TTTCCTTTTT CATCCCACTC CAGTTATACT 1020
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Seq ID NO: C40 DNA Sequence
Nucleic Acid Accession #: BC012089
Coding sequence: 1..2571

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CCCTTGAATT TGTTTTGGTT TGGCATAGGA AAAGCTACTG TATTTTTACT TCCGGCTCTA 2400
ATTTTTGCGG TAAAACTGGC TAAGTACTAT CGTCGAATGG ATTCGGAGGA CGTGTACGAT 2460
GATGTTGAAA CTATACCCAT GAAAAATATG GAAAATGGTA ATAATGGTTA TCATAAAGAT 2520
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Seq ID NO: C41 DNA Sequence

Nucleic Acid Accession #: NM_033049
Coding sequence: 28..1566

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GAAACTGCTA GCACCACAGC AAATACACCT TCTTTCCCAA CAGCTACTTC ACCTGCTCCC  240
CCCATAATTA GTACACATAG TTCCTCCACA ATTCCTACAC CTGCTCCCCC CATAATTAGT  300
ACACATAGTT CCTCCACAAT TCCTATACCT ACTGCTGCAG ACAGTGAGTC AACCACAAAT  360
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CAATCATCAG GGCCTCCCAC TGGCACCGCT TTATTGGAGA CCAGCACCCT AAACAGCACA  540
GGTCCCAGCA ATCCTTGCCA AGATGATCCC TGTGCAGATA ATTCGTTATG TGTTAAGCTG  600
CATAATACAA GTTTTTGCCT GTGTTTAGAA GGGTATTACT ACAACTCTTC TACATGTAAG  660
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GGAGACATAC GCATCAACTG TGGAGGTCCG AGGGGATGAG AAGGGATACC CACCACCTTT 2040
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Seq ID NO: C42 DNA Sequence
Nucleic Acid Accession #: NM_001432.1
Coding sequence: 167..676

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AACAAAGTGT AGCTCTGACA TGAATGGCTA TTGTTTGCAT GGACAGTGCA TCTATCTGGT  420
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CTTCTTTTTA ACCGTCCACC AACCTTTAAG CAAAGAGTAT GTGGCTTTGA CCGTGATTCT  540
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WO03042661 [file:///E:/WO03042661.pcp]


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Seq ID NO: C43 DNA Sequence
Nucleic Acid Accession #: AF011468.1
Coding sequence: 257..1468

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AATTGTGCTA CTTATACTGG TTCATAATCT GGAGGCAAGG TTCGACTGCA GCCGCCCCGT   1740
CAGCCTGTGC TAGGCATGGT GTCTTCACAG GAGGCAAATC CAGAGCCTGG CTGTGGGGAA   1800
AGTGACCACT CTGCCCTGAC CCCGATCAGT TAAGGAGCTG TGCAATAACC TTCCTAGTAC   1860
CTGAGTGAGT GTGTAACTTA TTGGGTTGGC GAAGCCTGGT AAAGCTGTTG GAATGAGTAT   1920
GTGATTCTTT TTAAGTATGA AAATAAAGAT ATATGTACAG ACTTGTATTT TTTCTCTGGT   1980
GGCATTCCTT TAGGAATGCT GTGTGTCTGT CCGGCACCCC GGTAGGCCTG ATTGGGTTTC   2040
TAGTCCTCCT TAACCACTTA TCTCCCATAT GAGAGTGTGA AAAATAGGAA CACGTGCTCT   2100
ACCTCCATTT AGGGATTTGC TTGGGATACA GAAGAGGCCA TGTGTCTCAG AGCTGTTAAG   2160
GGCTTATTTT TTTAAAACAT TGGAGTCATA GCATGTGTGT AAACTTTAAA TATGCAAATA   2220
AATAAGTATC TATGTCTAAA AAAAAAAAAA AAA                                2253
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Seq ID NO: C44 DNA Sequence
Nucleic Acid Accession #: NM_013372
Coding sequence: 63..617

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GTATGAGCCG CACAGCCTAC ACGGTGGGAG CCCTGCTTCT CCTCTTGGGG ACCCTGCTGC  120
CGGCTGCTGA AGGGAAAAAG AAAGGGTCCC AAGGTGCCAT CCCCCCGCCA GACAAGGCCC  180
AGCACAATGA CTCAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGGC  240
GGGGCCAAGG GCGGGGCACT GCCATGCCCG GGGAGGAGGT GCTGGAGTCC AGCCAAGAGG  300
CCCTGCATGT GACGGAGCGC AAATACCTGA AGCGAGACTG GTGCAAAACC CAGCCGCTTA  360
AGCAGACCAT CCACGAGGAA GGCTGCAACA GTCGCACCAT CATCAACCGC TTCTGTTACG  420
GCCAGTGCAA CTCTTTCTAC ATCCCCAGGC ACATCCGGAA GGAGGAAGGT TCCTTTCAGT  480
CCTGCTCCTT CTGCAAGCCC AAGAAATTCA CTACCATGAT GGTCACACTC AACTGCCCTG  540
AACTACAGCC ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT  600
CCATCGATTT GGATTAAGCC AAATCCAGGT GCACCCAGCA TGTCCTAGGA ATGCAGCCCC  660
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AACCCCCAGC TGCCTCCTGG CAGGAGCCTG CTTGTGCGTA GTTCGTGTGC ATGAGTGTGG  780
ATGGGTGCCT GTGGGTGTTT TTAGACACCA GAGAAAACAC AGTCTCTGCT AGAGAGCACT  840
CCCTATTTTG TAAACATATC TGCTTTAATG GGGATGTACC AGAAACCCAC CTCACCCCGG  900
CTCACATCTA AAGGGGCGGG GCCGTGGTCT GGTTCTGACT TTGTGTTTTT GTGCCCTCCT  960
GGGGACCAGA ATCTCCTTTC GGAATGAATG TTCATGGAAG AGGCTCCTCT GAGGGCAAGA 1020
GACCTGTTTT AGTGCTGCAT TCGACATGGA AAAGTCCTTT TAACCTGTGC TTGCATCCTC 1080
CTTTCCTCCT CCTCCTCACA ATCCATCTCT TCTTAAGTTG ATAGTGACTA TGTCAGTCTA 1140
ATCTCTTGTT TGCCAAGGTT CCTAAATTAA TTCACTTAAC CATGATGCAA ATGTTTTTCA 1200
TTTTGTGAAG ACCCTCCAGA CTCTGGGAGA GGCTGGTGTG GGCAAGGACA AGCAGGATAG 1260
TGGAGTGAGA AAGGGAGGGT GGAGGGTGAG GCCAAATCAG GTCCAGCAAA AGTCAGTAGG 1320
GACATTGCAG AAGCTTGAAA GGCCAATACC AGAACACAGG CTGATGCTTC TGAGAAAGTC 1380
TTTTCCTAGT ATTTAACAGA ACCCAAGTGA ACAGAGGAGA AATGAGATTG CCAGAAAGTG 1440
ATTAACTTTG GCCGTTGCAA TCTGCTCAAA CCTAACACCA AACTGAAAAC ATAAATACTG 1500
ACCACTCCTA TGTTCGGACC CAAGCAAGTT AGCTAAACCA AACCAACTCC TCTGCTTTGT 1560
CCCTCAGGTG GAAAAGAGAG GTAGTTTAGA ACTCTCTGCA TAGGGGTGGG AATTAATCAA 1620
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TCCATTCCAC TATTTCCCAT AATGCTTCTG AGAGCCACTA ACTTGATTGA TAAAGATCCT 1740
GCCTCTGCTG AGTGTACCTG ACAGTAAGTC TAAAGATGAR AGAGTTTAGG GACTACTCTG 1800
TTTTAGCAAG ARATATTKTG GGGGTCTTTT TGTTTTAACT ATTGTCAGGA GATTGGGCTA 1860
RAGAGAAGAC GACGAGAGTA AGGAAATAAA GGGRATTGCC TCTGGCTAGA GAGTAAGTTA 1920
GGTGTTAATA CCTGGTAGAA ATGTAAGGGA TATGACCTCC CTTTCTTTAT GTGCTCACTG 1980
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TCTGATTAAA CTTGGCCTAC TGGCAATGGC TACTTAGGAT TGATCTAAGG GCCAAAGTGC 2160
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TCCAGTGCTC TCCCATCTAA CAACTAAACA GGAGCCATTT CAAGGCGGGA GATATTTTAA 2460
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AGCAGTAATC TTCTTTTAGG AGCTTGTACC ACAGTCTTGC ACATAAGTGC AGATTTGGCT 2880
CAAGTAAAGA GAATTTCCTC AACACTAACT TCACTGGGAT AATCAGCAGC GTAACTACCC 2940
TAAAAGCATA TCACTAGCCA AAGAGGGAAA TATCTGTTCT TCTTACTGTG CCTATATTAA 3000
GACTAGTACA AATGTGGTGT GTCTTCCAAC TTTCATTGAA AATGCCATAT CTATACCATA 3060
TTTTATTCGA GTCACTGATG ATGTAATGAT ATATTTTTTC ATTATTATAG TAGAATATTT 3120
TTATGGCAAG ATATTTGTGG TCTTGATCAT ACCTATTAAA ATAATGCCAA ACACCAAATA 3180
TGAATTTTAT GATGTACACT TTGTGCTTGG CATTAAAAGA AAAAAACACA CATCCTGGAA 3240
GTCTGTAAGT TGTTTTTTGT TACTGTAGGT CTTCAAAGTT AAGAGTGTAA GTGAAAAATC 3300
TGGAGGAGAG GATAATTTCC ACTGTGTGGA ATGTGAATAG TTAAATGAAA AGTTATGGTT 3360
ATTTAATGTA ATTATTACTT CAAATCCTTT GGTCACTGTG ATTTCAAGCA TGTTTTCTTT 3420
TTCTCCTTTA TATGACTTTC TCTGAGTTGG GCAAAGAAGA AGCTGACACA CCGTATGTTG 3480
TTAGAGTCTT TTATCTGGTC AGGGGAAACA AAATCTTGAC CCAGCTGAAC ATGTCTTCCT 3540
GAGTCAGTGC CTGAATCTTT ATTTTTTAAA TTGAATGTTC CTTAAAGGTT AACATTTCTA 3600
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AAGCAATATT AAGAAAGACT TTAAATGTTA TTTTGGAAGA CTTACGATGC ATGTATACAA   3660
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AATGAAAAGT GGATAAACAG AACATTTATA AGTGATCAGT TAATGCCTAA GAGTGAAAGT   3780
AGTTCTATTG ACATTCCTCA AGATATTTAA TATCAACTGC ATTATGTATT ATGTCTGCTT   3840
AAATCATTTA AAAACGGCAA AGAATTATAT AGACTATGAG GTACCTTGCT GTGTAGGAGG   3900
ATGAAAGGGG AGTTGATAGT CTCATAAAAC TAATTTGGCT TCAAGTTTCA TGAATCTGTA   3960
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Seq ID NO: C45 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 200..2932

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TCCCTCGAGT TCTGGTGTGA AGAGATAAAT CACCAGTCAC AGACTATGCA CCCGACTGCT  180
GCTGTTCAGT CCAGGGAAAA TGAAAGTTGG AGTGCTGTGG CTCATTTCTT TCTTCACCTT  240
CACTGACGGC CACGGTGGCT TCCTGGGGAA AAATGATGGC ATCAAAACAA AAAAAGAACT  300
CATTGTGAAT AAGAAAAAAC ATCTAGGCCC AGTCGAAGAA TATCAGCTGC TGCTTCAGGT  360
GACCTATAGA GATTCCAAGG AGAAAAGAGA TTTGAGAAAT TTTCTGAAGC TCTTGAAGCC  420
TCCATTATTA TGGTCACATG GGCTAATTAG AATTATCAGA GCAAAGGCTA CCACAGACTG  480
CAACAGCCTG AATGGAGTCC TGCAGTGTAC CTGTGAAGAC AGCTACACCT GGTTTCCTCC  540
CTCATGCCTT GATCCCCAGA ACTGCTACCT TCACACGGCT GGAGCACTCC CAAGCTGTGA  600
ATGTCATCTC AACAACCTCA GCCAGAGTGT CAATTTCTGT GAGAGAACAA AGATTTGGGG  660
CACTTTCAAA ATTAATGAAA GGTTTACAAA TGACCTTTTG AATTCATCTT CTGCTATATA  720
CTCCAAATAT GCAAATGGAA TTGAAATTCA ACTTAAAAAA GCATATGAAA GAATTCAAGG  780
TTTTGAGTCG GTTCAGGTCA CCCAATTTCG AAATGGAAGC ATCGTTGCTG GGTATGAAGT  840
TGTTGGCTCC AGCAGTGCAT CTGAACTGCT GTCAGCCATT GAACATGTTG CCGAGAAGGC  900
TAAGACAGCC CTTCACAAGC TGTTTCCATT AGAAGACGGC TCTTTCAGAG TGTTCGGAAA  960
AGCCCAGTGT AATGACATTG TCTTTGGATT TGGGTCCAAG GATGATGAAT ATACCCTGCC 1020
CTGCAGCAGT GGCTACAGGG GAAACATCAC AGCCAAGTGT GAGTCCTCTG GGTGGCAGGT 1080
CATCAGGGAG ACTTGTGTGC TCTCTCTGCT TGAAGAACTG AACAAGAATT TCAGTATGAT 1140
TGTAGGCAAT GCCACTGAGG CAGCTGTGTC ATCCTTCGTG CAAAATCTTT CTGTCATCAT 1200
TCGGCAAAAC CCATCAACCA CAGTGGGGAA TCTGGCTTCG GTGGTGTCGA TTCTGAGCAA 1260
TATTTCATCT CTGTCACTGG CCAGCCATTT CAGGGTGTCC AATTCAACAA TGGAGGATGT 1320
CATCAGTATA GCTGACAATA TCCTTAATTC AGCCTCAGTA ACCAACTGGA CAGTCTTACT 1380
GCGGGAAGAA AAGTATGCCA GCTCACGGTT ACTAGAGACA TTAGAAAACA TCAGCACTCT 1440
GGTGCCTCCG ACAGCTCTTC CTCTGAATTT TTCTCGGAAA TTCATTGACT GGAAAGGGAT 1500
TCCAGTGAAC AAAAGCCAAC TCAAAAGGGG TTACAGCTAT CAGATTAAAA TGTGTCCCCA 1560
AAATACATCT ATTCCCATCA GAGGCCGTGT GTTAATTGGG TCAGACCAAT TCCAGAGATC 1620
CCTTCCAGAA ACTATTATCA GCATGGCCTC GTTGACTCTG GGGAACATTC TACCCGTTTC 1680
CAAAAATGGA AATGCTCAGG TCAATGGACC TGTGATATCC ACGGTTATTC AAAACTATTC 1740
CATAAATGAA GTTTTCCTAT TTTTTTCCAA GATAGAGTCA AACCTGAGCC AGCCTCATTG 1800
TGTGTTTTGG GATTTCAGTC ATTTGCAGTG GAACGATGCA GGCTGCCACC TAGTGAATGA 1860
AACTCAAGAC ATCGTGACGT GCCAATGTAC TCACTTGACC TCCTTCTCCA TATTGATGTC 1920
ACCTTTTGTC CCCTCTACAA TCTTCCCCGT TGTAAAATGG ATCACCTATG TGGGACTGGG 1980
TATCTCCATT GGAAGTCTCA TTTTATGCCT GATCATCGAG GCTTTGTTTT GGAAGCAGAT 2040
TAAAAAAAGC CAAACCTCTC ACACACGTCG TATTTGCATG GTGAACATAG CCCTGTCCCT 2100
CTTGATTGCT GATGTCTGGT TTATTGTTGG TGCCACAGTG GACACCACGG TGAACCCTTC 2160
TGGAGTCTGC ACAGCTGCTG TGTTCTTTAC ACACTTCTTC TACCTCTCTT TGTTCTTCTG 2220
GATGCTCATG CTTGGCATCC TGCTGGCTTA CCGGATCATC CTCGTGTTCC ATCACATGGC 2280
CCAGCATTTG ATGATGGCTG TTGGATTTTG CCTGGGTTAT GGGTGCCCTC TCATTATATC 2340
TGTCATTACC ATTGCTGTCA CGCAACCTAG CAATACCTAC AAAAGGAAAG ATGTGTGTTG 2400
GCTTAACTGG TCCAATGGAA GCAAACCACT CCTGGCTTTT GTTGTCCCTG CACTGGCTAT 2460
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TGGGGAAAGA CTGAGTCGGG ATGACAAGGC CACCATCATC CGCGTGGGGA AGAGCCTCCT 2580
CATTCTGACC CCTCTGCTAG GGCTCACCTG GGGCTTTGGA ATAGGAACAA TAGTGGACAG 2640
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CAAATTCTCA AAGCCTTTCA ACCCACTGCA AAACAAAGGC CATTATGCAT TTTCTCATAC 2880
TGGAGATTCC TCCGACAACA TCATGCTAAC TCAGTTTGTC TCAAATGAAT AAGGCAAGGA 2940
ATCATAAAAT CAAGAAAAAA TTTCCAGAAC AACTTGACAT TTAGAGACAA ATGTCAATGA 3000
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AATGTCTCAG TGGCTTCA                                                3078
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Seq ID NO: C46 DNA Sequence
Nucleic Acid Accession #: NM_000584.1
Coding sequence: 75..374

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CTGCAGCTCT GTGTGAAGGT GCAGTTTTGC CAAGGAGTGC TAAAGAACTT AGATGTCAGT  180
GCATAAAGAC ATACTCCAAA CCTTTCCACC CCAAATTTAT CAAAGAACTG AGAGTGATTG  240
AGAGTGGACC ACACTGCGCC AACACAGAAA TTATTGTAAA GCTTTCTGAT GGAAGAGAGC  300
TCTGTCTGGA CCCCAAGGAA AACTGGGTGC AGAGGGTTGT GGAGAAGTTT TTGAAGAGGG  360
CTGAGAATTC ATAAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT  420
GAAACTTCAA GCAAATCTAC TTCAACACTT CATGTATTGT GTGGGTCTGT TGTAGGGTTG  480
CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTTCA GTAAACAATG AATAGTTTTT  540
CATTGTACCA TGAAATATCC AGAACATACT TATATGTAAA GTATTATTTA TTTGAATCTA  600
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CAAAAAACAA CAAATAATTT TTAAATATAA GGATTTTCCT AGATATTGCA CGGGAGAATA   660
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GAATGGGTTT GCTAGAATGT GATATTTGAA GCATCACATA AAAATGATGG GACAATAAAT   780
TTTGCCATAA AGTCAAATTT AGCTGGAAAT CCTGGATTTT TTTCTGTTAA ATCTGGCAAC   840
CCTAGTCTGC TAGCCAGGAT CCACAAGTCC TTGTTCCACT GTGCCTTGGT TTCTCCTTTA   900
TTTCTAAGTG GAAAAAGTAT TAGCCACCAT CTTACCTCAC AGTGATGTTG TGAGGACATG   960
TGGAAGCACT TTAAGTTTTT TCATCATAAC ATAAATTATT TTCAAGTGTA ACTTATTAAC  1020
CTATTTATTA TTTATGTATT TATTTAAGCA TCAAATATTT GTGCAAGAAT TTGGAAAAAT  1080
AGAAGATGAA TCATTGATTG AATAGTTATA AAGATGTTAT AGTAAATTTA TTTTATTTTA  1140
GATATTAAAT GATGTTTTAT TAGATAAATT TCAATCAGGG TTTTTAGATT AAACAAAGAA  1200
ACAATTGGGT ACCCAGTTAA ATTTTCATTT CAGATAAACA ACAAATAATT TTTTAGTATA  1260
AGTACATTAT TGTTTATCTG AAAGTTTTAA TTGAACTAAC AATCCTAGTT TGATACTCCC  1320
AGTCTTGTCA TTGCCAGCTG TGTTGGTAGT GCTGTGTTGA ATTACGGAAT AATGAGTTAG  1380
AACTATTAAA ACAGCCAAAA CTCCACAGTC AATATTAGTA ATTTCTTGCT GGTTGAAACT  1440
TGTTTATTAT GTACAAATAG ATTCTTATAA TATTATTTAA ATGACTGCAT TTTTAAATAC  1500
AAGGCTTTAT ATTTTTAACT TTAAGATGTT TTTATGTGCT CTCCAAATTT TTTTTACTGT  1560
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Seq ID NO: C47 DNA Sequence
Nucleic Acid Accession #: NM_005603.1
Coding sequence: 1..3756

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GAACCAGAAC AAAACCGAGT CAACAGGGAA GCAGAGGAGA ACCGGGAGCC ATTCAGAAAA   180
GAATGTACAT GGCAAGTCAA AGCAAACGAT CGCAAGTACC ACGAACAACC TCACTTTATG   240
AACACAAAAT TCTTGTGTAT TAAGGAGAGT AAATATGCGA ATAATGCAAT TAAAACATAC   300
AAGTACAACG CATTTACCTT TATACCAATG AATCTGTTTG AGCAGTTTAA GAGAGCAGCC   360
AATTTATATT TCCTGGCTCT TCTTATCTTA CAGGCAGTTC CTCAAATCTC TACCCTGGCT   420
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GTGGACGATG TGGCTCGCCA TAAAATGGAT AAGGAAATCA ACAATAGGAC GTGTGAAGTC   540
ATTAAGGATG GCAGGTTCAA AGTTGCTAAG TGGAAAGAAA TTCAAGTTGG AGACGTCATT   600
CGTCTGAAAA AAAATGATTT TGTTCCAGCT GACATTCTCC TGCTGTCTAG CTCTGAGCCT   660
AACAGCCTCT GCTATGTGGA AACAGCAGAA CTGGACGGAG AAACCAATTT AAAATTTAAG   720
ATGTCACTTG AAATCACAGA CCAGTACCTC CAAAGAGAAG ATACATTGGC TACATTTGAT   780
GGTTTTATTG AATGTGAAGA ACCCAATAAC CGACTAGATA AGTTTACAGG AACACTATTT   840
TGGAGAAACA CAAGTTTTCC TTTGGATGCT GATAAAATTT TGTTACGTGG CTGTGTAATT   900
AGGAACACCG ATTTCTGCCA CGGCTTAGTC ATTTTTGCAG GTGCTGACAC TAAAATAATG   960
AAGAATAGTG GGAAAACCAG ATTTAAAAGA ACTAAAATTG ATTACTTGAT GAACTACATG  1020
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CCCATCTCTC TCTATGTCAG CGTGGAAGTG ATTCGTCTTG GACAGAGTCA CTTCATCAAC  1260
TGGGACCTGC AAATGTACTA TGCTGAGAAG GACACACCCG CAAAAGCTAG AACCACCACA  1320
CTCAATGAAC AGCTCGGGCA GATCCATTAT ATCTTCTCTG ATAAGACGGG GACACTCACA  1380
CAAAATATCA TGACCTTTAA AAAGTGCTGT ATCAACGGGC AGATATATGG GGACCATCGG  1440
GATGCCTCTC AACACAACCA CAACAAAATA GAGCAAGTTG ATTTTAGCTG GAATACATAT  1500
GCTGATGGGA AGCTTGCATT TTATGACCAC TATCTTATTG AGCAAATCCA GTCAGGGAAA  1560
GAGCCAGAAG TACGACAGTT CTTCTTCTTG CTCGCAGTTT GCCACACAGT CATGGTGGAT  1620
AGGACTGATG GTCAGCTCAA CTACCAGGCA GCCTCTCCCG ATGAAGGTGC CCTGGTAAAC  1680
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GAACTGGGCA CTGAAAGGAC TTACAATGTT CTTGCCATTT TGGACTTCAA CAGTGACCGG  1800
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ATTGAAGAAA AAGAATTTAC AGAATGGAAT AAAAAGTTTA TGGCTGCCAG TGTGGCCTCC  2040
ACCAACCGGG ACGAAGCTCT GGATAAAGTA TATGAGGAGA TTGAAAAAGA CTTAATTCTC  2100
CTGGGAGCTA CAGCTATTGA AGACAAGCTA CAGGATGGAG TTCCAGAAAC CATTTCAAAA  2160
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AAGAGGTACA AGAAAGCCAT CACGCTGGCC ATCGGAGATG GGGCCAATGA CGTGAACATG  2700
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TCGAGTGACT ATTCCTTTGC TCAGTTCCGA TATCTGCAGA GGCTACTGCT GGTGCATGGC  2820
CGATGGTCTT ACATAAGGAT GTGCAAGTTC CTACGATACT TCTTTTACAA AAACTTTGCC  2880
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GGGCTGCTCG ACCAGGATGT GAGTGACAAA CTGAGCCTCC GATTCCCTGG GTTATACATA  3060
GTGGGACAAA GAGACTTACT ATTCAACTAT AAGAGATTCT TTGTAAGCTT GTTGCATGGG  3120
GTCCTAACAT CGATGATCCT CTTCTTCATA CCTCTTGGAG CTTATCTGCA AACCGTAGGG  3180
CAGGATGGAG AGGCACCTTC CGACTACCAG TCTTTTGCCG TCACCATTGC CTCTGCTCTT  3240
GTAATAACAG TCAATTTCCA GATTGGCTTG GATACTTCTT ATTGGACTTT TGTGAATGCT  3300
TTTTCAATTT TTGGAAGCAT TGCACTTTAT TTTGGCATCA TGTTTGACTT TCATAGTGCT  3360
GGAATACATG TTCTCTTTCC ATCTGCATTT CAATTTACAG GCACAGCTTC AAACGCTCTG  3420
AGACAGCCAT ACATTTGGTT AACTATCATC CTGACTGTTG CTGTGTGCTT ACTACCCGTC  3480
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GTTGCCATTC GATTCCTGTC AATGACCATC TGGCCATCAG AAAGTGATAA GATCCAGAAG   3540
CATCGCAAGC GGTTGAAGGC GGAGGAGCAG TGGCAGCGAC GGCAGCAGGT GTTCCGCCGG   3600
GGCGTGTCAA CGCGGCGCTC GGCCTACGCC TTCTCGCACC AGCGGGGCTA CGCGGACCTC   3660
ATCTCCTCCG GGCGCAGCAT CCGCAAGAAG CGCTCGCCGC TTGATGCCAT CGTGGCGGAT   3720
GGCACCGCGG AGTACAGGCG CACCGGGGAC AGCTGA                              3756

Seq ID NO: C48 DNA Sequence
Nucleic Acid Accession #: XM_044533
Coding sequence: 238..2751

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GGAGGCGGGG GCCCCCGGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCCGCCCGTG   180
AGTCCGGCCG AGCCACCTGA GCCCGAGCCG CGGGACACCG TCGCTCCTGC TCTCCGAATG   240
CTGCGCACCG CGATGGGCCT GAGGAGCTGG CTCGCCGCCC CATGGGGCGC GCTGCCGCCT   300
CGGCCACCGC TGCTGCTGCT CCTGCTGCTG CTGCTCCTGC TGCAGCCGCC GCCTCCGACC   360
TGGGCGCTCA GCCCCCGGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCC ATTCCTCAGA   420
TTCGAAGCTG AACACATCTC CAACTACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC   480
CTGTACGTGG GTGCTCGAGA GGCCCTCTTT GCACTCAGTA GCAACCTCAG CTTCCTGCCA   540
GGCGGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCAG AGAAGAAACA GCAGTGCAGC   600
TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAAACTACA TCAAGATCCT CCTGCCGCTC   660
AGCGGCAGTC ACCTGTTCAC CTGTGGCACA GCAGCCTTCA GCCCCATGTG TACCTACATC   720
AACATGGAGA ACTTCACCCT GGCAAGGGAC GAGAAGGGGA ATGTCCTCCT GGAAGATGGC   780
AAGGGCCGTT GTCCCTTCGA CCCGAATTTC AAGTCCACTG CCCTGGTGGT TGATGGCGAG   840
CTCTACACTG GAACAGTCAG CAGCTTCCAA GGGAATGACC CGGCCATCTC GCGGAGCCAA   900
AGCCTTCGCC CCACCAAGAC CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG   960
GCCTCAGCCT ACATTCCTGA GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC   1020
TTTTTCTTCA GCGAGACTGG CCAGGAATTT GAGTTCTTTG AGAACACCAT TGTGTCCCGC   1080
ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC   1140
TCCTTCCTCA AGGCCCAGCT GCTGTGCTCA CGGCCCGACG ATGGCTTCCC CTTCAACGTG   1200
CTGCAGGATG TCTTCACGCT GAGCCCCAGC CCCCAGGACT GGCGTGACAC CCTTTTCTAT   1260
GGGGTCTTCA CTTCCCAGTG GCACAGGGGA ACTACAGAAG GCTCTGCCGT CTGTGTCTTC   1320
ACAATGAAGG ATGTGCAGAG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CCGTGAGACA   1380
CAGCAGTGGT ACACCGTGAC CCACCCGGTG CCCACACCCC GGCCTGGAGC GTGCATCACC   1440
AACAGTGCCC GGGAAAGGAA GATCAACTCA TCCCTGCAGC TCCCAGACCG CGTGCTGAAC   1500
TTCCTCAAGG ACCACTTCCT GATGGACGGG CAGGTCCGAA GCCGCATGCT GCTGCTGCAG   1560
CCCCAGGCTC GCTACCAGCG CGTGGCTGTA CACCGCGTCC CTGGCCTGCA CCACACCTAC   1620
GATGTCCTCT TCCTGGGCAC TGGTGACGGC CGGCTCCACA AGGCAGTGAG CGTGGGCCCC   1680
CGGGTGCACA TCATTGAGGA GCTGCAGATC TTCTCATCGG GACAGCCCGT GCAGAATCTG   1740
CTCCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCCTCAC ACTCGGGCGT AGTCCAGGTG   1800
CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCCTCGC CCGGGACCCC   1860
TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CACGTCAGCC TCTACCAGCC TCAGCTGGCC   1920
ACCAGGCCGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCGTCT   1980
TCGGTTGTGT CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC   2040
CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC   2100
TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCCTCCT GCCACGTGCT ACCCACTGGG   2160
GACCTGCTGC TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGCTGGTC ACTAGAGGAG   2220
GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC   2280
CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGCACCA   2340
GCTGGTGGCA AGGCCAGCTG GGGTGCAGAC AGGTCCTACT GGAAGGAGTT CCTGGTGATG   2400
TGCACGCTCT TTGTGCTGGC CGTGCTGCTC CCAGTTTTAT TCTTGCTCTA CCGGCACCGG   2460
AACAGCATGA AAGTCTTCCT GAAGCAGGGG GAATGTGCCA GCGTGCACCC CAAGACCTGC   2520
CCTGTGGTGC TGCCCCCTGA GACCCGCCCA CTCAACGGCC TAGGGCCCCC TAGCACCCCG   2580
CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT   2640
GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCCAGTGTGC   2700
CCCCGGCCCC GGGTCCGCCT TGGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT   2760
TCCAGAGGAC GCTGCCCTGG CTTCAGGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC   2820
TCCCCTCCGC TCTGCTCTTC GTGGAACACG ACCGTGGTGC CCGGCCCTTG GGAGCCTTGG   2880
GGCCAGCTGG CCTGCTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACCC AGACACCCAA   2940
ACAGCCGTGG CCCCAGAGGT CCTGGCCAAA TATGGGGGCC TGCCTAGGTT GGTGGAACAG   3000
TGCTCCTTAT GTAAACTGAG CCCTTTGTTT AAAAAACAAT TCCAAATGTG AAACTAGAAT   3060
GAGAGGGAAG AGATAGCATG GCATGCAGCA CACACGGCTG CTCCAGTTCA TGGCCTCCCA   3120
GGGGTGCTGG GGATGCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAAC CCTCACCAAC   3180
TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT   3240
CAGGACCAGC TTGGGCTGCG TGCGTTCTGC CTTGCCAGTC AGCCGAGGAT GTAGTTGTTG   3300
CTGCCGTCGT CCCACCACCT CAGGGACCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA   3360
GGTCCTGGGC TCGGACCCAA CTCCTGGACC TTTCCAGCCT GTATCAGGCT GTGGCCACAC   3420
GAGAGGACAG CGCGAGCTCA GGAGAGATTT CGTGACAATG TACGCCTTTC CCTCAGAATT   3480
CAGGGAAGAG ACTGTCGCCT GCCTTCCTCC GTTGTTGCGT GAGAACCCGT GTGCCCCTTC   3540
CCACCATATC CACCCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACTAA CTGCACCCTG   3600
GTCCTCTCCC CAGTCCCCAG TTCACCCTCC ATCCCTCACC TTCCTCCACT CTAAGGGATA   3660
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG   3720
ATGCACTTTA TGTCATTTTT TAATAAAGTC TGAAGAATTA CTGTTT                   3766

Seq ID NO: C49 DNA Sequence
Nucleic Acid Accession #: NM_007019.1
Coding sequence: 41..580

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CCGGGGTCCG GTGGGCAAAA GGCTACAGCA GGAGCTGATG ACCCTCATGA TGTCTGGCGA   180
TAAAGGGATT TCTGCCTTCC CTGAATCAGA CAACCTTTTC AAATGGGTAG GGACCATCCA   240
TGGAGCAGCT GGAACAGTAT ATGAAGACCT GAGGTATAAG CTCTCGCTAG AGTTCCCCAG   300
TGGCTACCCT TACAATGCGC CCACAGTGAA GTTCCTCACG CCCTGCTATC ACCCCAACGT   360
GGACACCCAG GGTAACATAT GCCTGGACAT CCTGAAGGAA AAGTGGTCTG CCCTGTATGA   420
TGTCAGGACC ATTCTGCTCT CCATCCAGAG CCTTCTAGGA GAACCCAACA TTGATAGTCC   480
CTTGAACACA CATGCTGCCG AGCTCTGGAA AAACCCCACA GCTTTTAAGA AGTACCTGCA   540
AGAAACCTAC TCAAAGCAGG TCACCAGCCA GGAGCCCTGA CCCAGGCTGC CCAGCCTGTC   600
CTTGTGTCGT CTTTTTAATT TTTCCTTAGA TGGTCTGTCC TTTTTGTGAT TTCTGTATAG   660
GACTCTTTAT CTTGAGCTGT GGTATTTTTG TTTTGTTTTT GTCTTTTAAA TTAAGCCTCG   720
GTTGAGCCCT TGTATATTAA ATAAATGCAT TTTTGTCCTT TTTTAAAAAA AAAAAAAAAA   780
AAA                                                                 783
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Seq ID NO: C50 DNA Sequence
Nucleic Acid Accession #: NM_014584.1
Coding sequence: 227..1633

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TGGCGATCGC TGAGAGGCAG GAGGGCCGAG GCGGGCCTGG GAGGCGGCCC GGAGGTGGGG  120
CGCCGCTGGG GCCGGCCCGC ACGGGCTTCA TCTGAGGGCG CACGGCCCGC GACCGAGCGT  180
GCGGACTGGC CTCCCAAGCG TGGGGCGACA AGCTGCCGGA GCTGCAATGG GCCGCGGCTG  240
GGGATTCTTG TTTGGCCTCC TGGGCGCCGT GTGGCTGCTC AGCTCGGGCC ACGGAGAGGA  300
GCAGCCCCCG GAGACAGCGG CACAGAGGTG CTTCTGCCAG GTTAGTGGTT ACTTGGATGA  360
TTGTACCTGT GATGTTGAAA CCATTGATAG ATTTAATAAC TACAGGCTTT TCCCAAGACT  420
ACAAAAACTT CTTGAAAGTG ACTACTTTAG GTATTACAAG GTAAACCTGA AGAGGCCGTG  480
TCCTTTCTGG AATGACATCA GCCAGTGTGG AAGAAGGGAC TGTGCTGTCA AACCATGTCA  540
ATCTGATGAA GTTCCTGATG GAATTAAATC TGCGAGCTAC AAGTATTCTG AAGAAGCCAA  600
TAATCTCATT GAAGAATGTG AACAAGCTGA ACGACTTGGA GCAGTGGATG AATCTCTGAG  660
TGAGGAAACA CAGAAGGCTG TTCTTCAGTG GACCAAGCAT GATGATTCTT CAGATAACTT  720
CTGTGAAGCT GATGACATTC AGTCCCCTGA AGCTGAATAT GTAGATTTGC TTCTTAATCC  780
TGAGCGCTAC ACTGGTTACA AGGGACCAGA TGCTTGGAAA ATATGGAATG TCATCTACGA  840
AGAAAACTGT TTTAAGCCAC AGACAATTAA AAGACCTTTA AATCCTTTGG CTTCTGGTCA  900
AGGGACAAGT GAAGAGAACA CTTTTTACAG TTGGCTAGAA GGTCTCTGTG TAGAAAAAAG  960
AGCATTCTAC AGACTTATAT CTGGCCTACA TGCAAGCATT AATGTGCATT TGAGTGCAAG 1020
ATATCTTTTA CAAGAGACCT GGTTAGAAAA GAAATGGGGA CACAACATTA CAGAATTTCA 1080
ACAGCGATTT GATGGAATTT TGACTGAAGG AGAAGGTCCA AGAAGGCTTA AGAACTTGTA 1140
TTTTCTCTAC TTAATAGAAC TAAGGGCTTT ATCCAAAGTG TTACCATTCT TCGAGCGCCC 1200
AGATTTTCAA CTCTTTACTG GAAATAAAAT TCAGGATGAG GAAAACAAAA TGTTACTTCT 1260
GGAAATACTT CATGAAATCA AGTCATTTCC TTTGCATTTT GATGAGAATT CATTTTTTGC 1320
TGGGGATAAA AAAGAAGCAC ACAAACTAAA GGAGGACTTT CGACTGCATT TTAGAAATAT 1380
TTCAAGAATT ATGGATTGTG TTGGTTGTTT TAAATGTCGT CTGTGGGGAA AGCTTCAGAC 1440
TCAGGGTTTG GGCACTGCTC TGAAGATCTT ATTTTCTGAG AAATTGATAG CAAATATGCC 1500
AGAAAGTGGA CCTAGTTATG AATTCCATCT AACCAGACAA GAAATAGTAT CATTATTCAA 1560
CGCATTTGGA AGAATTTCTA CAAGTGTGAA AGAATTAGAA AACTTCAGGA ACTTGTTACA 1620
GAATATTCAT TAAAGAAAAC AAGCTGATAT GTGCCTGTTT CTGGACAATG GAGGCGAAAG 1680
AGTGGAATTT CATTCAAAGG CATAATAGCA ATGACAGTCT TAAGCCAAAC ATTTTATATA 1740
AAGTTGCTTT TGTAAAGGAG AATTATATTG TTTTAAGTAA ACACATTTTT AAAAATTGTG 1800
TTAAGTCTAT GTATAATACT ACTGTGAGTA AAAGTAATAC TTTAATAATG TGGTACAAAT 1860
TTTAAAGTTT AATATTGAAT AAAAGGAGGA TTATCAAATT CATATATGAT AAAAGTGAAT 1920
GTTCTAAGTC TCTCAAACTA GCGTTTTATG TAATAATATG TAATATAAAT AAAACTATGG 1980
TAAATGTGAC AAGCATTTAA TAGGAAAATG CTAAGGAGGC CTCATAAATG ACCCATAATT 2040
ACCAACGTAG AATTTTTCAG TACATTTAGG GTTGCTGGAT TTAGCAAATA AAAATAAAGA 2100
TTGCCCAGTT AGATTTGAAT TTCAGATAAA CAATTAGTTT TTTAATATTT TACATGGAAT 2160
ATTTGGAAAA TACTTATACT AAAAAATTAT TTGTTTGAAA TTCACATTTA ACTGGGAGTC 2220
TTGTATTTTA TCTGGCAATC CTAAAATACA TTGGTATGAA ACAAATCACT TTTAGAAGTA 2280
TATTGCTATT TTGATTGGGT TGTTTTTGTG TGTAGAAACG TACAATAACA ACTCAAAGGC 2340
ACAGGAGATT TCTAAACATT GTGAAAAGTT GAATAGATTA TATATTTATT CTCATAATAC 2400
TTTCACTAAT ACTAAATAAA ATTTGGGGAA CACTTTTTAT TTTTATATAA TTTCCAATTT 2460
ACAGAAAAGT TTCAAAAATA GTACAAAGAG CTCTCTTACC CAGATTCACT AATTGTTCAT 2520
ACGTGCTTTA TCTTTCATGC TTTCTCTGTA CACACACACA CACACACAAA TTTTTCCTCA 2580
ATCATTTGAA AGTCAGTTAT AGGCATCATG CCCCTTAAAC CCTAAATACT TCAGTGTGTA 2640
ATACTGAATA ATTACTAAAA ATGATTTTCT CAGAAAAAAA AACTCCCACA ATTCTGGAAC 2700
TATAATACTG TAAGCCTTAG AATAAATAAT ACTTTCAAGT TCCAATCTAA AGTTCTTTTT 2760
GAGTTTTGTT GCCCGTTTTA TGCTTGATGT GTATAGTAAT AGGGTAGGCT ATTTATTTTA 2820
TTAAAATTTT TTTTAGAGAC AAGGTTTTGC TGTGTTGCCC AAGCTGGAAC TTGAACGACT 2880
GGGCTGAAGT GATCTTCCCA CCTCAGCCTC CCAAGTAGCT GGGAATACAG GTGTCTGCCA 2940
CCATACCCAG TTTCATTTTT GTTTTTTATA CCCGAAGTTC ATTTCCTTTG TCTCCCTAAA 3000
ACTGAACTGT AATTTTGGGA GGTTTTCATT AGTGGAAGCT CTTCATTTAT AAAGCTATTT 3060
GAAGGGGTTT AGGAATTTAT ATCACATGGT AATTGTAGAG AAAAAGAAGC TATATACCTC 3120
AAAATCGTGC CCTCTTTACA TATGTCTTAT CAGGTATAAC ATGTTGAAAT GTCACATTAG 3180
TAGTAAAGTG GGGTTTATTT ATATAGTGGT TAAGAAATGT CAGTTTACAC TGCTGTATAC 3240
TTCTTCTTCT GTGTCCCTAA GGCCTGGTAC AGTGCCAAGC ACATACTTGG TATCCAATAA 3300
ATATTTGTTG GATGAAAAAA AAAAAAAAAA AAAA                              3334
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Seq ID NO: C51 DNA Sequence
Nucleic Acid Accession #: NM_002888.1
Coding sequence: 37..723

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CCCGCTCCCT GGTCCGGGCC CAGGGGCCCG CGCCCCACCG CCCCGCTGCT CGCGCTGCTG  120
CTGTTGCTCG CCCCGGTGGC GGCGCCCGCG GGGTCCGGGG GCCCCGACGA CCCTGGGCAG  180
CCTCAGGATG CTGGGGTCCC GCGCAGGCTC CTGCAGCAGA AGGCGCGCGC GGCGCTTCAC  240
TTCTTCAACT TCCGGTCCGG CTCGCCCAGC GCGCTGCGAG TGCTGGCCGA GGTGCAGGAG  300
GGCCGCGCGT GGATTAATCC AAAAGAGGGA TGTAAAGTTC ACGTGGTCTT CAGCACAGAG  360
CGCTACAACC CAGAGTCTTT ACTTCAGGAA GGTGAGGGAC GTTTGGGGAA ATGTTCTGCT  420
CGAGTGTTTT TCAAGAATCA GAAACCCAGA CCAACCATCA ATGTAACTTG TACACGGCTC  480
ATCGAGAAAA AGAAAAGACA ACAAGAGGAT TACCTGCTTT ACAAGCAAAT GAAGCAACTG  540
AAAAACCCCT TGGAAATAGT CAGCATACCT GATAATCATG GACATATTGA TCCCTCTCTG  600
AGACTCATCT GGGATTTGGC TTTCCTTGGA AGCTCTTACG TGATGTGGGA AATGACAACA  660
CAGGTGTCAC ACTACTACTT GGCACAGCTC ACTAGTGTGA GGCAGTGGGT AAGAAAAACC  720
TGAAAATTAA CTTGTGCCAC AAGAGTTACA ATCAAAGTGG TCTCCTTAGA CTGAATTCAT  780
GTGAACTTCT AATTTCATAT CAAGAGTTGT AATCACATTT ATTTCAATAA ATATGTGAGT  840
TCCTGC                                                             846

Seq ID NO: C52 DNA Sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

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CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC  120
TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC  180
TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC  240
ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT  300
AAAGGACAAC GATGCCTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT  360
GAAAGAAAGA ATTTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA  420
AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG  480
AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT  540
GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAT CAGAATTCCA  600
CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT  660
GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTTGTATT ATACATTCAT  720
GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT  780
GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT  840
CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG  900
CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTTCAT GCAAATACAC ACTTCTTTCC  960
CCAAATATCA TGTAGCACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT 1020
TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT 1140
GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGGAC ACATTTGAAA 1260
TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTTGAAAAA TAAGCAAATG TATACCTAGC 1320
AATCACTTTT ACTTTTTGTA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
TTGTTCATGC CTATATACTG TAAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440
GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTTCTTTT TTAAAAAAAA AAA          1493

Seq ID NO: C53 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..609

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GTGAGCCGGC ACCCGGTCTT TTTCCTCACC GTGCCCGCAG TCCTGACAAT CACCTTCGGC  120
CTCAGCGCGC TCAACCGCTT CCAGCCCGAG GGCGACCTGG AGCGCCTGGT CGCTCCCAGC  180
CACAGCCTGG CCAAGATCGA GCGCAGCCTG GCCAGCAGCC TTTTCCCCCT GGACCAGTCC  240
AAAAGCCAGC TCTATTCGGA CTTACACACC CCTGGGAGGT ATGGCAGGGT GATCCTCCTC  300
TCCCCAACCG GGGACAATAT TTTGCTCCAG GCTGAGGGGA TCCTGCAGAC CCACCGAGCC  360
GTGCTGGAAA TGAAGGTGAA CCACAAGGGC TATAATTATA CTTTTTCCCA TCTGTGTGTG  420
TTGAGAAATC AGGATAAGAA ATGCGTGCTG GATGATATTA TTTCAGTGCT AGAGGATCTC  480
AGGCAGGCTG CCGTCTCCAA TAAGACAACA GCCAGGGTGC AAGTGAGGTA TCCCAACACT  540
AAATTAAAGG TATGCTCCTT CTGCATGCTT CTGCCAATTA AAGAGGCAGC ACTTCATTTC  600
TTGCCCTAA                                                          609

Seq ID NO: C54 DNA Sequence
Nucleic Acid Accession #: NM_002438.1
Coding sequence: 104..4474

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GCCCTCCTGT CCATCAGGAG AAGGAAAGGA TAAACCCTGG GCCATGAGGC TACCCCTGCT  120
CCTGGTTTTT GCCTCTGTCA TTCCGGGTGC TGTTCTCCTA CTGGACACCA GGCAATTTTT  180
AATCTATAAT GAAGATCACA AGCGCTGCGT GGATGCAGTG AGTCCCAGTG CCGTCCAAAC  240
CGCAGCTTGC AACCAGGATG CCGAATCACA GAAATTCCGA TGGGTGTCCG AATCTCAGAT  300
TATGAGTGTT GCATTTAAAT TATGCCTGGG AGTGCCATCA AAAACAGACT GGGTTGCTAT  360
CACTCTCTAT GCCTGTGACT CAAAAAGTGA ATTTCAGAAA TGGGAGTGCA AAAATGACAC  420
ACTTTTGGGG ATCAAAGGAG AAGATTTATT TTTTAACTAC GGCAACAGAC AAGAAAAGAA  480
TATTATGCTC TACAAGGGAT CGGGTTTATG GAGCAGGTGG AAGATCTATG GAACCACAGA  540
CAATCTGTGC TCCAGAGGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGGAGC  600
AACCTGTGCA TTCCCGTTCA AGTTTGAAAA CAAGTGGTAC GCAGATTGCA CGAGTGCTGG  660
GCGGTCGGAT GGATGGCTCT GGTGCGGAAC CACTACTGAC TATGACACAG ACAAGCTATT  720
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TGGATATTGT CCATTGAAAT TTGAGGGCAG TGAAAGCTTA TGGAATAAAG ACCCGCTGAC 780
CAGCGTTTCC TACCAGATAA ACTCCAAATC CGCTTTAACG TGGCACCAAG CGAGGAAAAG 840
CTGCCAACAA CAGAACGCTG AGCTCCTGAG CATCACAGAG ATACATGAGC AAACATACCT 900
GACAGGATTA ACCAGTTCCT TGACCTCAGG ACTCTGGATT GGACTTAACA GTCTGAGCTT 960
CAACAGCGGT TGGCAGTGGA GTGACCGCAG TCCTTTCCGA TATTTGAACT GGTTACCAGG 1020
AAGTCCATCA GCTGAACCTG GAAAAAGCTG TGTGTCACTA AATCCTGGAA AAAATGCTAA 1080
ATGGGAAAAT CTGGAATGTG TTCAGAAACT GGGCTATATT TGCAAAAAGG GCAACACCAC 1140
TTTAAATTCT TTTGTTATTC CCTCAGAAAG TGATGTGCCT ACTCACTGTC CTAGTCAGTG 1200
GTGGCCGTAT GCCGGTCACT GTTACAAGAT TCACAGAGAT GAGAAAAAAA TCCAGAGGGA 1260
TGCTCTGACC ACCTGCAGGA AGGAAGGCGG TGACCTCACA AGTATCCACA CCATCGAGGA 1320
ATTGGACTTT ATTATCTCCC AGCTAGGATA TGAGCCAAAT GACGAATTGT GGATCGGCTT 1380
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CAAATGGCTT CGTGGAGAAC CAAGCCATGA AAACAACAGA CAGGAGGATT GTGTGGTGAT 1500
GAAAGGCAAG GATGGGTACT GGGCAGATCG GGGCTGTGAG TGGCCTCTTG GCTACATCTG 1560
CAAGATGAAA TCACGAAGCC AAGGTCCAGA AATAGTGGAA GTCGAAAAAG GCTGCAGGAA 1620
AGGCTGGAAA AAACATCACT TTTACTGCTA TATGATTGGA CATACGCTTT CAACATTTGC 1680
AGAAGCAAAC CAAACCTGTA ATAATGAGAA TGCTTATTTA ACAACTATTG AAGACAGATA 1740
TGAACAAGCC TTCCTGACTA GTTTCGTTGG CTTAAGGCCT GAAAAATATT TCTGGACAGG 1800
ACTTTCAGAT ATACAAACCA AAGGGACTTT TCAGTGGACC ATCGAGGAAG AGGTTCGGTT 1860
CACCCACTGG AATTCAGATA TGCCAGGGCG AAAGCCAGGG TGTGTTGCCA TGAGAACCGG 1920
GATTGCAGGG GGCTTATGGG ATGTTTTGAA ATGTGATGAA AAGGCAAAAT TTGTGTGCAA 1980
GCACTGGGCA GAAGGAGTAA CCCACCCACC GAAGCCCACG ACGACTCCCG AACCCAAATG 2040
TCCGGAGGAT TGGGGCGCCA GCAGTAGAAC AAGCTTGTGT TTCAAGCTGT ATGCAAAAGG 2100
AAAACATGAG AAGAAAACGT GGTTTGAATC TCGAGATTTT TGTCGAGCTC TGGGTGGAGA 2160
CTTAGCTAGC ATCAATAACA AAGAGGAACA GCAAACAATA TGGCGATTAA TAACAGCTAG 2220
TGGAAGCTAC CACAAACTGT TTTGGTTGGG ATTGACATAT GGAAGCCCTT CAGAAGGTTT 2280
TACTTGGAGT GATGGTTCTC CTGTTTCATA TGAAAACTGG GCTTATGGAG AACCTAATAA 2340
TTATCAAAAT GTTGAATACT GTGGTGAGCT GAAAGGTGAC CCTACTATGT CTTGGAATGA 2400
TATTAATTGT GAACACCTTA ACAACTGGAT TTGCCAGATA CAAAAAGGAC AAACACCAAA 2460
ACCTGAGCCA ACACCAGCTC CTCAAGACAA TCCACCAGTT ACTGAAGATG GGTGGGTTAT 2520
TTACAAAGAC TACCAGTATT ATTTCAGCAA AGAGAAGGAA ACCATGGACA ATGCGCGAGC 2580
GTTTTGCAAG AGGAATTTTG GTGATCTTGT TTCTATTCAA AGTGAAAGTG AAAAGAAGTT 2640
TCTATGGAAA TATGTAAACA GAAATGATGC ACAGTCTGCA TATTTTATTG GTTTATTGAT 2700
CAGCTTGGAT AAAAAGTTTG CTTGGATGGA TGGAAGCAAA GTGGATTACG TGTCTTGGGC 2760
CACAGGTGAA CCCAATTTTG CAAATGAAGA TGAAAACTGT GTGACCATGT ATTCAAATTC 2820
AGGGTTTTGG AATGACATTA ACTGTGGCTA TCCAAACGCC TTCATTTGCC AGCGACATAA 2880
CAGTAGTATC AATGCTACCA CAGTTATGCC TACCATGCCC TCGGTCCCAT CAGGGTGCAA 2940
GGAAGGTTGG AATTTCTACA GCAACAAGTG TTTCAAAATC TTTGGATTTA TGGAAGAAGA 3000
AAGAAAAAAT TGGCAAGAGG CACGAAAAGC TTGTATAGGC TTTGGAGGGA ATCTGGTCTC 3060
CATACAAAAT GAAAAAGAGC AAGCATTTCT TACCTATCAC ATGAAGGACT CCACTTTCAG 3120
TGCCTGGACT GGGCTGAATG ATGTCAATTC AGAACACACG TTCCTTTGGA CGGATGGACG 3180
AGGAGTCCAT TACACAAACT GGGGGAAAGG TTACCCTGGT GGAAGAAGAA GCAGTCTTTC 3240
TTATGAAGAT GCTGACTGTG TTGTTATTAT TGGAGGTGCA TCAAATGAAG CAGGAAAATG 3300
GATGGATGAT ACCTGCGACA GTAAACGAGG CTACATATGC CAGACACGAT CCGACCCTTC 3360
CTTGACTAAT CCTCCAGCAA CGATTCAAAC AGATGGCTTT GTTAAATATG GCAAAAGCAG 3420
CTATTCACTC ATGAGACAAA AATTTCAATG GCATGAAGCG GAGACATACT GCAAGCTTCA 3480
CAATTCCCTT ATAGCCAGCA TTCTGGATCC CTACAGTAAT GCATTTGCGT GGCTGCAGAT 3540
GGAAACATCT AATGAACGTG TGTGGATCGC CCTGAACAGT AACTTGACTG ATAATCAATA 3600
CACTTGGACT GATAAGTGGA GGGTGAGGTA CACTAACTGG GCTGCTGATG AGCCCAAATT 3660
GAAATCAGCA TGTGTTTATC TGGATCTTGA TGGCTACTGG AAGACAGCAC ATTGCAATGA 3720
AAGTTTTTAC TTTCTCTGTA AAAGATCAGA TGAAATCCCT GCTACTGAAC CCCCACAACT 3780
GCCTGGCAGA TGCCCGGAGT CAGATCACAC AGCATGGATT CCTTTCCATG GTCACTGTTA 3840
CTATATTGAG TCCTCATATA CAAGAAACTG GGGCCAAGCT TCTCTGGAAT GTCTTCGAAT 3900
GGGTTCCTCT CTGGTTTCCA TTGAAAGTGC TGCAGAATCC AGTTTTCTGT CATATCGGGT 3960
TGAGCCACTT AAAAGTAAAA CCAATTTTTG GATAGGATTG TTCAGAAATG TTGAAGGGAC 4020
GTGGCTGTGG ATAAATAACA GTCCGGTCTC CTTTGTCAAC TGGAACACAG GAGATCCCTC 4080
TGGTGAACGG AATGATTGTG TAGCTTTACA TGCGTCTTCT GGGTTTTGGA GTAATATTCA 4140
CTGTTCTTCC TACAAAGGAT ATATTTGTAA AAGACCAAAA ATTATTGATG CTAAACCTAC 4200
TCATGAATTA CTTACAACAA AAGCTGACAC AAGGAAGATG GACCCTTCTA AACCGTCTTC 4260
CAACGTGGCC GGAGTAGTCA TCATTGTGAT CCTCCTGATT TTAACGGGTG CTGGCCTTGC 4320
CGCCTATTTC TTTTATAAGA AAAGACGTGT GCACCTACCT CAAGAGGGCG CCTTTGAAAA 4380
CACTCTGTAT TTTAACAGTC AGTCAAGCCC AGGAACTAGT GATATGAAAG ATCTCGTGGG 4440
CAATATTGAA CAGAATGAAC ACTCGGTCAT CTAGTACCTC AATGCGATTC TGAGATATTT 4500
GAATTTCATA AAATTGTAAC TGAAATTTAA AATTTTTAGT TCAATGTGAT TGTTTTCTTT 4560
AAAATGAGTA CTGAATTGTA CTGGTCTGTC CTTTTTTCCT TTGCCTAATT GAAGAAATAA 4620
TTGCTTGTTT TCTAGCCTGG CAAGATATTT TCATAAAAGA GGGATAACAA TGCTGATTAC 4680
TACCTTTTAA AATATTTTAG ATAAATGCAC AGCACCACAG CACCACATCT AAGCATTAGT 4740
GATGGGTAGC TGATGTCAGC TTCATGTGGA TTTTAAGCAC TCTAGAAACA ATGAAGCTTC 4800
TTGGCATATT TTAAGGAGCT CCCAAAATGT GTTACCTATT AAATTGTAAC TCAGCAAGTA 4860
GAAGACCATT TGAAAAGTCA GGTACAAATT TCCTCAAGTG GCATAAAAAT GTAGTCAGTT 4920
TTCTCTTTTA CCAGTTTTTA TTTCCACTCC AATTATTTAG AACTTTATTT GTACATGTGC 4980
AGAAGAATAA GGCAGCTGAG AATCTTGTTT CCCCCAAGAG AGTTTTACAG GCTGAGTGTT 5040
GCAAATGTGT TCTTTGTCCT GTTATATGTA TATCAGGAAT ACAAGGATGT GAAATAAAAC 5100
TGTAAATTTG CATAACTGGA TGTACTTAGA TAATGTGAAA TAAACATTAA AGACAAGGTC 5160
TATTTTTAAT AAAAAAAAAA AAAAA 5185

Seq ID NO: C55 DNA Sequence
Nucleic Acid Accession #: NM_024574.2
Coding sequence: 424..2130

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CCCGCCGCCC AGCCCCCGCA CGCTCCCTGC AGTTTAAAAG GACCTCCCGC CGCTTCTCGG  120
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CGCTGCCCCG GGATTCCCCA GCCCCGCGCG GCTCCCTACT CCACTTCGCA GCAACTTCGG   180
CGACCGCGCG CCGCCCGCCC TCGCCCGCCT TTGAAGTTTG CTGTGCCGAC CGCAAAGTTG   240
GGACACTTCA GCGGATTGAA TTTTTCTCTT TTATCTGCCT CCGTCCCCGC CCTCCAGGCT   300
TCTCGTTCCT GGATATTGGT GCTTAGCATC TTGGCAGGGT CCGGGGACGT GGACTATTTC   360
GCACACCACA CCACGGGGAG GGATTTTTTT CTATTTTCCC TACGAAAAAC AGATCTTTTT   420
AAGGATGGTG CTGCTCCACT GGTGCCTGCT GTGGCTCCTG TTTCCACTCA GCTCAAGGAC   480
CCAGAAGTTA CCCACCCGGG ATGAGGAACT TTTTCAGATG CAGATCCGGG ACAAGGCATT   540
TTTTCATGAT TCGTCAGTAA TTCCAGATGG AGCTGAAATT AGCAGTTATC TCTTTAGAGA   600
TACACCTAAA AGGTATTTCT TTGTGGTTGA AGAAGACAAT ACTCCATTAT CAGTCACAGT   660
GACGCCCTGT GATGCGCCTT TGGAGTGGAA GCTGAGCCTC CAGGAGCTGC CAGAGGACAG   720
GAGCGGGGAA GGCTCAGGTG ATCTGGAACC TCTTGAGCAG CAGAAGCAGC AGATCATTAA   780
TGAGGAAGGC ACTGAGTTAT TCTCCTACAA AGGCAATGAT GTTGAGTATT TTATATCGTC   840
TAGTTCCCCA TCCGGTTTAT ATCAGTTGGA TCTTCTTTCA ACAGAGAAAG ACACACATTT   900
CAAAGTATAT GCCACCACAA CTCCAGAATC TGATCAGCCA TACCCTGAGT TACCCTATGA   960
CCCAAGAGTA GATGTGACCT CACTGGGGCG CACCACGGTC ACTTTGGCCT GGAAACCAAG  1020
CCCCACTGCC TCTTTGCTGA AACAACCCAT TCAGTACTGT GTGGTCATCA ACAAAGAGCA  1080
CAATTTCAAA AGTCTCTGTG CAGTGGAAGC AAAACTGAGT GCAGATGATG CTTTTATGAT  1140
GGCACCGAAA CCTGGTCTGG ACTTCAGCCC CTTTGACTTT GCCCACTTTG GATTTCCTTC  1200
TGATAATTCA GGTAAAGAAC GCAGTTTCCA GGCAAAGCCT TCTCCAAAAC TGGGGCGTCA  1260
TGTCTACTCC AGGCCCAAGG TTGATATTCA GAAAATCTGC ATAGGAAACA AGAACATCTT  1320
CACCGTCTCT GATCTGAAAC CCGACACGCA GTACTACTTT GACGTATTTG TGGTCAACAT  1380
CAACAGCAAC ATGAGCACCG CTTATGTAGG TACCTTTGCC AGGACCAAGG AAGAAGCCAA  1440
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CTCTTGTCTG GATGCTGTCC AAATCCAAGT GAGAAGAGAT GGGAAACTTC TTCTGTCTCA  1620
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TCGACTGAAA GGAAACAAGA AAGGAGCATC TATGTTGAAA ATTCTAGCTA CCACAAGGCC  1740
TACTAAGCAG TCATTTCCCT CTCTTCCTGA AGACACAAGA ATCAAAGCCT TTGACAAGCT  1800
CCGTACCTGT TCCTCGGCCA CCGTGGCTTG GCTAGGCACT CAGGAAAGGA ACAAGTTTTG  1860
CATCTACAAA AAAGAAGTGG ATGATAACTA CAATGAAGAC CAGAAGAAAA GAGAGCAAAA  1920
CCAATGTCTA GGACCAGATA TAAGGAAGAA GTCAGAAAAG GTCCTCTGTA AATATTTCCA  1980
CAGTCAAAAC CTGCAGAAAG CAGTGACCAC AGAAACAATT AAAGGTCTTC AGCCTGGCAA  2040
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TAAGGTTGTG AAAACTAGAA AGTTCTGTTA GTTACCTTCT TATAGAGATA TATTATGTAG  2160
AACTCCAGGA GGGACATTAA ATCACTTTAA GTATAAACTG ACTACTCCCA CAGTTGAGAG  2220
AAGTTGTGAC CTGTACTTGT ACTATGGAAG GAAGGATATC AACGTGTGTA TATTGATGTT  2280
TATATAAGTA ACTCTTGAAG GAGACTTGTT CTAGCGTGCC CCATGGTACC TAGTGTGTGT  2340
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TGACCACTGC ATGAACTGCT TCTAAATTAT TTTATTACCT AAAAATTTAA AATATGCCAT  2460
TCATTGCACA CACCCACAAA TGCAAATCAT TCCTCTCTAT AGATGCTAGG ATATATATAA  2520
ATTATTTTAT AAATTCTTGT TTTAAATGTC AGTGTTTCTA TGATTGTAAA CTATTAAATT  2580
CTTTTCCTAT TAAAGTACAG ATCTAATCTA AGTATTATTA AGTTGATAGC CCTCTAGTCA  2640
GTTATATTGC TATTGTAAAT TCTTGTTTGT TGAGTAAAAT GTTTAAATAC TATATGTATC  2700
TCATGTACAA AGTTGACATA CATTATATTC ATGTACATAA AATTAAAGAG ATTAGATTAT  2760
ATACTGTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA               2808
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Seq ID NO: C56 DNA Sequence
Nucleic Acid Accession #: BC034229.1
Coding sequence: 373..1422

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CTTCCTCAGC CTGCTCAATG TGAAGCCCCT GATCATGATT CACTTCCACT TAATAAATAA  120
AGTGTTTACA AATCAGAATA ACTTTTAGAC AATATTAAGG TGGTAATCAT GAACAGAAAA  180
GATTTTGTAG TTCTTCCATG GGGAAAACCT GGAAATTCTG TAAAGCTAAA ATATAGCAAT  240
GTAATAATTA AAACAAAAGT CTAAGATTTG AAGAGATAAT TTGCTTCAGG ATTTTGATGG  300
AAGGCAAATG CTAACTTTAA AAACCAGATT TCGGAGAAGT ACAAAAGAAA TAGAAATGCT  360
CAAGAACTGC GAATGGAGAA AGTACAGTTA GAGTTTGAGA ACCAAGAGAT GGAGAAGAAA  420
CTGCAAGAAT TCCGATCCAC AAGAAACAAA GAAAAGGAAG ATAGAGAGTC AAGCGAGTAT  480
TACTGGAAAT CTGGAAAAGT GGGCAAATTG GTCAATCAAT CATATATGAT GTCACAAAAT  540
AAAGGAAATG TTGTTAAGTT TTCTGCTGGA AAAGTGAAAT TAAAATTGCT GAAGGAACAG  600
ATTCAAGAGC CAGTGAAACC AACAGTTAAT TATAAAATGG CAAATTCTTC AGAATGTGAA  660
AAACCCAAGA TAAATGGGAA AGTTTGTGGA CAGTGTGAGA ACAAAGCTGC TCTACTGGTA  720
TGCCTTGAAT GTGGAGAAGA TTATTGTTCA GGATGCTTTG CTAATGTTCA CCAGAAAGGG  780
GCACTAAAGC TCCACAGAAC AACTCTTTTG CAGGCAAGAT CTCAAATATT ATTCAATGTA  840
TTGGATGTTG CCCATCAGTT TATAAAGGAT GTTAATCCAG ATGAACCCAA AGAGGAGAAT  900
AATTCTACAA AGGAAACCAG TAAAATTCAA CATAAACCCA AATCTGTACT TCTCCAGAGG  960
AGCAGCTCTG AGGTAGAAAT TACAACGATG AAAAGAGCAC AACGTACAAA ACCAAGAAAG 1020
AGTCTGTTGT GTGAAGGGTC ATTCGATGAA GAAGCTTCTG CACAGTCCTT TCAGGAAGTG 1080
TTAAGTCAAT GGAGAACCGG AAATCATGAT GACAACAAGA AACAGAATTT ACATGCAGCA 1140
GTAAAAGACT CATTGGAAGA ATGCGAAGTA CAGACTAATC TGAAAATTTG GAGAGAACCA 1200
CTTAATATTG AACTTAAAGA AGACATTCTA TCCTATATGG AAAAATTATG GCTTAAAAAA 1260
CACAGGAGAA CTCCACAAGA GCAACTTTTT AAATGCTACC AGATACGTTC CCACATCCAC 1320
ATGAAACCAC TGGTGATGCA CAGTGTTCTC AAAATGAAAA CGATGAAGAT AGTGATGGTG 1380
AGGAGACCAA AGTACAACAC ACAGCTCTTT TATTGCCAGT AGAAACATTA AACATAGAGA 1440
GACCTGAACC ATCTCTGAAG ATAGTCGAAC TGGATGATAC TTATGAAGAG GAATTTGAAG 1500
AAGCAGAAAA TATTGTGCCT TACAAAGTTA AATTAGCTGA TGCAGACAGT CAACGAAGTT 1560
GTGCTTTTCA TGATTGTCAG AAGAATAGCT TTCCATATGA AAATGGCATC CATCAACATC 1620
ATGTTTTCGA TAAGGGAAAG AGAGACTTCT TAAATCTTTG TCTGAGAAAC AGCTCTACTT 1680
ATTATAAAGA TAATTCAAAA GGAGAAACTT CAAACACAGA TTTTGACAAC ATCGTGGATC 1740
CTGATGTGTA TTCTTCTGAC ATTGAAAAAA TTGAGGAAAG CACCTCCTTT GAAAGAAATT 1800
TAAAGGAGAA AAATATAGGT TTAGAAAGTA ATCAAAAGTC TGATGATTCC TGTGTATCAC 1860
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TTGAAAGCAA GGACACTTTG CTAGGTAGAG ATTTAGAAAA AGCTCCCATT GAGGAGAAAT   1920
TATCTCAAGA CATCAAAGAA TCCTTGGAAT TGAGCAATCT GTATAAGAGG CCAAGCTTTG   1980
AAGAATCAAA AACTACAAAG TCATCACTGT TGTTACAAGA AATAGCCTGC AGAAGTAAGC   2040
CTATAACAAA ACAATATCAA GGACTTGAGA GATTCTTTAT TTTTGATACA AATGAAAGAC   2100
TCAACTTACT TCCTTCTCAT CGTTTAGAAT GCAACAATTC CAGTACTAGG ATTACACTTG   2160
CAGGTCAGAA ATCACAGAGA CCTTCAACAG CAAATTTTCC ACTTTCCAAC TCTGTTAAAG   2220
AAAGCTCCAG TTGCCTTTCA TCCTCTCATC CTCGATCAAG AAGTGCAGCT GCTCAATCAT   2280
CATCTAGAGC TGCTTCTGAA ATTTCAGAAA TTGAATATAT TGATATTACT GACCAGAATG   2340
AGCTTTCCTT AGATGACACT ACTGATCAAC ATACTTTAGA CAATTTGGAA AAAGAATTAC   2400
AAGTGCTGAG ATCTCTTGCA GATACTTCAG AAAAGCTTTA CAGCTTAACC TCAGAAGAGT   2460
TCCCAGATTT CAGCAGCCAA TCACTGAATA TAAGTCAGAT TTCCACAGAT TTCCTTAAGA   2520
CCTCACATGT GAGGGGTCCC TGTGGAGTTG AGGAATTGAG CTGTTCTGGA AGAGATACCA   2580
AAATTCAGTC TTTGCTGTCA CTTTCTGAGA GCAGTACAGA TGAGGAGGAG GAAGATTTTC   2640
TCAACAAGCA ACATGTCATC ACACTACCGT GGTCAAAGAG TACTTAAAGA TTATTTGTTC   2700
ATTACTGTTT CCATTTTGTA CCCAGAGTAA AGCAAACAAC TGAGAAAAGT AACCAAGTGA   2760
TTACCTATCC AAGTGCTGGA GATTTTGATT ACTAATGTCT TTGATGTTTC AAGGCTACAA   2820
ACTAATAAAA GTAAAATTAT AAGTTCAAAA AAATTTTTAA AAAAAAAAAT AAAAAA       2876
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Seq ID NO: C57 DNA Sequence
Nucleic Acid Accession #: NM_024687.1
Coding sequence: 138..1706

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AAGACATTCT ATCCTATATG GAAAAATTAT GGCTTAAAAA ACACAGGAGA ACTCCACAAG   180
AGCAACTTTT TAAAATGCTA TCAGATACGT TCCCACATCC ACATGAAACC ACTGGTGATG   240
CACAGTGTTC TCAAAATGAA AACGATGAAG ATAGTGATGG TGAGGAGACC AAAGTACAAC   300
ACACAGCTCT TTTATTGCCA GTAGAAACAT TAAACATAGA GAGACCTGAA CCATCTCTGA   360
AGATAGTCGA ACTGGATGAT ACTTATGAAG AGGAATTTGA AGAAGCAGAA AATATTGTGC   420
CTTACAAAGT TAAATTAGCT GATGCAGACA GTCAACGAAG TTGTGCTTTT CATGATTGTC   480
AGAAGAATAG CTTTCCATAT GAAAATGGCA TCCATCAACA TCATGTTTTC GATAAGGGAA   540
AGAGAGACTT CTTAAATCTT TGTCTGAGAA ACAGCTCTAC TTATTATAAA GATAATTCAA   600
AAGGAGAAAC TTCAAACACA GATTTTGACA ACATCGTGGA TCCTGATGTG TATTCTTCTG   660
ACATTGAAAA AATTGAGGAA AGCACCTCCT TTGAAAGAAA TTTAAAGGAG AAAAATATAG   720
GTTTAGAAAG TAATCAAAAG TCTGATGATT CCTGTGTATC ACTTGAAAGC AAGGACACTT   780
TGCTAGGTAG AGATTTAGAA AAAGCTCCCA TTGAGGAGAA ATTATCTCAA GACATCAAAG   840
AATCCTTGGA ATTGAGCAAT CTGTATAAGA GGCCAAGCTT TGAAGAATCA AAAACTACAA   900
AGTCATCACT GTTGTTACAA GAAATAGCCT GCAGAAGTAA GCCTATAACA AAACAATATC   960
AAGGACTTGA GAGATTCTTT ATTTTTGATA CAAATGAAAG ACTCAACTTA CTTCCTTCTC   1020
ATCGTTTAGA ATGCAACAAT TCCAGTACTA GGATTACACT TGCAGAAGAC AGAGAATGGA   1080
TTCCAGACCA TAGCTTAAGT GAATATGCTG ATAATGCAAT TGTCTTGGGT GTTCTGCAGG   1140
GTGCTCAGAG TCCATCATCA AGTAGAAAAC AGCAAAAGAT GGGTCAGAAA TCACAGAGAC   1200
CTTCAACAGC AAATTTTCCA CTTTCCAACT CTGTTAAAGA AAGCTCCAGT TGCCTTTCAT   1260
CCTCTCATCC TCGATCAAGA AGTGCAGCTG CTCAATCATC ATCTAGAGCT GCTTCTGAAA   1320
TTTCAGAAAT TGAATATATT GATATTACTG ACCAGAATGA GCTTTCCTTA GATGACACTA   1380
CTGATCAACA TACTTTAGAC AATTTGGAAA AAGAATTACA AGTGCTGAGA TCTCTTGCAG   1440
ATACTTCAGA AAAGCTTTAC AGCTTAACCT CAGAAGAGTT CCCAGATTTC AGCAGCCAAT   1500
CACTGAATAT AAGTCAGATT TCCACAGATT TCCTTAAGAC CTCACATGTG AGGGGTCCCT   1560
GTGGAGTTGA GGAATTGAGC TGTTCTGGAA GAGATACCAA AATTCAGTCT TTGCTGTCAC   1620
TTTCTGAGAG CAGTACAGAT GAGGAGGAGG AAGATTTTCT CAACAAGCAA CATGTCATCA   1680
CACTACCGTG GTCAAAGAGT ACTTAAAGAT TATTTGTTCA TTACTGTTTC CATTTTGTAC   1740
CCAGAGTAAA GCAAACAACT GAGAAAAGTA ACCAAGTGAT TACCTATCCA AGTGCTGGAG   1800
ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAATAAAAG TAAAATTATA   1860
AGTTCAAAAA AAAAAAAAAA AAAA                                          1884
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Seq ID NO: C58 DNA Sequence
Nucleic Acid Accession #: NM_005408.1
Coding sequence: 76..372

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CTCTTAACCT TCAACATGAA AGTCTCTGCA GTGCTTCTGT GCCTGCTGCT CATGACAGCA   120
GCTTTCAACC CCCAGGGACT TGCTCAGCCA GATGCACTCA ACGTCCCATC TACTTGCTGC   180
TTCACATTTA GCAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACCACC   240
AGCAGGTGTC CCCAGAAGGC TGTCATCTTC AGAACCAAAC TGGGCAAGGA GATCTGTGCT   300
GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCCGGAA AGCTCACACC   360
CTGAAGACTT GAACTCTGCT ACCCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT   420
TCCATTCTCC TCTGGCCTCC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT   480
AGGATGCATT CGGTTTTGTG ATTCAAAATG TACTATGTGT TAAGTAATAT TGGCTATTAT   540
TTGACTTGTT GCTGGTTTGG AGTTTATTTG AGTATTGCTG ATCTTTTCTA AAGCAAGGCC   600
TTGAGCAAGT AGGTTGCTGT CTCTAAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT   660
GGGTTTGTAT TCGGTTCCCA GGGGTTGAGA GCATGCCTGT GGGAGTCATG GACATGAAGG   720
GATGCTGCAA TGTAGGAAGG AGAGCTCTTT GTGAATGTGA GGTGTTGCTA AATATGTTAT   780
TGTGGAAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATTT   840
AAAATCTCCA AAAAAAAAAA                                               860
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Seq ID NO: C59 DNA Sequence
Nucleic Acid Accession #: AK097746.1
Coding sequence: 185..2224

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ATTTTCCTTT TTATTATGTG CCAATCTTCT TCTGGCAAGG AAAGAGATTG AATACCAGGA   180
ACTGATGTTT CTTTTAACTG GAGGAGTAAG TCTTAAAAGT GCTGAGAAAA ATCCTGATCC   240
AACTTGGCTA CAGGACAAAA GCTGGGAGGA AATCTGTCGG GCAAGTGAAT TTCCTGCCTT   300
CAGAGGACTC AGGCAACATT TTTGTGAACA TATATATGAA TGGCGAGAAA TCTATGACAG   360
TAAAGAGCCA CATAATGCTA AATTTCCAGC ACCAATGGAT AAGAACCTAA ATGAACTACA   420
GAAAATAATA ATTCTTCGGT GTTTAAGACC TGATAAGATA ACCCCAGCTA TAACAAACTA   480
TGTAACTGAC AAACTAGGGA AAAAGTTTGT AGAGCCTCCA CCATTTGATT TGACAAAGAG   540
TTACTTGGAT TCAAATTGCA CCATTCCCTT AATTTTTGTT CTATCTCCAG GAGCAGATCC   600
TATGGCCAGC CTGCTGAAAT TTGCAAATGA TAAATCTATG TCTGGAAATA AGTTTCAAGC   660
TATTTCACTG GGACAGGGAC AAGGACCGAT TGCAGCAAAA ATGATTAAAG CAGCAATTGA   720
AGAAGGAACT TGGGTGTGCC TACAGAATTG CCATCTTGCA GTGTCCTGGA TGCCCATGTT   780
GGAAAAAATA TGTGAAGATT TTACCTCTGA AACCTGTAAC TCATCCTTTA GGCTTTGGCT   840
GACAAGCTAT CCATCTTCAA AATTCCCAGT AACAATTCTA CAGAATGGAG TAAAAATGAC   900
TAATGAACCT CCCACGGGTC TTCGGCTGAA TCTCCTTCAA TCATATCTCA CTGATCCAGT   960
TTCTGATCCT GAGTTTTTCA AGGGATGCCG TGGAAAGGAA CTGTTATTTA TCAATGAATA   1020
TGATACAATT CCATTTGAAG CTATATCTTA CCTGACTGGG GAGTGTAATT ATGGAGGAAG   1080
AGTGACAGAC GATTGGGACA GACGTCTTCT ATTAACCATG CTGGCTGACT TTTATAATCT   1140
GTACATAGTT GAAAACCCTC ATTATAAGTT TTCTCCCAGT GGAAACTATT TTGCACCTCC   1200
TAAAGGCACT TATGAGGACT ACATTGAATT CATTAAGAAA CTTCCATTTA CTCAACACCC   1260
TGAGATATTT GGATTACATG AAAACGTTGA CATCTCCAAG GATCTTCAAC AAACAAAAAC   1320
CCTCTTTGAG TCCTTGCTCC TCACCCAGGG AGGCTCCAAA CAGACAGGAG CCTCAGGAAG   1380
TACTGATCAG ATTCTGTTAG AAATTACCAA AGATATCCTC AACAAGCTCC CTAGTGATTT   1440
CGACATTGAA ATGGCACTAC GGAAGTATCC TGTGAGATAT GAAGAAAGCA TGAATACTGT   1500
GTTAGTACAA GAAATGGAAA GATTTAACAA TTTAATTATA ACTATACGTA ACACTCTACG   1560
GGACCTTGAA AAAGCTATTA AGGGTGTGGT TGTGATGGAT TCTGCATTGG AGGCACTCTC   1620
CAGTAGCTTA CTTGTTGGAA ATGCCTACGA AATATGGGCC AAACGTTCAT ACCCAAGCCT   1680
TAAGCCCCTG GGAAGTTACA TCACAGATTT CCTAGCCCGG TTGAACTTTT TACAGGACTG   1740
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TTTAACTGGA GCTATGCAGA ATTATGCCAG AAAATATACC ACCCCTATTG ATTTGCTAGG   1860
ATATGAATTT GAGGTTATCC CATCTGATAC ATCTGACACA TCACCAGAAG ATGGTGTTTA   1920
TATCCACGGA CTGTATCTCG ATGGCGCACG CTGGGACCGA GAAAGTGGAT TGCTTGCTGA   1980
ACAATATCCC AAACTTCTGT TTGACCTGAT GCCCATCATA TGGATAAAAC CAACTCAAAA   2040
ATCTCGGATT ATAAAGTCGG ATGCCTATGT CTGTCCCCTC TACAAGACAA GTGAACGTAA   2100
AGGAACTCTT TCCACTACGG GACATTCTAC TAACTTTGTC ATTGCAATGT TGTTAAAAAC   2160
AGACCAACCT ACTCGGCACT GGATCAAGCG CGGGGTTGCT TTGCTTTGTC AGTTGGATGA   2220
CTAAATTGGA CAAATTTATA AAACATCCAA AAGTTT                             2256
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Seq ID NO: C60 DNA Sequence
Nucleic Acid Accession #: J02761.1
Coding sequence: 14..1159

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GCTCTGTGGC CCAGGCACTG CTGCCTGGAC CACCTCATCC TTGGCCTGTG CCCAGGGCCC   120
TGAGTTCTGG TGCCAAAGCC TGGAGCAAGC ATTGCAGTGC AGAGCCCTAG GGCATTGCCT   180
ACAGGAAGTC TGGGGACATG TGGGAGCCGA TGACCTATGC CAAGAGTGTG AGGACATCGT   240
CCACATCCTT AACAAGATGG CCAAGGAGGC CATTTTCCAG GACACGATGA GGAAGTTCCT   300
GGAGCAGGAG TGCAACGTCC TCCCCTTGAA GCTGCTCATG CCCCAGTGCA ACCAAGTGCT   360
TGACGACTAC TTCCCCCTGG TCATCGACTA CTTCCAGAAC CAGACTGACT CAAACGGCAT   420
CTGTATGCAC CTGGGCCTGT GCAAATCCCG GCAGCCAGAG CCAGAGCAGG AGCCAGGGAT   480
GTCAGACCCC CTGCCCAAAC CTCTGCGGGA CCCTCTGCCA GACCCTCTGC TGGACAAGCT   540
CGTCCTCCCT GTGCTGCCCG GGGCCCTCCA GGCGAGGCCT GGGCCTCACA CACAGGATCT   600
CTCCGAGCAG CAATTCCCCA TTCCTCTCCC CTATTGCTGG CTCTGCAGGG CTCTGATCAA   660
GCGGATCCAA GCCATGATTC CCAAGGGTGC GCTAGCTGTG GCAGTGGCCC AGGTGTGCCG   720
CGTGGTACCT CTGGTGGCGG GCGGCATCTG CCAGTGCCTG GCTGAGCGCT ACTCCGTCAT   780
CCTGCTCGAC ACGCTGCTGG GCCGCATGCT GCCCCAGCTG GTCTGCCGCC TCGTCCTCCG   840
GTGCTCCATG GATGACAGCG CTGGCCCAAG GTCGCCGACA GGAGAATGGC TGCCGCGAGA   900
CTCTGAGTGC CACCTCTGCA TGTCCGTGAC CACCCAGGCC GGGAACAGCA GCGAGCAGGC   960
CATACCACAG GCAATGCTCC AGGCCTGTGT TGGCTCCTGG CTGGACAGGG AAAAGTGCAA   1020
GCAATTTGTG GAGCAGCACA CGCCCCAGCT GCTGACCCTG GTGCCCAGGG GCTGGGATGC   1080
CCACACCACC TGCCAGGCCC TCGGGGTGTG TGGGACCATG TCCAGCCCTC TCCAGTGTAT   1140
CCACAGCCCC GACCTTTGAT GAGAACTCAG CTGTCCAGCT GCAAAGGAAA AGCCAAGTGA   1200
GACGGGCTCT GGGACCATGG TGACCAGGCT CTTCCCCTGC TCCCTGGCCC TCGCCAGCTG   1260
CCAGGCTGAA AAGAAGCCTC AGCTCCCACA CCGCCCTCCT CACCTCCCTT CCTCGGCAGT   1320
CACTTCCACT GGTGGACCAC GGGCCCCCAG CCCTGTGTCG GCCTTGTCTG TCTCAGCTCA   1380
ACCACAGTCT GACACCAGAG CCCACTTCCA TCCTCTCTGG TGTGAGGCAC AGCGAGGGCA   1440
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AAAAACCAGC CACTGCTTTA CAGGACAGGG GGTTGAAGCT GAGCCCCGCC TCACACCCAC   1560
CCCCATGCAC TCAAAGATTG GATTTTACAG CTACTTGCAA TTCAAAATTC AGAAGAATAA   1620
AAAATGGGAA CATACAGAAC TCTAAAAGAT AGACATCAGA AATTGTTAAG TTAAGCTTTT   1680
TCAAAAAATC AGCAATTCCC CAGCGTAGTC AAGGGTGGAC ACTGCACGCT CTGGCATGAT   1740
GGGATGGCGA CCGGGCAAGC TTTCTTCCTC GAGATGCTCT GCTGCTTGAG AGCTATTGCT   1800
TTGTTAAGAT ATAAAAAGGG GTTTCTTTTT GTCTTTCTGT AAGGTGGACT TCCAGATTTT   1860
GATTGAAAGT CCTAGGGTGA TTCTATTTCT GCTGTGATTT ATCTGCTGAA AGCTCAGCTG   1920
GGGTTGTGCA AGCTAGGGAC CCATTCCTGT GTAATACAAT GTCTGCACCA ATGCTAATAA   1980
AGTCCTATTC TCTTTTAAAA AAAAAAAAAA AAAAAAAACG GAATTC                  2026
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Seq ID NO: C61 DNA Sequence

Nucleic Acid Accession #: NM_139172.1
Coding sequence: 19..552

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GGGGTCTGGG GAGGTGACAT GTTGGGCTGT GGGATCCCAG CGCTGGGCCT GCTCCTGCTG   60
CTGCAGGGCT CGGCAGACGG AAATGGAATC CAGGGATTCT TCTACCCATG GAGCTGTGAG  120
GGTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC  180
TGCCTGCGTC TCCGGTGCTG CTACCGCAAT GGGGTCTGCT ACCACCAGCG TCCAGACGAA  240
AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGGACGT GCAGCGGCCT CCTCCTCCTG  300
AGCTGCAGCA TCTGCTTGTT CTGGTGGGCC AAGCGCCGGG ACGTGCTGCA TATGCCCGGT  360
TTCCTGGCGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCAA GCACCGAGGG  420
ACCAAGAAGA CGCCGTCCAC GGGCAGCGTG CCAGTCGCCC TGTCCAAAGA GTCCAGGGAT  480
GTGGAGGGAG GCACCGAGGG GGAAGGGACG GAGGAGGGTG AGGAGACAGA GGGCGAGGAA  540
GAGGAGGATT AGGGGAGTCC CCGGGGGACT GCTCAATACA GATACGGTGG ACG          593
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Seq ID NO: C62 DNA Sequence
Nucleic Acid Accession #: NM_054023.2
Coding sequence: 98..379

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ATTTTTAAAC TCCTGAAAAA TATCCCAGAT AACTGTCATG AAGCTGGTAA CTATCTTCCT  120
GCTGGTGACC ATCAGCCTTT GTAGTTACTC TGCTACTGCC TTCCTCATCA ACAAAGTGCC  180
CCTTCCTGTT GACAAGTTGG CACCTTTACC TCTGGACAAC ATTCTTCCCT TTATGGATCC  240
ATTAAAGCTT CTTCTGAAAA CTCTGGGCAT TTCTGTTGAG CACCTTGTGG AGGGGCTAAG  300
GAAGTGTGTA AATGAGCTGG GACCAGAGGC TTCTGAAGCT GTGAAGAAAC TGCTGGAGGC  360
GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGGAAGATGA  420
TGCTCCTATC CTCCCTGCCT GAAACCTGTT CTACCAATTA TAGATCAAAT GCCCTAAAAT  480
GTAGTGACCC GTGAAAAGGA CAAATAAAGC AATGAATACT AAAAAAAAAA AAAAAAAAAA  540
AAAAAAAAAA                                                          550
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Seq ID NO: C63 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2874

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TGGATGTCGA GAGGAGCATA TCAGCGGAGG AACACACGGG CAGCTGGACG TCCAGAGGAA  120
TGCACTGACA GAAACTGGCA TGCTGGCAGA ACACGTGGAA TTTGGCTGGG GCAGTTGGAG  180
GAGAGATGTT CAGATGTGTT CGGAGTTTCT TTCTTCTGGT GGGTTCGTGG TCTCGCTGGC  240
TCAGGAGCGA AGCTGCAGAC CTTCACGCCA GCCCAGGAAG GGGCTCCCAC AGTGCAGCGG  300
CAGGCTGAAG CGCTCCTCAA GTGCCGCCAG AGTGGGCGTC CAGGCAGAGG AGGCGCCGAG  360
AGCGAGCGAG CGAGGGATGC CAGCATGCTG TCACCTCTCA GTGCTGCCAT GCGAAACTAC  420
CCAACGTCCT CTACCATCCC TCCAAGAAGA TCCTACTCTC CAACCGAAAT TGCTCACAAG  480
AGTTACTCCT GCAGCCTTCC AGACATGAAA ATCTCCATGG CAGAATCTGG CCCCTCCTTG  540
GATAGCCTTG ACATTCTGGA GGATGGCGAG TCTGGGTCAC CATTTCTTGT GACTCATTTG  600
TACTTTCTGG GGGTTGTCAC CACTGGGATG GAACAACTAG ATTTTGAAAC AGGACCAAAC  660
ATATTTGATT TGCAGATTTA TGTGAAGGAT GAGGTTGGTG TCACAGACCT GCAAGTCCTG  720
ACTGTCCAGG TAACAGATGT GAACGAGCCA CCTCAGTTTC AAGGCAACTT GGCAGAAGAT  780
CATCTCCGTG CAGACCAGCC ACATTTCAAT GCTCATAGTC ACACGTACGT GAGGGTAGTG  840
GCTACTGCAT TGGCCAGGCA CAGGCTTAGA TCTAGCATTG GTTCCCCCTT CCTGGGCACC  900
TTCTGTGTTG TGGTGGGCAT GCAGTATTTC CTGATTTCTC CCCCAAAGAG CTTCAGAATG  960
TCTGCTAATG GCACCCTCTT CTCCACAACA GAATTGGACT TTGAAGCAGG ACACAGAAGT 1020
TTCCATCTCA TCGTGGAGGT GAGGGACAGT GGAGGCCTCA AAGCCTCCAC AGAGCTCCAG 1080
GTGAACATCG TGAACCTCAA CGACGAAGTC CCTCGCTTTA CCAGCCCGAC ACGAGTGTAC 1140
ACAGTCCTGG AGGAACTGAG TCCAGGAACC ATCGTGGCCA ATATCACAGC GGAGGATCCT 1200
GATGATGAAG GTTTTCCCAG CCACCTCCTC TACAGCATTA CCACTGTTAG CAAATATTTC 1260
ATGATAAATC AGTTGACTGG TACAATCCAA GTGGCCCAAA GGATAGACCG AGATGCAGGT 1320
GAATTGAGAC AAAATCCCAC CATTTCCCTG GAAGTTCTAG TGAAGGACAG ACCATATGGG 1380
GGTCAGGAGA ATCGCATCCA GATAACCTTC ATTGTGGAAG ACGTCAACGA CAATCCTGCC 1440
ACATGCCAAA AGTTCACCTT CAGATCCAGT CTCCACCCTG CTCTGTGCTC CAAGACGCTG 1500
ACCTGGATGG ATACCGTATT AGACTGTTTT CATGCTGCTG ATAAAGATAT ACCTGTGACT 1560
GGGCGATTTA CAAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAAGC 1620
CTCACAATCA TGGCAGAAGG CAAGGAGGAG CAAGTCACAT CTTACATGGA TGGCAGCAGG 1680
CAAAGAGATA GAGCTTGTGT AGGGAAACTC CTCCTTATAA AGCCATCAGA TCTCATGAGA 1740
CTTAGTCACT ATCACGAGAA CAACTCAGGA AAGACTTGCC CCCATGATTC CATTTCCTCC 1800
TACCAGGTCC CTCCCACAAC ATGTAGGAAT TCAAGAATCC AGGCCACCAA CAACGAAGAC 1860
ACAAGCTCTG TCACTGTTAC TGTGAACATC CTTGAAGAAA ATGATGAAAA GCCAATTTGT 1920
ACTCCAAACT CTTATTTCCT GGCCCTCCCA GTGGATCTGA AAGTTGGCAC AAATATTCAG 1980
AATTTCAAGC TGACATGTAC CGACCTTGAT TCCAGCCCCA GATCTTTCCG TTATTCCATT 2040
GGCCCAGGTA ACGTCAACAA TCATTTCACC TTCTCTCCCA ATGCTGGTTC CAATGTCACA 2100
CGCCTGCTGC TTACATCTCG CTTTGACTAT GCTGGTGGGT TTGATAAGAT CTGGGACTAC 2160
AAGCTACTTG TCTACGTAAC TGATGACAAC TTGATGTCTG ACAGGAAGAA AGCGGAGGCT 2220
CTTGTTGAGA CAGGAACAGT GACACTGAGT ATTAAAGTCA TTCCCCACCC AACCACTATC 2280
ATCACCACGA CCCCCAGGCC CAGGGTCACC TATCAGGTCC TGAGGAAAAA CGTTTACTCT 2340
CCATCTGCAT GGTACGTGCC GTTTGTCATC ACTTTGGGCT CCATATTGCT TCTGGGTCTC 2400
CTCGTGTACC TGGTCGTCCT ATTGGCCAAA GCCATCCACA GACACTGCCC CTGCAAGACT 2460
GGGAAGAACA AGGAACCTCT GACAAAGAAA GGAGAAACGA AGACTGCAGA GAGAGACGTC 2520
GTGGTGGAAA CTATCCAGAT GAACACTATC TTTGATGGAG AAGCCATAGA TCCAGAGCCT 2580
GAGCAAGCTT CACTCGAGCT CTATGCCCTG CTGCCCAGCT GCTGCGACCC TAGTCCAGTA 2640
ACCCTAAGAA AGGTCCAGGT GTGTGGGGAG AGTGAAGAGA CCGGTCAGTG TTCCGGCCAC 2700
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ATCACACTTC CCGGCAAGAT TCCAGTCGAT GACCCAAGGA AACAGGAAAC AGGCCTGCAG   2760
GGTGATTTCG AGGTCTGGAC TCTATGCCCC GCTGTGAAGG TGGTTGTAGG CAGCCCTCAA   2820
GCTGAACGGT GCATTCGATT GGCTCTCAGT CTGAAAAAGT ACAGTTCTGA TTAA         2874
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Seq ID NO: C64 DNA Sequence
Nucleic Acid Accession #: XM_168571.1
Coding sequence: 155..988

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CCTGATGATG AAGGTTTTCC CAGCCACCTC CTCTACAGCA TTACCACTGT TAGCAAATAT   120
TTCATGATAA ATCAGTTGAC TGGTACAATC CAAGTGGCCC AAAGGATAGA CCGAGATGCA   180
GGTGAATTGA GACAAAATCC CACCATTTCC CTGGAAGTTC TAGTGAAGGA CAGACCATAT   240
GGGGGTCAGG AGAATCGCAT CCAGATAACC TTCATTGTGG AAGACGTCAA CGACAATCCT   300
GCCACATGCC AAAAGTTCAC CTTCAGCATT ATGGTGCCGG AAAGAACAGC CAAGGGGACG   360
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TTCAACTTCA CCATGCCATC TGGAGTGGGG AGCGGCAGCA GATTTTTACA GGATCCAGCT   480
GGCTCTGGGA AGATTGTGCT GATTGGTGAT CTAGACTACG AAAATCCAAG TAACCTAGCA   540
GCCGGCAATA AATATACGGT GATAATCCAG GTGCAGGATG TGGCCCCCCC TTACTATAAA   600
AATAACGTCT ACGTTTATAT CCTAACAAGC CCAGAAAATG AGTTTCCTCT CATTTTTGAT   660
AGGCCATCCT ATGTATTTGA TGTGTCAGAA AGAAGGCCCG CCCAGGGTCA CCTATCAGGT   720
CCTGAGGAAA AACGTTTACT CTCCATCTGC ATGGTACGTG CCGTTTGTCA TCACTTTGGG   780
CTCCATATTG CTTCTGGGTC TCCTCGTGTA CCTGGTCGTC CTATTGGCCA AAGCCATCCA   840
CAGACACTGC CCCTGCAAGA CTGGGAAGAA CAAGGAACCT CTGACAAAGA AAGGAGAAAC   900
GAAGACTGCA GAGAGAGACG TCGTGGTGGA AACTATCCAG ATGAACACTA TCTTTGATGG   960
AGAAGCCATA GATCCAGTGA CCGGGGAAAC ATATGAATTC AACTCAAAAA CTGGAGCCAG   1020
AAAGTGGAAA GATCCACTAA CCCAAATGCC AAAATGGAAA GAGTCCAGCC ACCAGGGAGC   1080
TGCCCCACGC AGAGTCACTG CTGGGGAAGG GATGGGGTCA CTGAGAAGTG CCAACTGGGA   1140
AGAAGATGAG CTGAGTGGCA AAGCGTGGGC TGAGGATGCT GGTCTGGGTT CCAGAAATGA   1200
GGGTGGCAAG CTGGGCAACC CAAAGAACAG AAATCCAGCC TTCATGAACA GGGCTTACCC   1260
CAAACCACAC CCAGGAAAGT AAACGGGGTC TAAGGAGGGG CCTGTCAATC ACTGAGATGC   1320
TGCCTCACCC TAAATTCTAT GGGGATGGTG TGGGCATGGT GTAGGGGGGA AAATGTGGGC   1380
TGAGGGGATT CAGACATCCA GGGTCAAACA TGGGATGTTT GACAAATTTT TAAACAAATA   1440
GAAAGGGGTT TGATCACATA GTTGCGTGTT CTGAAATGAT ACAGGAACAT TTTCTATCAG   1500
ATTTCAGAAC TACCTGTGCT TCTGATAAGC AAGACTGTTA ACTTTGGGGT GTGGAATTGT   1560
TGTGTTTCTT CTTTGCATTG ACTGCTAGGA AGCTCTATTC TGTTCACCAT AGAAAGTTTG   1620
TAGGAATTCC TGACATAAAT AGTGAAGACT ATCCTTACAT CTGGTTTCCA CCTTATTTTC   1680
CTGCCCTCGT TTTAACATCA CCCAGATTTC TTCAGTTATA AATATGCCAT ACACCTTTGT   1740
AAGTCACCTC AAATCTTCTT CAAAAGAAGC AGAACAGTGA AAAAAACAGA TGAGTAAGTT   1800
AAGAGTTGGT CATCTGGAAA GAAGAAAACT CAGTAGGCAC CTTCTTTTGT TTTTTCTTGT   1860
GGTGTCCGGA TCAGCATCCT GCATGTGAGA TTCATCCACG TTGTCCTGTC TAGCAGTAGT   1920
TCAGTTCTCT TCATGGTTAT GTCTGGTTTC ATTCTATGAT TATATCACAA TTTATCTATT   1980
CTACACTTGG GTGGCAGCTG CTTCAGATTT TTTACTTTTA AAAAATATAC TTAAAAGTGA   2040
ACTACAGGCA GGGCATGATG GCTCATGCCT GTAATGCCAG CACTTTGCCA AGGTGGGCAG   2100
ATCACCTAAG GTCAGGAGTT CAAGATCAGC CTGGCCTAGA TGGCAAAACC CTGTCTCTAC   2160
TAAAAAATAC AAAAATTAGC TTGGTGTGGT GGTGGGCACA TGTAATCCCA GCTACTTGGG   2220
AGGCTGAGGT AGGGAGAACT GCTTAAACCT GAGAGGTGGA GGTTACAGTG AGTTGAGATT   2280
GTGCCACTGC ACTCTAGCCT GGGTGACAAA GCAAGACTCC ATCTCAGAAA AAAAAAATAA   2340
AAGTGAATTA CAACACT                                                  2357
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Seq ID NO: C65 DNA Sequence
Nucleic Acid Accession #: NM_005266.3
Coding sequence: 122..1198

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ACACAAGGCA GCAAGCACTG GGAGACGAAA GTTTTGGCAT CTGTTCCCTG GCTGTGCCAA   120
GATGGGCGAT TGGAGCTTCC TGGGAAATTT CCTGGAGGAA GTACACAAGC ACTCGACCGT   180
GGTAGGCAAG GTCTGGCTCA CTGTCCTCTT CATATTCCGT ATGCTCGTGC TGGGCACAGC   240
TGCTGAGTCT TCCTGGGGGG ATGAGCAGGC TGATTTCCGG TGTGATACGA TTCAGCCTGG   300
CTGCCAGAAT GTCTGCTACG ACCAGGCTTT CCCCATCTCC CACATTCGCT ACTGGGTGCT   360
GCAGATCATC TTCGTCTCCA CGCCCTCTCT GGTGTACATG GGCCACGCCA TGCACACTGT   420
GCGCATGCAG GAGAAGCGCA AGCTACGGGA GGCCGAGAGG GCCAAAGAGG TCCGGGGCTC   480
TGGCTCTTAC GAGTACCCGG TGGCAGAGAA GGCAGAACTG TCCTGCTGGG AGGAAGGGAA   540
TGGAAGGATT GCCCTCCAGG GCACTCTGCT CAACACCTAT GTGTGCAGCA TCCTGATCCG   600
CACCACCATG GAGGTGGGCT TCATTGTGGG CCAGTACTTC ATCTACGGAA TCTTCCTGAC   660
CACCCTGCAT GTCTGCCGCA GGAGTCCCTG TCCCCACCCG GTCAACTGTT ACGTATCCCG   720
GCCCACAGAG AAGAATGTCT TCATTGTCTT TATGCTGGCT GTGGCTGCAC TGTCCCTCCT   780
CCTTAGCCTG GCTGAACTCT ACCACCTGGG CTGGAAGAAG ATCAGACAGC GATTTGTCAA   840
ACCGCGGCAG CACATGGCTA AGTGCCAGCT TTCTGGCCCC TCTGTGGGCA TAGTCCAGAG   900
CTGCACACCA CCCCCCGACT TTAATCAGTG CCTGGAGAAT GGCCCTGGGG GAAAATTCTT   960
CAATCCCTTC AGCAATAATA TGGCCTCCCA ACAAAACACA GACAACCTGG TCACCGAGCA   1020
AGTACGAGGT CAGGAGCAGA CTCCTGGGGA AGGTTTCATC CAGGTTCGTT ATGGCCAGAA   1080
GCCTGAGGTG CCCAATGGAG TCTCACCAGG TCACCGCCTT CCCCATGGCT ATCATAGTGA   1140
CAAGCGACGT CTTAGTAAGG CCAGCAGCAA GGCAAGGTCA GATGACCTAT CAGTGTGACC   1200
CTCCTTTATG GGAGGATCAG GACCAGGTGG GAACAAAGGA GGCTCAGAGA GGAAAGACGT   1260
GTCCCTTCTG AACTGATGCT TTCTCACTGT CATCACTGCT TGGCTCCTTT GAGCCCCGGG   1320
TCTCAATGAC GTTGCTCATT AATTCTAGAA ACTATAACCA GGGCTCTGGG ATAGTAAGAG   1380
AGGTGACAAC CCACCCAGAC TGCAGTTCCC TCCCCACCCT CTACCCAGTA TACGAAGCCT   1440
TTCAGATTAC TCATGAAACA GGGTAGAGGG AAAGAAGGGA AGCATGGCAA AAGCTGGCCT   1500
GGAAGGGATA GCCAGAGGGA TAGAATGACT CTCTCTCTAC ATACCAGCAG CATACCAAAT   1560
GCGTTCTCTA AGTTCCTACC TCCTTGACCT GATCACCCTC CCTCCTCCAA GGAAGAGCTC   1620
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AAAGTTCCCA GCCAATAGAC AGCATGAATC AAGGAACTTG CATTATATGT GCTCTTGAAT   1680
CTGTTGTCTC CATGGACCAT TCCTCGGAGT AGTGGTGAGA TGGCCTTGGG TTGCCCTTGG   1740
CTTCTCCTCC CTCTACTCAG CCTTAAAAAG GGCTTCTTGG AACTTTACCA GCAGCCTCAG   1800
CTTTACAAAT GCCTTGGTAT GTACCTCTGG CAAATGCCCT GGTATGTACC TCTGGCAAAT   1860
GCCCCACCTT GGTGATGTTG CAACCTTTCC TTCTGCTAGG GTGTACACCT AGCCTGTGCA   1920
GGTGTCAGCC CTGCTAGGGA GTCACTGTAC ACACAAACTC TACTGGAATT CCTGCCAACA   1980
TCTGTCACCC TGCAGCTCCT TTACAGTTCA ATCCAATGAT AGAAACCATC CCTTCCCTTT   2040
CTCCCTTGGC TGTTCACCCA GCCATTCCCT GAAGGCCTTA CCAACAGGAA TATCCAAGAA   2100
GCTGTTGTCC TCTCTCGAAC CCTGACCAGA TCATCAGCCA CTGAGGCCAG TGGAATTTCC   2160
CCAGGCCTTG TTAAAAAAAA AAAAAAAAAA                                    2190

Seq ID NO: C66 DNA Sequence
Nucleic Acid Accession #: NM_014459.2
Coding sequence: 738..3407

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TTTCATCACG GGAGGCGAGC AGCAAGTAAG AATTTCACTT TCGGATCTGC CTAGAGACAC   240
ACCTCCCTGC TCCCTCCCCC ACTCGATGTG AAGAGTATTC CGGAGTCTCC GGGCGGGAGT   300
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CTCTCCCAGA CGAGATTTCC TTCTTATCGC CTGCCTCATC GCTCAAGTTT GAGCCTCCCG   420
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TGCTCCAAGC CCCTGCAGCT CTGCTGCACC GCAGCTTCTC ACCCAGTGCG GATGCTGTAG   540
ATCAACAGGT TCAGGGAACT TGAGCAGAAT AAGGAGAGAC CACCGGGTGC CGCAGCTCGG   600
GTGCAGAGGG AAAAAAGGAC CCATAGACTT GTGGCTCGCG TCGCGCGCGC ACGCTGCGCC   660
AGGGCCCCAG GCTGGCGCGC ACTCCCTCTC TGGCTCCTCC AGTCCGATTG CTCCTGCCCC   720
CACCTTACAG GTCTGGGATG TACCTTTCCA TCTGTTGCTG CTTTCTTCTA TGGGCCCCTG   780
CCCTCACTCT CAAGAACCTC AACTACTCCG TGCCGGAGGA GCAAGGGGCC GGCACGGTGA   840
TCGGGAACAT CGGCAGGGAT GCTCGACTGC AGCCTGGGCT TCCGCCTGCA GAGCGCGGCG   900
GCGGAGGGCG CAGCAAGTCG GGTAGCTACC GGGTGCTGGA GAACTCCGCA CCGCACCTGC   960
TGGACGTGGA CGCAGACAGC GGGCTCCTCT ACACCAAGCA GCGCATCGAC CGCGAGTCCC   1020
TGTGCCGCCA CAATGCCAAG TGCCAGCTGT CCCTCGAGGT GTTCGCCAAC GACAAGGAGA   1080
TCTGCATGAT CAAGGTAGAG ATCCAGGACA TCAACGACAA CGCGCCCTCC TTCTCCTCGG   1140
ACCAGATCGA AATGGACATC TCGGAGAACG CTGCTCCGGG CACCCGCTTC CCCCTCACCA   1200
GCGCACATGA CCCCGACGCC GGCGAGAATG GGCTCCGCAC CTACCTGCTC ACGCGCGACG   1260
ATCACGGCCT CTTTGGACTG GACGTTAAGT CCCGCGGCGA CGGCACCAAG TTCCCAGAAC   1320
TGGTCATCCA GAAGGCTCTG GACCGCGAGC AACAGAATCA CCATACGCTC GTGCTGACTG   1380
CCCTGGACGG TGGCGAGCCT CCACGTTCCG CCACCGTACA GATCAACGTG AAGGTGATTG   1440
ACTCCAACGA CAACAGCCCG GTCTTCGAGG CGCCATCCTA CTTGGTGGAA CTGCCCGAGA   1500
ACGCTCCGCT GGGTACAGTG GTCATCGATC TGAACGCCAC CGACGCCGAT GAAGGTCCCA   1560
ATGGTGAAGT GCTCTACTCT TTCAGCAGCT ACGTGCCTGA CCGCGTGCGG GAGCTCTTCT   1620
CCATCGACCC CAAGACCGGC CTAATCCGTG TGAAGGGCAA TCTGGACTAT GAGGAAAACG   1680
GGATGCTGGA GATTGACGTG CAGGCCCGAG ACCTGGGGCC TAACCCTATC CCAGCCCACT   1740
GCAAAGTCAC GGTCAAGCTC ATCGACCGCA ACGACAATGC GCCGTCCATC GGTTTCGTCT   1800
CCGTGCGCCA GGGGGCGCTG AGCGAGGCCG CCCCTCCCGG CACCGTCATC GCCCTGGTGC   1860
GGGTCACTGA CCGGGACTCT GGCAAGAACG GACAGCTGCA GTGTCGGGTC CTAGGCGGAG   1920
GAGGGACGGG CGGCGGCGGG GGCCTGGGCG GGCCCGGGGG TTCCGTCCCC TTCAAGCTTG   1980
AGGAGAACTA CGACAACTTC TACACGGTGG TGACTGACCG CCCGCTGGAC CGCGAGACAC   2040
AAGACGAGTA CAACGTGACC ATCGTGGCGC GGGACGGGGG CTCTCCTCCC CTCAACTCCA   2100
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GGCTCTACGT GCTTCAGGTG CACGAGAACA ACATCCCGGG AGAGTACCTG GGCTCTGTGC   2220
TCGCCCAGGA TCCCGACCTG GGCCAGAACG GCACCGTATC CTACTCTATC CTGCCCTCGC   2280
ACATCGGCGA CGTGTCTATC TACACCTATG TGTCTGTGAA TCCCACGAAC GGGGCCATCT   2340
ACGCCCTGCG CTCCTTTAAC TTCGAGCAGA CCAAGGCTTT TGAGTTCAAG GTGCTTGCTA   2400
AGGACTCGGG GGCGCCCGCG CACTTGGAGA GCAACGCCAC GGTGAGGGTG ACAGTGCTAG   2460
ACGTGAATGA CAACGCGCCA GTGATCGTGC TCCCCACGCT GCAGAACGAC ACCGCGGAGC   2520
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GCGACTTCGG CGAGAGCGGG CGTCTCACCT ACGAGATCGT GGACGGCAAC GACGACCACC   2640
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TGACGCCCGT GGTGGAGCTG GTGGTGAAGG TGACCGACCA CGGCAAGCCT ACCCTGTCCG   2760
CAGTGGCCAA GCTCATCATC CGCTCGGTGA GCGGATCCCT TCCCGAGGGG GTACCACGGG   2820
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ATCTCAAACC GGCCTCCAAC AACCTGACTG TCCCTCAGGG GCACGCGGGC TGCCACACCA   3240
GCTTCACCGG ACAAGGGACT AATGCAAGCG AGACCCCTGC CACTCGGATG TCCATAATTC   3300
AGACAGACAA TTTTCCCGCA GAGCCCAATT ACATGGGCAG CAGGCAGCAG TTTGTTCAAA   3360
GTATTTCAGT AGCTCCACGT TTAAGGACCC AGAAAGAGCC AGCCTGAGAG ACAGTGGGCA   3420
CGGGGACAGT GATCAGGCTG ACAGTGACCA AGACACTAAC AAAGGCTCCT GCTGTGACAT   3480
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TCTCTTTGTA CCTACAGTTG AAGCTAATGT TGAGACTGAG ACTTACGAAA CTGTGAATCC   3720
CACTGGGAAA AAGACTTTTT GTACATTTGG AAAAGACAAG CGAGAGCACA CTATTCTCAT   3780
TGCCAACGTT AAACCTTATT TAAAAGCCAA ACGTGCCCTG AGCCCTCTCC TCCAAGAGGT   3840
CCCCTCAGCA TCAAGCAGCC CAACCAAGGC GTGCATCGAG CCTTGCACCT CAACAAAAGG   3900
CTCCCTGGAT GGCTGTGAAG CAAAACCAGG AGCCCTGGCT GAAGCAAGCA GTCAGTACTT   3960
GCCCACTGAC AGTCAATATC TGTCACCTAG TAAGCAACCA AGAGACCCTC CCTTCATGGC   4020
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CGACCCTGTG GCTGTGAGAA AGTGAAAAAA GAAAAAAAAA AAGGCATTGG CATTTTCTTG   4260
TCTCTTCTGT TGATTTAAAA ATGATCCCTC CTGGTGATAA CCCATTTTAC AGGGATGAAG   4320
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CTGTTTACCT ATAAACCCCA TACAAAGCAG GGTCATAATT TGTGATCTGT GGTGGATTTC   4680
TAGCAGTCAT CACAGGCTTC TACTGAAAGT CCTGAAAAGA CCTTGCAGTA GTCCAAGCTA   4740
CACCAAACAT TAACACATAT TTGTGGTAAA CATTTCTGTA TAAAGTTACC TGACACACAT   4800
ATAAACACAA GGAACATTCC ATATCATTAG TCGAAAACAA AAACAAAAAA AAAACCTTTG   4860
GTCATTTGTA AGACATCTCA TGTCATATAA AAGTTAAATG TAAAAAGATA CAGTCCATTT   4920
TGTCCTGCAC ACACGTAGAC TAATTCACGT CAAAAAAAAA AAAAAA                  4966
```

Seq ID NO: C67 DNA Sequence
Nucleic Acid Accession #: NM_005601.2
Coding sequence: 101..598

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1          11         21         31         41         51
|          |          |          |          |          |
CCCAGGAGTC TGGGTGCACA GCCTCCTTCT CTCTGAGATT CAAGAGTCTG ATCAGCAGCC   60
TCTTCCTCCT CCAGGACCCA GAAGCCCTGA GCTTATCCCC ATGGAGCTCT GCCGGTCCCT   120
GGCCCTGCTG GGGGGCTCCC TGGGCCTGAT GTTCTGCCTG ATTGCTTTGA GCACCGATTT   180
CTGGTTTGAG GCTGTGGGTC CCACCCACTC AGCTCACTCG GGCCTCTGGC CAACAGGGCA   240
TGGGGACATC ATATCAGGCT ACATCCACGT GACGCAGACC TTCAGCATTA TGGCTGTTCT   300
GTGGGCCCTG GTGTCCGTGA GCTTCCTGGT CCTGTCCTGC TTCCCCTCAC TGTTCCCCCC   360
AGGCCACGGC CCGCTTGTCT CAACCACCGC AGCCTTTGCT GCAGCCATCT CCATGGTGGT   420
GGCCATGGCG GTGTACACCA GCGAGCGGTG GGACCAGCCT CCACACCCCC AGATCCAGAC   480
CTTCTTCTCC TGGTCCTTCT ACCTGGGCTG GGTCTCAGCT ATCCTCTTGC TCTGTACAGG   540
TGCCCTGAGC CTGGGTGCTC ACTGTGGCGG TCCCCGTCCT GGCTATGAAA CCTTGTGAGC   600
AGAAGGCAAG AGCGGCAAGA TGAGTTTTGA GCGTTGTATT CCAAAGGCCT CATCTGGAGC   660
CTCGGGAAAG TCTGGTCCTA CATTTGCCCG CCCTTCCAGC CCTTCCCCAG CCCCTCCTCT   720
TGTTTCTTCA TTCATTCAAC AAAATTTGGC TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA   780
AAA                                                                783
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Seq ID NO: C68 DNA Sequence
Nucleic Acid Accession #: NM_006433.2
Coding sequence: 129..566

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1          11         21         31         41         51
|          |          |          |          |          |
GTATCTGTGG TAAACCCAGT GACACGGGGG AGATGACATA CAAAAAGGGC AGGACCTGAG   60
AAAGATTAAG CTGCAGGCTC CCTGCCCATA AAACAGGGTG TGAAAGGCAT CTCAGCGGCT   120
GCCCCACCAT GGCTACCTGG GCCCTCCTGC TCCTTGCAGC CATGCTCCTG GGCAACCCAG   180
GTCTGGTCTT CTCTCGTCTG AGCCCTGAGT ACTACGACCT GGCAAGAGCC CACCTGCGTG   240
ATGAGGAGAA ATCCTGCCCG TGCCTGGCCC AGGAGGGCCC CCAGGGTGAC CTGTTGACCA   300
AAACACAGGA GCTGGGCCGT GACTACAGGA CCTGTCTGAC GATAGTCCAA AAACTGAAGA   360
AGATGGTGGA TAAGCCCACC CAGAGAAGTG TTTCCAATGC TGCGACCCGG GTGTGTAGGA   420
CGGGGAGGTC ACGATGGCGC GACGTCTGCA GAAATTTCAT GAGGAGGTAT CAGTCTAGAG   480
TTACCCAGGG CCTCGTGGCC GGAGAAACTG CCCAGCAGAT CTGTGAGGAC CTCAGGTTGT   540
GTATACCTTC TACAGGTCCC CTCTGAGCCC TCTCACCTTG TCCTGTGGAA GAAGCACAGG   600
CTCCTGTCCT CAGATCCCGG GAACCTCAGC AACCTCTGCC GGCTCCTCGC TTCCTCGATC   660
CAGAATCCAC TCTCCAGTCT CCCTCCCCTG ACTCCCTCTG CTGTCCTCCC CTCTCACGAG   720
AATAAAGTGT CAAGCAAG                                                738
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Seq ID NO: C69 DNA Sequence
Nucleic Acid Accession #: NM_002985.2
Coding sequence: 69..344

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1          11         21         31         41         51
|          |          |          |          |          |
GCTGCAGAGG ATTCCTGCAG AGGATCAAGA CAGCACGTGG ACCTCGCACA GCCTCTCCCA   60
CAGGTACCAT GAAGGTCTCC GCGGCAGCCC TCGCTGTCAT CCTCATTGCT ACTGCCCTCT   120
GCGCTCCTGC ATCTGCCTCC CCATATTCCT CGGACACCAC ACCCTGCTGC TTTGCCTACA   180
TTGCCCGCCC ACTGCCCCGT GCCCACATCA AGGAGTATTT CTACACCAGT GGCAAGTGCT   240
CCAACCCAGC AGTCGTCTTT GTCACCCGAA AGAACCGCCA AGTGTGTGCC AACCCAGAGA   300
AGAAATGGGT TCGGGAGTAC ATCAACTCTT TGGAGATGAG CTAGGATGGA GAGTCCTTGA   360
ACCTGAACTT ACACAAATTT GCCTGTTTCT GCTTGCTCTT GTCCTAGCTT GGGAGGCTTC   420
CCCTCACTAT CCTACCCCAC CCGCTCCTTG AAGGGCCCAG ATTCTACCAC ACAGCAGCAG   480
TTACAAAAAC CTTCCCCAGG CTGGACGTGG TGGCTCACGC CTGTAATCCC AGCACTTTGG   540
GAGGCCAAGG TGGGTGGATC ACTTGAGGTC AGGAGTTCGA GACCAGCCTG GCCAACATGA   600
TGAAACCCCA TCTCTACTAA AAATACAAAA AATTAGCCGG GCGTGGTAGC GGGCGCCTGT   660
AGTCCCAGCT ACTCGGGAGG CTGAGGCAGG AGAATGGCGT GAACCCGGGA GGCGGAGCTT   720
GCAGTGAGCC GAGATCGCGC CACTGCACTC CAGCCTGGGC GACAGAGCGA GACTCCGTCT   780
CAAAAAAAAA AAAAAAAAAA AAAATACAAA AATTAGCCGG GCGTGGTGGC CCACGCCTGT   840
AATCCCAGCT ACTCGGGAGG CTAAGGCAGG AAAATTGTTT GAACCCAGGA GGTGGAGGCT   900
GCAGTGAGCT GAGATTGTGC CACTTCACTC CAGCCTGGGT GACAAAGTGA GACTCCGTCA   960
CAACAACAAC AACAAAAAGC TTCCCCAACT AAAGCCTAGA AGAGCTTCTG AGGCGCTGCT   1020
TTGTCAAAAG GAAGTCTCTA GGTTCTGAGC TCTGGCTTTG CCTTGGCTTT GCCAGGGCTC   1080
```

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TGTGACCAGG AAGGAAGTCA GCATGCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACTC   1140
TTAAGCTTCC GCCGTCTCAA CCCCTCACAG GAGCTTACTG GCAAACATGA AAAATCGGCT   1200
TACCATTAAA GTTCTCAATG CAACCATAAA AAAAAAA                            1237
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Seq ID NO: C70 DNA Sequence
Nucleic Acid Accession #: NM_022154.2
Coding sequence: 1381..1722

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CATATGTACG CAAATCCTGG GGCGTTTGCA AACCCGGATC CGGGGCGTCT GGCCCCATGC   120
CCGGCCGGGC GTTTGAGGGC TACTGCCACG CAGCGTTTCT GGAGCCTGCC GGCTGGTGCC   180
CTGGTGGCCT TTATCTCTGT CCCCCTTTGT CCTCTTTATC TCAGGCTCTC CAGGAGGCCG   240
GGGGGCCCAC TCCGCCTATC GCTCCCCTCG GCTACGCTGC CACTCCAATG CCCCGCAGGT   300
CGCGAGCTGC TGTTCTTTCG AAGGCGCCGG AGAACCAGGG GCGTCCCGCG CCACCTCTGA   360
CTCGGAGCAG CGCCGAGCAC TGACGCTCCC GCCCTTGGGC AAGGACGCCA GTGCGCCCGC   420
GCGCGTCCCT CTGCGCGGCA GCCCGTCGCG GGCCCTCAAG GGGAAGCCCA GGCCAGGATG   480
GCCCCGGGTC GCGCGGTGGC CGGGCTCCTG TTGCTGGCGG CCGCCGGCCT CGGAGGAGTG   540
GCGGAGGGGC CAGGGCTAGC CTTCAGCGAG GATGTGCTGA GCGTGTTCGG CGCGAATCTG   600
AGCCTGTCGG CGGCGCAGCT CCAGCACTTG CTGGAGCAGA TGGGAGCCGC CTCCCGCGTG   660
GGCGTCCCGG AGCCTGGCCA GCTGCACTTC AACCAGTGTT TAACTGCTGA AGAGATCTTT   720
TCCCTTCATG GCTTTTCAAA TGCTACCCAA ATAACCAGCT CCAAATTCTC TGTCATCTGT   780
CCAGCAGTCT TACAGCAATT GAACTTTCAC CCATGTGAGG ATCGGCCCAA GCACAAAACA   840
AGACCAAGTC ATTCAGAAGT TTGGGGATAT GGATTCCTGT CAGTGACGAT TATTAATCTG   900
GCATCTCTCC TCGGATTGAT TTTGACTCCA CTGATAAAGA AATCTTATTT CCCAAAGATT   960
TTGACCTTTT TTGTGGGGCT GGCTATTGGG ACTCTTTTTT CAAATGCAAT TTTCCAACTT   1020
ATTCCAGAGG CATTTGGATT TGATCCCAAA GTCGACAGTT ATGTTGAGAA GGCAGTTGCT   1080
GTGTTTGGTG GATTTTACCT ACTTTTCTTT TTTGAAAGAA TGCTAAAGAT GTTATTAAAG   1140
ACATATGGTC AGAATGGTCA TACCCACTTT GGAAATGATA ACTTTGGTCC TCAAGAAAAA   1200
ACTCATCAAC CTAAAGCATT ACCTGCCATC AATGGTGTGA CATGCTATGC AAATCCTGCT   1260
GTCACAGAAG CTAATGGACA TATCCATTTT GATAATGTCA GTGTGGTATC TCTACAGGAT   1320
GGAAAAAAAG AGCCAAGTTC ATGTACCTGT TTGAAGGGGC CCAAACTGTC AGAAATAGGG   1380
ACGATTGCCT GGATGATAAC GCTCTGCGAT GCCCTCCACA ATTTCATCGA TGGCCTGGCG   1440
ATTGGGGCTT CCTGCACCTT GTCTCTCCTT CAGGGACTCA GTACTTCCAT AGCAATCCTA   1500
TGTGAGGAGT TTCCCCACGA GTTAGGAGAC TTTGTGATCC TACTCAATGC AGGGATGAGC   1560
ACTCGACAAG CCTTGCTATT CAACTTCCTT TCTGCATGTT CCTGCTATGT TGGGCTAGCT   1620
TTTGGCATTT TGGTGGGCAA CAATTTCGCT CCAAATATTA TATTTGCACT TGCTGGAGGC   1680
ATGTTCCTCT ATATTTCTCT GGCAGATATG TTTCCAGAGA TGAATGATAT GCTGAGAGAA   1740
AAGGTAACTG GAAGAAAAAC CGATTTCACC TTCTTCATGA TTCAGAATGC TGGAATGTTA   1800
ACTGGATTCA CAGCCATTCT ACTCATTACC TTGTATGCAG GAGAAATCGA ATTGGAGTAA   1860
TAGAAAATGG AAGATGGTGT TGTTAATAAA GGCATTTAAT AGATAAAAAC ATCTCCAAAA   1920
AGGATTTTGA AGCTGATCCT ATTTAGTTAA AAAGATAATT TTGCTTTCAA CTGTAGGTCC   1980
AGAAAACTAA TTATTGGCAT CAGTCTGTGA AATAGTCCAT TATTTGTTGT TAAAAATGCT   2040
TCAAAAGGTT TTCAGTGTCA GTCTGAGATG CCTGGTATAT AGGAGCCTTT GGGAAATACT   2100
TATTTTTCAG TATTCCATGC ATATTAGATA TCACCATGAA GCAAGAGACA TGCATTCTAT   2160
AATCATGTAG ACACTCAGAC TCAGGGGAAA ATACAAGTTA TATCCTGAAA GCCTTTAAAA   2220
CTCTATGGTA GGATCAAAGA TTCAAATGGT TTCAGAGAGG TTTTATTTCA ATTAATTTGT   2280
TCTAGTGCTT TCAAGAGCAA GTACATCAAA ATGTAGAAGG TAAAATGTAT GCAACACTAA   2340
TATAAATTAT TCCAAGTCTT TAAGGAGCCA AAGAAAAAAA AGATTTCTCA CAGCTTTTTG   2400
TTCTGTTTTG TATTTCAATT AGGAACTTGC AGTATTATTT TGAAAACCAT TCTAAAATAA   2460
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TCGCTAAGTN TAAACTTCAC CAGATTCCAC GAAAAGCTGG ATAGCTTTTT TTCTGACTTA   2580
TGTTGTGGTT GCACCCCTCA CAAATGGCAG AACAGTATGT AAAGCTGGTA ACACCTCGGT   2640
TTCAGTGCAC CATGTGTTTG CTTTGTGAAG GTGAAGAATA TGTTGGTTTA GAGAAAGAAA   2700
TTGGATGTAA TTTTATGCAA TTTACTTTTA AAGACAAACA TAACTATTTA GCAGAGAATA   2760
TTTTAATAAA TGCAAAACAA CAGCTGGACT GCTGTACATC AAGGACAGAT TAACTGGAAA   2820
ACATATGTTC CTTATGTGTG ATTGAGAGCC ATTCAGAAAA GACTTCCTTT GTGTTCAGCC   2880
TATACTTTTC CATATGGTAT ACCTTGAAAA AAATTAGCAC ACCATGGTTA TTTTTCTACC   2940
TTTTATAAAA GACAGAGCCT GTTTACTCAT TTAGAAGATA GAGAAAATTG GTCTAAAATT   3000
GAACATCCTA GATTCACACT CCCAAGTCAC TTAAGGTGAT TTGATGGTGA GGAAAATGAT   3060
TGACAAAGCC CAACAATGAT CTCAGGAATT ACATTTTCCA ACAGACCAAA AAATGTTTTC   3120
ATGTAGCAGC AATGCAGATT TGGTGAATAT TTAATATATA TTTTAGTATG TATTTCACTT   3180
TATGACTGAC AATTAAAAAA TATTGTTTGG CCAAATAGTA AACACCCTTT TGAAACCATG   3240
AAAAAA                                                             3246
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Seq ID NO: C71 DNA Sequence
Nucleic Acid Accession #: NM_004184.2
Coding sequence: 188..1603

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CTCAACTGCC CAGCGTGACC AGTGGCCACC TCTGCAGTGT CTTCCACAAC CTGGTCTTGA   120
CTCGTCTGCT GAACAAATCC TCTGACCTCA GGCCGGCTGT GAACGTAGTT CCTGAGAGAT   180
AGCAAACATG CCCAACAGTG AGCCCGCATC TCTGCTGGAG CTGTTCAACA GCATCGCCAC   240
ACAAGGGGAG CTCGTAAGGT CCCTCAAAGC GGGAAATGCG TCAAAGGATG AAATTGATTC   300
TGCAGTAAAG ATGTTGGTGT CATTAAAAAT GAGCTACAAA GCTGCCGCGG GGGAGGATTA   360
CAAGGCTGAC TGTCCTCCAG GGAACCCAGC ACCTACCAGT AATCATGGCC CAGATGCCAC   420
AGAAGCTGAA GAGGATTTTG TGGACCCATG GACAGTACAG ACAAGCAGTG CAAAAGGCAT   480
AGACTACGAT AAGCTCATTG TTCGGTTTGG AAGTAGTAAA ATTGACAAAG AGCTAATAAA   540
CCGAATAGAG AGAGCCACCG GCCAAAGACC ACACCACTTC CTGCGCAGAG GCATCTTCTT   600
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CTCACACAGA GATATGAATC AGGTTCTTGA TGCCTATGAA AATAAGAAGC CATTTTATCT 660
GTACACGGGC CGGGGCCCCT CTTCTGAAGC AATGCATGTA GGTCACCTCA TTCCATTTAT 720
TTTCACAAAG TGGCTCCAGG ATGTATTTAA CGTGCCCTTG GTCATCCAGA TGACGGATGA 780
CGAGAAGTAT CTGTGGAAGG ACCTGACCCT GGACCAGGCC TATGGCGATG CTGTTGAGAA 840
TGCCAAGGAC ATCATCGCCT GTGGCTTTGA CATCAACAAG ACTTTCATAT TCTCTGACCT 900
GGACTACATG GGGATGAGCT CAGGTTTCTA CAAAAATGTG GTGAAGATTC AAAAGCATGT 960
TACCTTCAAC CAAGTGAAAG GCATTTTCGG CTTCACTGAC AGCGACTGCA TTGGGAAGAT 1020
CAGTTTTCCT GCCATCCAGG CTGCTCCCTC CTTCAGCAAC TCATTCCCAC AGATCTTCCG 1080
AGACAGGACG GATATCCAGT GCCTTATCCC ATGTGCCATT GACCAGGATC CTTACTTTAG 1140
AATGACAAGG GACGTCGCCC CCAGGATCGG CTATCCTAAA CCAGCCCTGT TGCACTCCAC 1200
CTTCTTCCCA GCCCTGCAGG GCGCCCAGAC CAAAATGAGT GCCAGCGACC CAAACTCCTC 1260
CATCTTCCTC ACCGACACGG CCAAGCAGAT CAAAACCAAG GTCAATAAGC ATGCGTTTTC 1320
TGGAGGGAGA GACACCATCG AGGAGCACAG GCAGTTTGGG GGCAACTGTG ATGTGGACGT 1380
GTCTTTCATG TACCTGACCT TCTTCCTCGA GGACGACGAC AAGCTCGAGC AGATCAGGAA 1440
GGATTACACC AGCGGAGCCA TGCTCACCGG TGAGCTCAAG AAGGCACTCA TAGAGGTTCT 1500
GCAGCCCTTG ATCGCAGAGC ACCAGGCCCG GCGCAAGGAG GTCACGGATG AGATAGTGAA 1560
AGAGTTCATG ACTCCCCGGA AGCTGTCCTT CGACTTTCAG TAGCACTCGT TTTACATATG 1620
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CCACCTGTAG GCTTCTGTCT CATGGTAATT ACTGGGCCTG GCCTCTGTAA GCCTGTGTAT 1740
GTTATCAATA CTGTTTCTTC CTGTGAGTTC CATTATTTCT ATCTCTTATG GGCAAAGCAT 1800
TGTGGGTAAT TGGTGCTGGC TAACATTGCA TGGTCGGATA GAGAAGTCCA GCTGTGAGTC 1860
TCTCCCCAAA GCAGCCCCAC AGTGGAGCCT TCGGCTGGAA GTCCATGGGC CACCCTGTTC 1920
TTGTCCATGG AGGACTTCCG AGGGTTCCAA GTATACTCTT AAGACCCACT CTGTTTAAAA 1980
ATATATATTC TATGTATGCG TATATGGAAT TGAAATGTCA TTATTGTAAC CTAGAAAGTG 2040
CTTTGAAATA TTGATGTGGG GAGGTTTATT GAGCACAAGA TGTATTTCAG CCCATGCCCC 2100
CTCCCAAAAA GAAATTGATA AGTAAAAGCT TCGTTATACA TTTGACTAAG AAATCACCCA 2160
GCTTTAAAGC TGCTTTTAAC AATGAAGATT GAACAGAGTT CAGCAATTTT GATTAAATTA 2220
AGACTTGGGG GTGAAACTTT CCAGTTTACT GAACTCCAGA CCATGCATGT AGTCCACTCC 2280
AGAAATCATG CTCGCTTCCC TTGGCACACC AGTGTTCTCC TGCCAAATGA CCCTAGACCC 2340
TCTGTCCTGC AGAGTCAGGG TGGCTTTTCC CCTGACTGTG TCCGATGCCA AGGAGTCCTG 2400
GCCTCCGCAG ATGCTTCATT TTGACCCTTG GCTGCAGTGG AAGTCAGCAC AGAGCAGTGC 2460
CCTGGCTGTG TCCTGGACGG GTGGACTTAG CTAGGGAGAA AGTCGAGGCA GCAGCCCTCG 2520
AGGCCCTCAC AGATGTCTAG GCAGGCCTCA TTTCATCACG CAGCATGTGC AGGCCTGGAA 2580
GAGCAAAGCC AAATCTCAGG GAAGTCCTTG GTTGATGTAT CTGGGTCTCC TCTGGAGCAC 2640
TCTGCCCTCC TGTCACCCAG TAGAGTAAAT AAACTTCCTT GGCTCCTAAA AAA 2693

Seq ID NO: C72 DNA Sequence
Nucleic Acid Accession #: NM_004938.1
Coding sequence: 337..4632

1 11 21 31 41 51

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GCCTCCGACA GCGCTCCGGA GGGACCGGGG GAGCTCCCAG GCGCCCGGGA CTGGAGACTG 240
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AGTCCCCTGG GCTTTGGTGA GGCGTGACAG TTTATCATGA CCGTGTTCAG GCAGGAAAAC 360
GTGGATGATT ACTACGACAC CGGCGAGGAA CTTGGCAGTG GACAGTTTGC GGTTGTGAAG 420
AAATGCCGTG AGAAAAGTAC CGGCCTCCAG TATGCCGCCA AATTCATCAA GAAAAGGAGG 480
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AAGGAGATCC AGCACCCCAA TGTCATCACC CTGCACGAGG TCTATGAGAA CAAGACGGAC 600
GTCATCCTGA TCTTGGAACT CGTTGCAGGT GGCGAGCTGT TTGACTTCTT AGCTGAAAAG 660
GAATCTTTAA CTGAAGAGGA AGCAACTGAA TTTCTCAAAC AAATTCTTAA TGGTGTTTAC 720
TACCTGCACT CCCTTCAAAT CGCCCACTTT GATCTTAAGC CTGAGAACAT AATGCTTTTG 780
GATAGAAATG TCCCCAAACC TCGGATCAAG ATCATTGACT TTGGGTTGGC CCATAAAATT 840
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ATCCATGCCA TCAACGATGA CAATGTCCCA GGCCTGCAGC ACCTTCTGGG CTCATTATCC 1440
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CACGGCTATT ACTCTGTGGC CAAAGCCCTT TGTGAAGCCG GCTGTAACGT GAACATCAAG 1860
AACCGAGAAG GAGAGACGCC CCTCCTGACA GCCTCTGCCA GGGGCTACCA CGACATCGTG 1920
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GATACGCACC GAGGACTCTT CATCCAGCAG CTCCGACCCA CACAGAACCT GCAGCCAAGA 2400
ATTAAGCTCA AGCTGTTTGG CCACTCGGGA TCCGGGAAAA CCACCCTTGT AGAATCTCTC 2460
AAGTGTGGGC TGCTGAGGAG CTTTTTCAGA AGGCGTCGGC CCAGACTGTC TTCCACCAAC 2520

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TCCAGCAGGT TCCCACCTTC ACCCCTGGCT TCTAAGCCCA CAGTCTCAGT GAGCATCAAC   2580
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GATTTCAGCG TGTGGGAGTT CTCTGGAAAT CCTGTGTATT TCTGCTGTTA TGACTATTTT   2820
GCTGCAAATG ATCCCACGTC AATCCATGTT GTTGTCTTTA GTCTAGAAGA GCCCTATGAG   2880
ATCCAGCTGA ACCCAGTGAT TTTCTGGCTC AGTTTCCTGA AGTCCCTTGT CCCAGTTGAA   2940
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CACGCTGACA TCATGAATGT TCCTCGACCG GCTGGAGGCG AGTTTGGATA TGACAAAGAC   3060
ACATCGTTGC TGAAAGAGAT TAGGAACAGG TTTGGAAATG ATCTTCACAT TTCAAATAAG   3120
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CTGCAAGAAA TACGAAGCCA GATTGTTTCG GTCTGTCCTC CCATGACTCA CCTGTGTGAG   3240
AAAATCATCT CCACGCTGCC TTCCTGGAGG AAGCTCAATG GACCCAACCA GCTGATGTCG   3300
CTGCAGCAGT TTGTGTACGA CGTGCAGGAC CAGCTGAACC CCCTGGCCAG CGAGGAGGAC   3360
CTCAGGCGCA TTGCTCAGCA GCTCCACAGC ACAGGCGAGA TCAACATCAT GCAAAGTGAA   3420
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CCAGGGCTCC TGACCGTGAA GCATTACCTG AGCCCCCAGC AGCTGCGGGA GCACCATGAG   4080
CCCGTCATGA TCTACCAGCC ACGGGACTTC TTCCGGGCAC AGACTCTGAA GGAAACCTCA   4140
CTGACCAACA CCATGGGGGG GTACAAGGAA AGCTTCAGCA GCATCATGTG CTTCGGGTGT   4200
CACGACGTCT ACTCACAGGC CAGCCTCGGC ATGGACATCC ATGCATCAGA CCTGAACCTC   4260
CTCACTCGGA GGAAACTGAG TCGCCTGCTG GACCCGCCCG ACCCCCTGGG GAAGGACTGG   4320
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TACCCTGAGA GCACAGTGGG CACCCTCATG TCCAAACTGA GGGAGCTGGG TCGCCGGGAT   4500
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CAGGAGGCCT ATGCCTCGAG CTGCAACAGC GGCACCTCTT ACAATTCCAT TAGCTCTGTT   4620
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GGGTGATGTA GCCCATCCTT CCCTTTGGAG ATGCTGAGGG TGTTTCTTCC TGCACCCACA   4740
GCCAGGGGGA TGCCACTCCT CCCTCCGGCT TGACCTGTTT CTCTGCCGCT ACCTCCCTCC   4800
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CTCCAGTACC TTGCTTCTTA CTGATAATTT TGCTGGAATT CCTAACTTTT CAATGACATT   4980
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TGTATTTCTT ATACGCTTTT CTGTGTTATA CCATTTCCTC AGCTTATCTC TTTTATATTT   5100
GTAGGAGAAA CTCCCATGTA TGGAATCCCA CTGTATGATT TATAAACAGA CAATATGTGA   5160
GTGCCTTTTG CAGAAGAGGG TGTGTTTGAA ATCATCGGAG TCAGCCAGGA GCTGTCACCA   5220
AGGAAACGCT ACCTCTCTGT CCCTTGCTGT ATGCTGATCA TCGCCAGAGG TGCTTCACCC   5280
TGAGTTTTGT TTTGTATTGT TTTCTGACAG TTTTTCTGTT TTGTTTGGCA AGGAAAGGGG   5340
AGAAGGGAAT CCTCCTCCAG GGTGATTTTA TGATCAGTGT TGTTGCTCTA GGAAGACATT   5400
TTTCCGTTTG CTTTTGTTCC AATGTCAATG TGAACGTCCA CATGAAACCT ACACACTGTC   5460
ATGCTTCATC ATTCCCTCTC ATCTCAGGTA GAAGGTTGAC ACAGTTGTAG GGTTACAGAG   5520
ACCTATGTAA GAATTCAGAA GACCCCTGAC TCATCATTTG TGGCAGTCCC TTATAATTGG   5580
TGCATAGCAG ATGGTTTCCA CATTTAGATC CTGGTTTCAT AACTTCCTGT ACTTGAAGTC   5640
TAAAAGCAGA AAATAAAGGA AGCAAGTTTT CTTCCATGAT TTTAAATTGT GATCGAGTTT   5700
TAAATTGATA GGAGGGAACA TGTCCTAATT CTTCTGTCCT GAGAAGCATG TAATGTTAAT   5760
GTTATATCAT ATGTATATAT ATATATGCAC TATGTATATA CATATATATT AATACTGGTA   5820
TTTTTACTTA ATCTATAAAA TGTCGTTAAA AAGTTGTTTG TTTTTTTCTT TTTTTATAAA   5880
TAAACTGTTG CTCGTTAAAA AAAAAAAAAA                                    5910
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Seq ID NO: C73 DNA Sequence
Nucleic Acid Accession #: NM_002081.1
Coding sequence: 222..1898

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GGCTTTTGTT GTCTCCGCCT CCTCGGCCGC CGCCGCCTCT GGACCGCGAG CCGCGCGCGC   120
CGGGACCTTG GCTCTGCCCT TCGCGGGCGG GAACTGCGCA GGACCCGGCC AGGATCCGAG   180
AGAGGCGCGG GCGGGTGGCC GGGGGCGCCG CCGGCCCCGC CATGGAGCTC CGGGCCCGAG   240
GCTGGTGGCT GCTATGTGCG GCCGCAGCGC TGGTCGCCTG CGCCCGCGGG GACCCGGCCA   300
GCAAGAGCCG GAGCTGCGGC GAGGTCCGCC AGATCTACGG AGCCAAGGGC TTCAGCCTGA   360
GCGACGTGCC CCAGGCGGAG ATCTCGGGTG AGCACCTGCG GATCTGTCCC CAGGGCTACA   420
CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA   480
CCGCGCTCCG GGACAGCAGC CGCGTCCTGC AGGCCATGCT TGCCACCCAG CTGCGCAGCT   540
TCGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC   600
CCGGCGCCTT CGGAGAGCTG TACACGCAGA ACGCGAGGGC CTTCCGGGAC CTGTACTCAG   660
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GGGCCCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCCTGATG   780
ACTACCTGGA CTGCCTGGGC AAGCAGGCCG AGGCGCTGCG GCCCTTCGGG GAGGCCCCGA   840
GAGAGCTGCG CCTGCGGGCC ACCCGTGCCT TCGTGGCTGC TCGCTCCTTT GTGCAGGGCC   900
TGGGCGTGGC CAGCGACGTG GTCCGGAAAG TGGCTCAGGT CCCCCTGGGC CCGGAGTGCT   960
CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCCT GGGAGTCCCC GGCGCCAGGC   1020
CCTGCCCTGA CTATTGCCGA AATGTGCTCA AGGGCTGCCT TGCCAACCAG GCCGACCTGG   1080
ACGCCGAGTG GAGGAACCTC CTGGACTCCA TGGTGCTCAT CACCGACAAG TTCTGGGGTA   1140
CATCGGGTGT GGAGAGTGTC ATCGGCAGCG TGCACACGTG GCTGGCGGAG GCCATCAACG   1200
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CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCAT CCAGGGCTGC GGGAACCCCA   1260
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TCCTGGCCCT TACAGTAGCC AGGCCCCGGT GGCGGTAACT GCCCCAAGGC CCCAGGGACA   1920
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CAGGGCTCAG AGTGACCCTC GGCTGTCACC TGCTCACAGG GATGCTGGTG GCTGGTGAGA   2880
CCCCGCACTG CACACGGGAA TGCCTAGGTC CCTTCCCGAC CCAGCCAGCT GCACTGCAGG   2940
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TGTCCTTGTT CATGGAGAGC TGTTCGCTCC TCCCAGATGG CTTCGGAGGC CCGCAGGGCC   3060
CACCTTGGAC CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC   3120
CTGGACGGGC CCTCCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG   3180
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TCCTGAACCG ACTGACCCTG AGGAGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCGTCC   3300
CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC   3360
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Seq ID NO: C74 DNA Sequence
Nucleic Acid Accession #: BC030205.1
Coding sequence: 45..878

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AATACAAGCT CACCTACGCA GAAGCTAAGG CGGTGTGTGA ATTTGAAGGC GGCCATCTCG  240
CAACTTACAA GCAGCTAGAG GCAGCCAGAA AAATTGGATT TCATGTCTGT GCTGCTGGAT  300
GGATGGCTAA GGGCAGAGTT GGATACCCCA TTGTGAAGCC AGGGCCCAAC TGTGGATTTG  360
GAAAAACTGG CATTATTGAT TATGGAATCC GTCTCAATAG GAGTGAAAGA TGGGATGCCT  420
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GACTCAAGTA TGGTCAGCGT ATTCACCTGA GTTTTTTAGA TTTTGACCTT GAAGATGACC  600
CAGGTTGCTT GGCTGATTAT GTTGAAATAT ATGACAGTTA CGATGATGTC CATGGCTTTG  660
TGGGAAGATA CTGTGGAGAT GAGCTTCCAG ATGACATCAT CAGTACAGGA AATGTCATGA  720
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CAATGGATCC TGTATCCAAA TCCAGTCAAG GAAAAAATAC AAGTACTACT TCTACTGGAA  840
ATAAAAACTT TTTAGCTGGA AGATTTAGCC ACTTATAAAA AAAAAAAAAG GATGATCAAA  900
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GCGTTAACAT TTTCATATTT TTTTCTTTCA GTCATTTTTC TATTTGTGGT ATATGTATAT 1140
ATGTACCTAT ATGTATTTGC ATTTGAAATT TTGGAATCCT GCTCTATGTA CAGTTTTGTA 1200
TTATACTTTT TAAATCTTGA ACTTTATAAA CATTTTCTGA AATCATTGAT TATTCTACAA 1260
AAACATGATT TTAAACAGCT GTAAAATATT CTATGATATG AATGTTTTAT GCATTATTTA 1320
AGCCTGTCTC TATTGTTGGA ATTTCAGGTC ATTTTCATAA ATATTGTTGC AATAAATATC 1380
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Seq ID NO: C75 DNA Sequence
Nucleic Acid Accession #: NM_001982.1
Coding sequence: 199..4227

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WO03042661 [file://E:/WO03042661.pcl]


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GGCCTGAGTG TGACCGGCGA TGCTGAGAAC CAATACCAGA CACTGTACAA GCTCTACGAG   360
AGGTGTGAGG TGGTGATGGG GAACCTTGAG ATTGTGCTCA CGGGACACAA TGCCGACCTC   420
TCCTTCCTGC AGTGGATTCG AGAAGTGACA GGCTATGTCC TCGTGGCCAT GAATGAATTC   480
TCTACTCTAC CATTGCCCAA CCTCCGCGTG GTGCGAGGGA CCCAGGTCTA CGATGGGAAG   540
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TATCTGGTCA TAAAGAGAGA GAGTGGGCCT GGAATAGCCC CTGGGCCAGA GCCCCATGGT  3180
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AGTGAACGGT GCCCCCGTCC AGTCTCTCTA CACCCAATGC CACGGGGATG CCTGGCATCA  3480
GAGTCATCAG AGGGGCATGT AACAGGCTCT GAGGCTGAGC TCCAGGAGAA AGTGTCAATG  3540
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TTTCAGGGGC CTGGACATCA GGCCCCCCAT GTCCATTATG CCCGCCTAAA AACTCTACGT  4140
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CCCAAGGCTA ATGCCCAGAG AACGTAACTC CTGCTCCCTG TGGCACTCAG GGAGCATTTA  4260
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TTGACACAAA ATTCTTATGG TATGTAGCCA GCTGTGCACT TTCTTCTCTT TCCCAACCCC  4440
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Seq ID NO: C76 DNA Sequence

Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC  240
AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG  300
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CGCCCCCAGC TCGCCGCCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG  600
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GAGGCCTCCT TCCCTGCTGG AGTGGACAGC AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
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ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCCTGT CCTGCTCATT 1500
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Seq ID NO: C77 DNA Sequence
Nucleic Acid Accession #: NM_004207.1
Coding sequence: 63..1460

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AGGCCGTCAG TGTCTTCTTC AAGGAGCTCA TACAGGAGTT TGGGATCGGC TACAGCGACA  240
CAGCCTGGAT CTCCTCCATC CTGCTGGCCA TGCTCTACGG GACAGGTCCG CTCTGCAGTG  300
TGTGCGTGAA CCGCTTTGGC TGCCGGCCCG TCATGCTTGT GGGGGGTCTC TTTGCGTCGC  360
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CCGCGGGCTT CGTGGCGGGG CTTGGGAAGG TGCGGCCCTA CTCCGTCTAC CTCTTCAGCT  960
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TGCTGATGGA GGCGGTGGCC GTGCTCGTCG GGCCCCCTTC GGGAGGCAAA CTCCTGGATG 1200
CGACCCACGT CTACATGTAC GTGTTCATCC TGGCGGGGGC CGAGGTGCTC ACCTCCTCCC 1260
TGATTTTGCT GCTGGGCAAC TTCTTCTGCA TTAGGAAGAA GCCCAAAGAG CCACAGCCTG 1320
AGGTGGCGGC CGCGGAGGAG GAGAAGCTCC ACAAGCCTCC TGCAGACTCG GGGGTGGACT 1380
TGCGGGAGGT GGAGCATTTC CTGAAGGCTG AGCCTGAGAA AAACGGGGAG GTGGTTCACA 1440
CCCCGGAAAC AAGTGTCTGA GTGGCTGGGC GGGGCCGGCA GGCACAGGGA GGAGGTACAG 1500
AAGCCGGCAA CGCTTGCTAT TTATTTTACA AACTGGACTG GCTCAGGCAG GGCCACGGCT 1560
GGGCTCCAGC TGCCGGCCCA GCGGATCGTC GCCCGATCAG TGTTTTGAGG GGGAAGGTGG 1620
CGGGGTGGGA ACCGTGTCAT TCCAGAGTGG ATCTGCGGTG AAGCCAAGCC GCAAGGTTAC 1680
AAGGCATCCT CACCAGGGGC CCCGCCTGCT GCTCCCAGGT GGCCTGCGGC CACTGCTATG 1740
CTCAAGGACC TGGAAACCCA TGCTTCGAGA CAACGTGACT TTAATGGGAG GGTGGGTGGG 1800
CCGCAGACAG GCTGGCAGGG CAGGTGCTGC GTGGGGCCCT CTCCAGCCCG TCCTACCCTG 1860
GGCTCACATG GGGCCTGTGC CCACCCCTCT TGAGTGTCTT GGGGACAGCT CTTTCCACCC 1920
CTGGAAGATG GAAATAAACC TGCGTGTGGG TGGAGTGTTC TCGTGCCGAA TTCAAAAAGC 1980
TT                                                                 1982
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Seq ID NO: C78 DNA Sequence
Nucleic Acid Accession #: NM_000358.1
Coding sequence: 48..2099

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1          11         21         31         41         51
|          |          |          |          |          |
GCTTGCCCGT CGGTCGCTAG CTCGCTCGGT GCGCGTCGTC CCGCTCCATG GCGCTCTTCG   60
TGCGGCTGCT GGCTCTCGCC CTGGCTCTGG CCCTGGGCCC CGCCGCGACC CTGGCGGGTC  120
CCGCCAAGTC GCCCTACCAG CTGGTGCTGC AGCACAGCAG GCTCCGGGGC CGCCAGCACG  180
GCCCCAACGT GTGTGCTGTG CAGAAGGTTA TTGGCACTAA TAGGAAGTAC TTCACCAACT  240
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GCAAGCAGTG GTACCAAAGG AAAATCTGTG GCAAATCAAC AGTCATCAGC TACGAGTGCT   300
GTCCTGGATA TGAAAAGGTC CCTGGGGAGA AGGGCTGTCC AGCAGCCCTA CCACTCTCAA   360
ACCTTTACGA GACCCTGGGA GTCGTTGGAT CCACCACCAC TCAGCTGTAC ACGGACCGCA   420
CGGAGAAGCT GAGGCCTGAG ATGGAGGGGC CCGGCAGCTT CACCATCTTC GCCCCTAGCA   480
ACGAGGCCTG GGCCTCCTTG CCAGCTGAAG TGCTGGACTC CCTGGTCAGC AATGTCAACA   540
TTGAGCTGCT CAATGCCCTC CGCTACCATA TGGTGGGCAG GCGAGTCCTG ACTGATGAGC   600
TGAAACACGG CATGACCCTC ACCTCTATGT ACCAGAATTC CAACATCCAG ATCCACCACT   660
ATCCTAATGG GATTGTAACT GTGAACTGTG CCCGGCTCCT GAAAGCCGAC CACCATGCAA   720
CCAACGGGGT GGTGCACCTC ATCGATAAGG TCATCTCCAC CATCACCAAC AACATCCAGC   780
AGATCATTGA GATCGAGGAC ACCTTTGAGA CCCTTCGGGC TGCTGTGGCT GCATCAGGGC   840
TCAACACGAT GCTTGAAGGT AACGGCCAGT ACACGCTTTT GGCCCCGACC AATGAGGCCT   900
TCGAGAAGAT CCCTAGTGAG ACTTTGAACC GTATCCTGGG CGACCCAGAA GCCCTGAGAG   960
ACCTGCTGAA CAACCACATC TTGAAGTCAG CTATGTGTGC TGAAGCCATC GTTGCGGGGC  1020
TGTCTGTAGA GACCCTGGAG GGCACGACAC TGGAGGTGGG CTGCAGCGGG GACATGCTCA  1080
CTATCAACGG GAAGGCGATC ATCTCCAATA AAGACATCCT AGCCACCAAC GGGGTGATCC  1140
ACTACATTGA TGAGCTACTC ATCCCAGACT CAGCCAAGAC ACTATTTGAA TTGGCTGCAG  1200
AGTCTGATGT GTCCACAGCC ATTGACCTTT TCAGACAAGC CGGCCTCGGC AATCATCTCT  1260
CTGGAAGTGA GCGGTTGACC CTCCTGGCTC CCCTGAATTC TGTATTCAAA GATGGAACCC  1320
CTCCAATTGA TGCCCATACA AGGAATTTGC TTCGGAACCA CATAATTAAA GACCAGCTGG  1380
CCTCTAAGTA TCTGTACCAT GGACAGACCC TGGAAACTCT GGGCGGCAAA AAACTGAGAG  1440
TTTTTGTTTA TCGTAATAGC CTCTGCATTG AGAACAGCTG CATCGCGGCC CACGACAAGA  1500
GGGGGAGGTA CGGGACCCTG TTCACGATGG ACCGGGTGCT GACCCCCCCA ATGGGGACTG  1560
TCATGGATGT CCTGAAGGGA GACAATCGCT TTAGCATGCT GGTAGCTGCC ATCCAGTCTG  1620
CAGGACTGAC GGAGACCCTC AACCGGGAAG GAGTCTACAC AGTCTTTGCT CCCACAAATG  1680
AAGCCTTCCG AGCCCTGCCA CCAAGAGAAC GGAGCAGACT CTTGGGAGAT GCCAAGGAAC  1740
TTGCCAACAT CCTGAAATAC CACATTGGTG ATGAAATCCT GGTTAGCGGA GGCATCGGGG  1800
CCCTGGTGCG GCTAAAGTCT CTCCAAGGTG ACAAGCTGGA AGTCAGCTTG AAAAACAATG  1860
TGGTGAGTGT CAACAAGGAG CCTGTTGCCG AGCCTGACAT CATGGCCACA AATGGCGTGG  1920
TCCATGTCAT CACCAATGTT CTGCAGCCTC CAGCCAACAG ACCTCAGGAA AGAGGGGATG  1980
AACTTGCAGA CTCTGCGCTT GAGATCTTCA AACAAGCATC AGCGTTTTCC AGGGCTTCCC  2040
AGAGGTCTGT GCGACTAGCC CCTGTCTATC AAAAGTTATT AGAGAGGATG AAGCATTAGC  2100
TTGAAGCACT ACAGGAGGAA TGCACCACGG CAGCTCTCCG CCAATTTCTC TCAGATTTCC  2160
ACAGAGACTG TTTGAATGTT TTCAAAACCA AGTATCACAC TTTAATGTAC ATGGGCCGCA  2220
CCATAATGAG ATGTGAGCCT TGTGCATGTG GGGGAGGAGG GAGAGAGATG TACTTTTTAA  2280
ATCATGTTCC CCCTAAACAT GGCTGTTAAC CCACTGCATG CAGAAACTTG GATGTCACTG  2340
CCTGACATTC ACTTCCAGAG AGGACCTATC CCAAATGTGG AATTGACTGC CTATGCCAAG  2400
TCCCTGGAAA AGGAGCTTCA GTATTGTGGG GCTCATAAAA CATGAATCAA GCAATCCAGC  2460
CTCATGGGAA GTCCTGGCAC AGTTTTTGTA AAGCCCTTGC ACAGCTGGAG AAATGGCATC  2520
ATTATAAGCT ATGAGTTGAA ATGTTCTGTC AAATGTGTCT CACATCTACA CGTGGCTTGG  2580
AGGCTTTTAT GGGGCCCTGT CCAGGTAGAA AAGAAATGGT ATGTAGAGCT TAGATTTCCC  2640
TATTGTGACA GAGCCATGGT GTGTTTGTAA TAATAAAACC AAAGAAACAT A            2691
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Seq ID NO: C79 DNA Sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109..2940

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ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA   60
ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG  120
AGCATTGCAG GTCCTATTTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA  180
GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC  240
ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG  300
ATAACTGAAG CTTCATTTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTCAGAAAT  360
ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA  420
TCATATGAAA AGGCAAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA  480
TACACCCTAC AATACAGAGG GTGTGGAAAA GAGGGAAAAT ACATTCATTT CACACCTAAT  540
TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT  600
GAATGGGCCC ACCTCCGTTG GGGTGTGTTC GATGAGTATA ACAATGACAA ACCTTTCTAC  660
ATAAATGGGC AAAATCAAAT TAAAGTGACA AGGTGTTCAT CTGACATCAC AGGCATTTTT  720
GTGTGTGAAA AAGGTCCTTG CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA  780
GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA  840
AGTTTATCTT CTGTGGTTGA ATTTTGTAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC  900
CTACAGAACC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC  960
TTTCACCACA GCTTTCCCAT GAATGGGACT GAGCTTCCAC CTCCTCCCAC ATTCTCGCTT 1020
GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAATTTT ATTTGATGCA GATTGTTGAA 1140
ATTCATACCT TCGTGGGCAT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCCAGCTA 1200
CACCAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
TCAGCTAAAA CAGACATCAG CATTTGTTCA GGGCTTAAGA AAGGATTTGA GGTGGTTGAA 1320
AAACTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
CTTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC 1440
CTGGGTTCAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
TTCTTTGTTC CAGATATATC AAACTCCAAT AGCATGATTG ATGCTTTCAG TAGAATTTCC 1560
TCTGGAACTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAATGTC 1620
AAACCTCACC ATCAATTGAA AAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT 1740
GGACGAAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAACAA TACCCATCAT 1860
TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA 1920
GCCACTGTGG AAGCCTTTGT GGAAAGAGAC AGCCTCCATT TTCCTCATCC TGTGATGATT 1980
TATGCCAATG TGAAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTCAC TGCCACAGTT 2040
GAGCCAGAGA CTGGAGATCC TGTTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT 2100
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GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTTTCT CCTTTGCTGC AAATGGTAGA   2160
TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCAGC CCACTCTATT   2220
CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT   2280
GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC   2340
AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCCACCC TGATGTGTTT   2400
CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT   2460
TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG   2520
AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA   2580
AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC   2640
ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT   2700
GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCCAGGCG   2760
CCTCTGTTTA TTCCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA   2820
GGAGTTTTAA CAGCAATGGG TTTGATAGGA ATCATTTGCC TTATTATAGT TGTGACACAT   2880
CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA   2940
ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCTTCG ACTACAAAAA   3000
CATACTAACA AAGTCAAATT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTTGTACA   3060
ATACAGATAA GATTTTTACA TGGTAGATCA ACAATTCTTT TTGGGGGTAG ATTAGAAAAC   3120
CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAAGTAAT GTCTTTAAAG   3180
GCAAAGGGAA GGGTAAAGTC GGACCAGTGT CAAGGAAAGT TTGTTTTATT GAGGTGGAAA   3240
AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA   3300
TCATTTAGTT ACTTTGATTA ATTTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG   3360
TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT   3420
CTTGCTATTT TGTTATATAT ATTTCAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT   3480
TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT   3540
TTTATGACAA AGGTCTATTG AATTTATTTG TNTGTAAGTT TCTACTCCCA TCAAAGCAGC   3600
TTTCTAAGTT TATTGCCTTG GGTTATTATG GAATGATAGT TATAGCCCCN TATAATGCCT   3660
TACCTAGGAA A                                                       3671
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Seq ID NO: C80 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1413

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ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCTGAAC   60
AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTTGGTG AAAGATACTT AGAAAAATTT  120
TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAAAATGA AATATAGTGG AAACTTAATG  180
AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC  240
ACATCTACCC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCCGATGT CCATCATTTC  300
AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT  360
TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAAGC TTTCCAAGTA  420
TGGAGTAATG TTACCCCCTT GAAATTCAGC AAGATTAACA CAGGCATGGC TGACATTTTG  480
GTGGTTTTTG CCCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC  540
CTAGCCCATG CTTTTGGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC  600
GAATTCTGGA CTACACATTC AGGAGGCACA AACTTGTTCC TCACTGCTGT TCACGAGATT  660
GGCCATTCCT TAGGTCTTGG CCATTCTAGT GATCCAAAGG CCGTAATGTT CCCCACCTAC  720
AAATATGTTG ACATCAACAC ATTTCGCCTC TCTGCTGATG ACATACGTGG CATTCAGTCC  780
CTGTATGGAG ACCCAAAAGA GAACCAACGC TTGCCAAATC CTGACAATTC AGAACCAGCT  840
CTCTGTGACC CCAATTTGAG TTTTGATGCT GTCACTACCG TGGGAAATAA GATCTTTTTC  900
TTCAAAGACA GGTTCTTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA  960
ATTTCTTCCT TATGGCCAAC CTTGCCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020
AGAAATCAAG TTTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080
GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTC CTAACTTTGT GAAAAAAATT 1140
GATGCAGCTG TTTTTAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAGTAT 1200
TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCTGGTT ATCCCAAACT GATTACCAAG 1260
AACTTCCAAG GAATCGGGCC TAAAATTGAT GCAGTCTTCT ACTCTAAAAA CAAATACTAC 1320
TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAACG TATCACCAAA 1380
ACACTGAAAA GCAATAGCTG GTTTGGTTGT TGA                               1413
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Seq ID NO: C81 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1413

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCTGAAC   60
AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTTGGTG AAAGATACTT AGAAAAATTT  120
TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAAAATGA AATATAGTGG AAACTTAATG  180
AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC  240
ACATCTACCC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCCGATGT CCATCATTTC  300
AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT  360
TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAAGC TTTCCAAGTA  420
TGGAGTAATG TTACCCCCTT GAAATTCAGC AAGATTAACA CAGGCATGGC TGACATTTTG  480
GTGGTTTTTG CCCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC  540
CTAGCCCATG CTTTTGGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC  600
GAATTCTGGA CTACACATTC AGGAGGCACA AACTTGTTCC TCACTGCTGT TCACGCCATT  660
GGCCATTCCT TAGGTCTTGG CCATTCTAGT GATCCAAAGG CCGTAATGTT CCCCACCTAC  720
AAATATGTTG ACATCAACAC ATTTCGCCTC TCTGCTGATG ACATACGTGG CATTCAGTCC  780
CTGTATGGAG ACCCAAAAGA GAACCAACGC TTGCCAAATC CTGACAATTC AGAACCAGCT  840
CTCTGTGACC CCAATTTGAG TTTTGATGCT GTCACTACCG TGGGAAATAA GATCTTTTTC  900
TTCAAAGACA GGTTCTTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA  960
ATTTCTTCCT TATGGCCAAC CTTGCCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020
AGAAATCAAG TTTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080
GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTC CTAACTTTGT GAAAAAAATT 1140
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GATGCAGCTG TTTTTAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAGTAT   1200
TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCTGGTT ATCCCAAACT GATTACCAAG   1260
AACTTCCAAG GAATCGGGCC TAAAATTGAT GCAGTCTTCT ACTCTAAAAA CAAATACTAC   1320
TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAACG TATCACCAAA   1380
ACACTGAAAA GCAATAGCTG GTTTGGTTGT TGA                                1413
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Seq ID NO: C82 DNA Sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

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1          11         21         31         41         51
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AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT   60
TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT   120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG   180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT   240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT   300
AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC   360
ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACAACAGCC CTCCAAACAA   420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA   480
CAATTGCTGT GGCGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC   540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA   600
AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG   660
CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG   720
ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG   780
AATTGAATAT TAAGAA                                                  796
```

Seq ID NO: C83 DNA Sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71..2560

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1          11         21         31         41         51
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AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT   60
CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG   120
CTGGCTGCAG TGCGCGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC   180
CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG   240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA   300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC   360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC   420
TGAAAATGGC AAGGGTCCCT TCCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG   480
AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT   540
CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTTGAAT AAGCCACTGG ACCGGGAGGA   600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA   660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA   720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAGGT   780
GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT   840
CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTTC ACCATTCACC GGAGCACAGG   900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC   960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA   1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT   1080
GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC   1140
CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT   1200
TACCATCACC ACCCACCCTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA   1260
TTTTGAGGCC AAAAACCAGC ACACCCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT   1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC   1380
ACCTGTGTTT GTCCCACCCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA   1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG   1500
CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTCACAGC   1560
TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT   1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC   1680
ACTGATTGAT GTCAATGACC ATGGCCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA   1740
CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC   1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA   1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT   1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT   1980
GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAGGGAG GTTTCATCCT   2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCCTCCTG CTGGTGCTGC TTTTGTTGGT   2100
GAGAAAGAAG CGGAAGATCA AGGAGCCCCT CCTACTCCCA GAAGATGACA CCCGTGACAA   2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA   2220
GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC   2280
CATCATCCCG ACACCCATGT ACCGTCCTCG GCCAGCCAAC CCAGATGAAA TCGGCAACTT   2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCACA GCCCCGCCCT ACGACACCCT   2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC   2460
CTCCGCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA   2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCCTGCC TGCAGGGCTG   2580
GGGACCAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG   2640
GACTTCGGAG CTTGTCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG   2700
ACGTTAGAGT GGTTGCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC   2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC   2820
TCTTACCTGC CGTAAAATGC TCAACCCTGT GTCCTGGGCC TGGGCCTGCT GTGACTGACC   2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT   2940
TTTTTTTAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT   3000
GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTTCCAGAC CCCAATGCCT CCCATTCGGA   3060
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TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT   3120
GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT   3180
TAAAGAAACT TTTCCCAGAA AAAAA                                      3205

Seq ID NO: C84 DNA Sequence
Nucleic Acid Accession #: NM_005629.1
Coding sequence: 639..2546

1          11         21         31         41         51
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TAGTCGGAGC GAGGTGGCGA GTCGCTGAGC CCGCCGCGGC CCCGAGAGCG GCTGCAGCCG   60
CCGCCGCCGG GAAGGAGAGG GCGAGGCGCG CCCGAGCCGC CGCCGCCGCC GCCACCGCCG  120
CCGCCGCCAC CACCGCCACC GGAGTCGCGG GCCAGCCGGG CAGCCTCCGC GGGCCCCGGC  180
CGGGGCGGGG GGCGCGGGCC ACAGGCCCCT GCTCCGGCCG TCGTTTGCAG ACCGCGGGCG  240
CCGATGTCGC CCGCGCCCCG TTAGGATGAG TCTCGGGTCG GGCGAGGAGC CGCCGCAGCC  300
GCCGCCGCCC GAGCCGCGGG CAGGAGCCTC GGGAGCCGCC GCCGCCGCCG CCGCCGCCCG  360
GCCGGGCCCC GACGCCGCCC GCGCGCCCCC GGGCCCCCGA CACACATGAG ATTCTTCAGG  420
CTCACTTTCA AGTGCTTCGT GGACTGCTTC TGACTGCGCC GCCCGCGCCC CGCACCCCGC  480
CGTCCGCCCG CCGCCCCGTC CCCCGGCCCG GCCGCCCCCC GGCCCCCGGC CGGCCCGCGC  540
CCTCGGGGCC CTCCCCGGTG CCGCCGGTGC CCCCCGCCTG ACCGCCGCCC CCCGTGAGGC  600
GCCGCGACCC CGGCCCGGCC GTGCGGCCCG CCGGGGCCAT GGCGAAGAAG AGCGCCGAGA  660
ACGGCATCTA TAGCGTGTCC GGCGACGAGA AGAAGGGCCC CCTCATCGCG CCCGGGCCCG  720
ACGGGGCCCC GGCCAAGGGC GACGGCCCCG TGGGCCTGGG GACACCCGGC GGCCGCCTGG  780
CCGTGCCGCC GCGCGAGACC TGGACGCGCC AGATGGACTT CATCATGTCG TGCGTGGGCT  840
TCGCCGTGGG CTTGGGCAAC GTGTGGCGCT TCCCCTACCT GTGCTACAAG AACGGCGGAG  900
GTGTGTTCCT TATTCCCTAC GTCCTGATCG CCCTGGTTGG AGGAATCCCC ATTTTCTTCT  960
TAGAGATCTC GCTGGGCCAG TTCATGAAGG CCGGCAGCAT CAATGTCTGG AACATCTGTC 1020
CCCTGTTCAA AGGCCTGGGC TACGCCTCCA TGGTGATCGT CTTCTACTGC AACACCTACT 1080
ACATCATGGT GCTGGCCTGG GGCTTCTATT ACCTGGTCAA GTCCTTTACC ACCACGCTGC 1140
CCTGGGCCAC ATGTGGCCAC ACCTGGAACA CTCCCGACTG CGTGGAGATC TTCCGCCATG 1200
AAGACTGTGC CAATGCCAGC CTGGCCAACC TCACCTGTGA CCAGCTTGCT GACCGCCGGT 1260
CCCCTGTCAT CGAGTTCTGG GAGAACAAAG TCTTGAGGCT GTCTGGGGGA CTGGAGGTGC 1320
CAGGGGCCCT CAACTGGGAG GTGACCCTTT GTCTGCTGGC CTGCTGGGTG CTGGTCTACT 1380
TCTGTGTCTG GAAGGGGGTC AAATCCACGG GAAAGATCGT GTACTTCACT GCTACATTCC 1440
CCTACGTGGT CCTGGTCGTG CTGCTGGTGC GTGGAGTGCT GCTGCCTGGC GCCCTGGATG 1500
GCATCATTTA CTATCTCAAG CCTGACTGGT CAAAGCTGGG GTCCCCTCAG GTGTGGATAG 1560
ATGCGGGGAC CCAGATTTTC TTTTCTTACG CCATTGGCCT GGGGGCCCTC ACAGCCCTGG 1620
GCAGCTACAA CCGCTTCAAC AACAACTGCT ACAAGGACGC CATCATCCTG GCTCTCATCA 1680
ACAGTGGGAC CAGCTTCTTT GCTGGCTTCG TGGTCTTCTC CATCCTGGGC TTCATGGCTG 1740
CAGAGCAGGG CGTGCACATC TCCAAGGTGG CAGAGTCAGG GCCGGGCCTG GCCTTCATCG 1800
CCTACCCGCG GGCTGTCACG CTGATGCCAG TGGCCCCACT CTGGGCTGCC CTGTTCTTCT 1860
TCATGCTGTT GCTGCTTGGT CTCGACAGCC AGTTTGTAGG TGTGGAGGGC TTCATCACCG 1920
GCCTCCTCGA CCTCCTCCCG GCCTCCTACT ACTTCCGTTT CCAAAGGGAG ATCTCTGTGG 1980
CCCTCTGTTG TGCCCTCTGC TTTGTCATCG ATCTCTCCAT GGTGACTGAT GGCGGGATGT 2040
ACGTCTTCCA GCTGTTTGAC TACTACTCGG CCAGCGGCAC CACCCTGCTC TGGCAGGCCT 2100
TTTGGGAGTG CGTGGTGGTG GCCTGGGTGT ACGGAGCTGA CCGCTTCATG GACGACATTG 2160
CCTGTATGAT CGGGTACCGA CCTTGCCCCT GGATGAAATG GTGCTGGTCC TTCTTCACCC 2220
CGCTGGTCTG CATGGGCATC TTCATCTTCA ACGTTGTGTA CTACGAGCCG CTGGTCTACA 2280
ACAACACCTA CGTGTACCCG TGGTGGGGTG AGGCCATGGG CTGGGCCTTC GCCCTGTCCT 2340
CCATGCTGTG CGTGCCGCTG CACCTCCTGG GCTGCCTCCT CAGGGCCAAG GGCACCATGG 2400
CTGAGCGCTG GCAGCACCTG ACCCAGCCCA TCTGGGGCCT CCACCACTTG GAGTACCGAG 2460
CTCAGGACGC AGATGTCAGG GGCCTGACCA CCCTGACCCC AGTGTCCGAG AGCAGCAAGG 2520
TCGTCGTGGT GGAGAGTGTC ATGTGACAAC TCAGCTCACA TCACCAGCTC ACCTCTGGTA 2580
GCCATAGCAG CCCCTGCTTC AGCCCCACCG CACCCCTCCA GGGGGCCTGC CTTTCCCTGA 2640
CACTTTTGGG GTCTGCCTGG GGGAGGAGGG GAGAAAGCAC CATGAGTGCT CACTAAAACA 2700
ACTTTTTCCA TTTTTAATAA AACGCCAAAA ATATCACAAC CCACCAAAAA TAGATGCCTC 2760
TCCCCCTCCA GCCCTAGCCG AGCTGGTCCT AGGCCCCGCC TAGTGCCCCA CCCCCACCCA 2820
CAGTGCTGCA CTCCTCCTGC CCCTGCCACG CCCACCCCCT GCCCACCTCT CCAGGCTCTG 2880
CTCTGCAGCA CACCCGTGGG TGACCCCTCA CCCCAGAAGC AGCAGTGGCA GCTTGGGAAA 2940
TGTGAGGAAG GGAAGGAGGG AGAGACGGGA GGGAGGAGAG AGAGGAGAAG GGAGGCAGGG 3000
GAGGGGCAGC AGAACCAAGG CAAATATTTC AGCTGGGCTA TACCCCTCTC CCCATCCCTG 3060
TTATAGAAGC TTAGAGAGCC AGCCAGCAAT GGAACCTTCT GGTTCCTGCG CCAATCGCCA 3120
CCAGTATCAA TTGTGTGAGC TTGGGTGCGA GTGCACGCGT GCGTGAGTAC GGAGAGTATA 3180
TATAGATCTC TATCTCTTAG CAAAGGTGAA TGCCAGATGT AAATGGCGCC TCTGGGCAAA 3240
GGAGGCTTGT ATTTTGCACA TTTTATAAAA ACTTGAGAGA ATGAGATTTC TGCTTGTATA 3300
TTTCTAAAAA GAGGAAGGAG CCCAAACCAT CCTCTCCTTA CCACTCCCAT CCCTGTGAGC 3360
CCTACCTTAC CCCTCTGCCC CTAGCCAAGG AGTGTGAATT TATAGATCTA ACTTTCATAG 3420
GCAAAACAAA AGCTTCGAGC TGTTGCGTGT GTGAGTCTGT TGTGTGGATG TGCGTGTGTG 3480
GTCCCCAGCC CCAGACTGGA TTGGAAAAGT GCATGGTGGG GGCCTCGGGG CTGTCCCCAC 3540
GCTGTCCCTT TGCCACAAGT CTGTGGGGCA AGAGGCTGCA ATATTCCGTC CTGGGTGTCT 3600
GGGCTGCTAA CCTGGCCTGC TCAGGCTTCC CACCCTGTGC GGGGCACACC CCCAGGAAGG 3660
GACCCTGGAC ACGGCTCCCA CGTCCAGGCT TAAGGTGGAT GCACTTCCCG CACCTCCAGT 3720
CTTCTGTGTA GCAGCTTTAA CCCACGTTTG TCTGTCACGT CCAGTCCCGA GACGGCTGAG 3780
TGACCCCAAG AAAGGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGCTGGGTGA 3840
GGGTGGCGGG CCTGCGGGGA CATTCTACTG TGCTAAAAAG CCACTGCAGA CATAGCAATA 3900
AAAACATGTC ATTTTCC                                               3917

Seq ID NO: C85 DNA Sequence
Nucleic Acid Accession #: NM_006516.1
Coding sequence: 180..1658

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TAGTCGCGGG TCCCCGAGTG AGCACGCCAG GGAGCAGGAG ACCAAACGAC GGGGGTCGGA   60
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GTCAGAGTCG CAGTGGGAGT CCCCGGACCG GAGCACGAGC CTGAGCGGGA GAGCGCCGCT   120
CGCACGCCCG TCGCCACCCG CGTACCCGGC GCAGCCAGAG CCACCAGCGC AGCGCTGCCA   180
TGGAGCCCAG CAGCAAGAAG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC   240
TTGGCTCCCT GCAGTTTGGC TACAACACTG GAGTCATCAA TGCCCCCCAG AAGGTGATCG   300
AGGAGTTCTA CAACCAGACA TGGGTCCACC GCTATGGGGA GAGCATCCTG CCCACCACGC   360
TCACCACGCT CTGGTCCCTC TCAGTGGCCA TCTTTTCTGT TGGGGGCATG ATTGGCTCCT   420
TCTCTGTGGG CCTTTTCGTT AACCGCTTTG GCCGGCGGAA TTCAATGCTG ATGATGAACC   480
TGCTGGCCTT CGTGTCCGCC GTGCTCATGG GCTTCTCGAA ACTGGGCAAG TCCTTTGAGA   540
TGCTGATCCT GGGCCGCTTC ATCATCGGTG TGTACTGCGG CCTGACCACA GGCTTCGTGC   600
CCATGTATGT GGGTGAAGTG TCACCCACAG CCTTTCGTGG GGCCCTGGGC ACCCTGCACC   660
AGCTGGGCAT CGTCGTCGGC ATCCTCATCG CCCAGGTGTT CGGCCTGGAC TCCATCATGG   720
GCAACAAGGA CCTGTGGCCC CTGCTGCTGA GCATCATCTT CATCCCGGCC CTGCTGCAGT   780
GCATCGTGCT GCCCTTCTGC CCCGAGAGTC CCCGCTTCCT GCTCATCAAC CGCAACGAGG   840
AGAACCGGGC CAAGAGTGTG CTAAAGAAGC TGCGCGGGAC AGCTGACGTG ACCCATGACC   900
TGCAGGAGAT GAAGGAAGAG AGTCGGCAGA TGATGCGGGA GAAGAAGGTC ACCATCCTGG   960
AGCTGTTCCG CTCCCCCGCC TACCGCCAGC CCATCCTCAT CGCTGTGGTG CTGCAGCTGT  1020
CCCAGCAGCT GTCTGGCATC AACGCTGTCT TCTATTACTC CACGAGCATC TTCGAGAAGG  1080
CGGGGGTGCA GCAGCCTGTG TATGCCACCA TTGGCTCCGG TATCGTCAAC ACGGCCTTCA  1140
CTGTCGTGTC GCTGTTTGTG GTGGAGCGAG CAGGCCGGCG GACCCTGCAC CTCATAGGCC  1200
TCGCTGGCAT GGCGGGTTGT GCCATACTCA TGACCATCGC GCTAGCACTG CTGGAGCAGC  1260
TACCCTGGAT GTCCTATCTG AGCATCGTGG CCATCTTTGG CTTTGTGGCC TTCTTTGAAG  1320
TGGGTCCTGG CCCCATCCCA TGGTTCATCG TGGCTGAACT CTTCAGCCAG GGTCCACGTC  1380
CAGCTGCCAT TGCCGTTGCA GGCTTCTCCA ACTGGACCTC AAATTTCATT GTGGGCATGT  1440
GCTTCCAGTA TGTGGAGCAA CTGTGTGGTC CCTACGTCTT CATCATCTTC ACTGTGCTCC  1500
TGGTTCTGTT CTTCATCTTC ACCTACTTCA AAGTTCCTGA GACTAAAGGC CGGACCTTCG  1560
ATGAGATCGC TTCCGGCTTC CGGCAGGGGG GAGCCAGCCA AAGTGATAAG ACACCCGAGG  1620
AGCTGTTCCA TCCCCTGGGG GCTGATTCCC AAGTGTGAGT CGCCCCAGAT CACCAGCCCG  1680
GCCTGCTCCC AGCAGCCCTA AGGATCTCTC AGGAGCACAG GCAGCTGGAT GAGACTTCCA  1740
AACCTGACAG ATGTCAGCCG AGCCGGGCCT GGGGCTCCTT TCTCCAGCCA GCAATGATGT  1800
CCAGAAGAAT ATTCAGGACT TAACGGCTCC AGGATTTTAA CAAAAGCAAG ACTGTTGCTC  1860
AAATCTATTC AGACAAGCAA CAGGTTTTAT AATTTTTTTA TTACTGATTT TGTTATTTTT  1920
ATATCAGCCT GAGTCTCCTG TGCCCACATC CCAGGCTTCA CCCTGAATGG TTCCATGCCT  1980
GAGGGTGGAG ACTAAGCCCT GTCGAGACAC TTGCCTTCTT CACCCAGCTA ATCTGTAGGG  2040
CTGGACCTAT GTCCTAAGGA CACACTAATC GAACTATGAA CTACAAAGCT TCTATCCCAG  2100
GAGGTGGCTA TGGCCACCCG TTCTGCTGGC CTGGATCTCC CCACTCTAGG GGTCAGGCTC  2160
CATTAGGATT TGCCCCTTCC CATCTCTTCC TACCCAACCA CTCAAATTAA TCTTTCTTTA  2220
CCTGAGACCA GTTGGGAGCA CTGGAGTGCA GGGAGGAGAG GGGAAGGGCC AGTCTGGGCT  2280
GCCGGGTTCT AGTCTCCTTT GCACTGAGGG CCACACTATT ACCATGAGAA GAGGGCCTGT  2340
GGGAGCCTGC AAACTCACTG CTCAAGAAGA CATGGAGACT CCTGCCCTGT TGTGTATAGA  2400
TGCAAGATAT TTATATATAT TTTTGGTTGT CAATATTAAA TACAGACACT AAGTTATAGT  2460
ATATCTGGAC AAGCCAACTT GTAAATACAC CACCTCACTC CTGTTACTTA CCTAAACAGA  2520
TATAAATGGC TGGTTTTTAG AAACATGGTT TTGAAATGCT TGTGGATTGA GGGTAGGAGG  2580
TTTGGATGGG AGTGAGACAG AAGTAAGTGG GGTTGCAACC ACTGCAACGG CTTAGACTTC  2640
GACTCAGGAT CCAGTCCCTT ACACGTACCT CTCATCAGTG TCCTCTTGCT CAAAAATCTG  2700
TTTGATCCCT GTTACCCAGA GAATATATAC ATTCTTTATC TTGACATTCA AGGCATTTCT  2760
ATCACATATT TGATAGTTGG TGTTCAAAAA AACACTAGTT TTGTGCCAGC CGTGATGCTC  2820
AGGCTTGAAA TCGCATTATT TTGAATGTGA AGGGAA                             2856
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Seq ID NO: C86 DNA Sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

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GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG   60
TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGGCGGCC GAGGAGAAGG AAGAGGCGCG  120
GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCAGGCG AGGGCGAGGG  180
CGTGACCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT  240
TATCGGCTCG GGCATCTTCG TGACGCCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCCGGG  300
GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA  360
CGCGGAGCTC GGCACCACCA TCTCCAAATC GGGCGGCGAC TACGCCTACA TGCTGGAGGT  420
CTACGGCTCG CTGCCCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCTTC  480
ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCGC TCTTCCCCAC  540
CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC  600
GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCGCCGC  660
CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA  720
TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACTGGATG TGGGGAACAT  780
TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAATTACT TGAATTTCGT  840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCCTG GCCATCATCA TCTCCCTGCC  900
CATCGTGACG CTGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCCACCGA  960
GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
GTCCTGGATC ATCCCCGTCT TCGTGGGCCT GTCCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTCACATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGTCC CTCGTGTTCA CGTGTGTGAT 1200
GACGCTGCTC TACGCCTTCT CCAAGGACAT CTTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TGCGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
CCTCTTCCTG ATCGCCGTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC              1609
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Seq ID NO: C87 DNA Sequence
Nucleic Acid Accession #: NM_005268.1

Coding sequence: 168..989

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TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCGAAAAC CTTCCCCGCT   60
TCTGGATATG AAATTCAAGC TGCTTGCTGA GTCCTATTGC CGGCTGCTGG GAGCCAGGAG  120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA  180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC  240
TGTCTCTGGT CTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA  300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGTCTGCT  360
TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA  420
CATGCCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTCAG GAGAAGAGGC  480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG  540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT  600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC  660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA  720
TTTTCACCCT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTCGTGGAGC  780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCCTGGC AGCAAGGAAA GCTCAAGCCA  840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCCTG CAAACAAGAC GACCTCCTTT  900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCCTCC TCTCTTACCA GACCGCCCCC  960
GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
TCAACTCCAG CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC                    1243
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Seq ID NO: C88 DNA Sequence
Nucleic Acid Accession #: NM_005130
Coding sequence: 98..802

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1          11         21         31         41         51
|          |          |          |          |          |
CTCTACCTGA CACAGCTGCA GCCTGCAATT CACTCCCACT GCCTGGGATT GCACTGGATC   60
CGTGTGCTCA GAACAAGGTG AACGCCCAGC TGCAGCCATG AAGATCTGTA GCCTCACCCT  120
GCTCTCCTTC CTCCTACTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAGTGAA  180
GAATGGACTT CACAGCAAAG TGGTCTCAGA ACAAAAGGAC ACTCTGGGCA ACACCCAGAT  240
TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAAGACC AAGCCAACTG  300
CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT  360
GGACCATGAA TTTTCCTGTG TCTTTGCTGG CAATCCAACC TCATGCCTAA AGCTCAAGGA  420
TGAGAGAGTC TATTGGAAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG  480
ATATTCCAAG ACAGCTGTGA AAACCAGAGT GTGCAGAAAG GATTTTCCAG AATCCAGTCT  540
TAAGCTAGTC AGCTCCACTC TATTTGGGAA CACAAAGCCC AGGAAGGAGA AAACAGAGAT  600
GTCCCCCAGG GAGCACATCA AGGGCAAAGA GACCACCCCC TCTAGCCTAG CAGTGACCCA  660
GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA  720
GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACATTCT TCCTCAGCAT  780
AGTGCAGGAC ACGTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA  840
TGTCGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCCAAAA TATGAACTTT  900
TGTGCTTAGT GAGTGCAACG AAATATTTAA ACAAGTTTTG TATTTTTTGC TTTTGTGTTT  960
TGGAATTTGC CTTATTTTTC TTGGATGCGA TGTTCAGAGG CTGTTTCCTG CAGCATGTAT 1020
TTCCATGGCC CACACAGCTA TGTGTTTGAG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
GAGTGATAAT TTCAGTGCAA CGAACTTTCT GCTGAATTAA TGGTAATAAA ACTCTGGGTG 1140
TTTTTCAAAA AAAAAAAAAA AAA                                         1163
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Seq ID NO: C89 DNA Sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 274..927

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1          11         21         31         41         51
|          |          |          |          |          |
ACTTGGTCCC AGCCGATAAA TCTGGGGCAG CGCGCGGTAG GAGCTGCGGG CGGCCAGGCC   60
CCTTCCTGCG TCCGCACCTG GCCCCGCGCG CCCCTCTCGG GCGTCCGGCT TCCGGCGTCC  120
TGGCGGCTCG GGTGGCGGCG GTTCGGGCGG CCGCCTGGCT GCTCCTCGGG GCGGCGACGG  180
GGCTCACGCG CGGGCCCGCC ACGGCCTTCA CCGCCGCGCG CTCTGACGCC GGCATAAGGG  240
CCATGTGTTC TGAAATTATT TTGAGGCAAG AAGTTTTGAA AGATGGTTTC CACAGAGACC  300
TTTTAATCAA AGTGAAGTTT GGGGAAAGCA TTGAGGACTT GCACACGTGC CGTCTCTTAA  360
TTAAACAGGA CATTCCTGCA GGACTTTATG TGGATCCGTA TGAGTTGGCT TCATTACGAG  420
AGAGAAACAT AACAGAGGCA GTGATGGTTT CAGAAAATTT TGATATAGAG GCCCCTAACT  480
ATTTGTCCAA GGAGTCTGAA GTTCTCATTT ATGCCAGACG AGATTCACAG TGCATTGACT  540
GTTTTCAAGC CTTTTTGCCT GTGCACTGCC GCTATCATCG GCCGCACAGT GAAGATGGAG  600
AAGCCTCGAT TGTGGTCAAT AACCCAGATT TGTTGATGTT TTGTGACCAA GAGTTCCCGA  660
TTTTGAAATG CTGGGCTCAC TCAGAAGTGG CAGCCCCTTG TGCTTTGGAT AATGAGGATA  720
TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC  780
CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC  840
TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAAATATGG CCATTTTTCC CTATAAGTTT  900
TATGTAGTTA AATGCTTCCT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG  960
TTCTTCTAGA ATTAATTACT TTTATCTTTT GTCTTCATTT GTGGCCAAAA TTATGTTTAC 1020
TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGCTCTA TTGCATGGAT 1080
CCTTGGTAAT CCTCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTCTGC TAAATTAATG 1140
TTTATTTTGT GAGAAGTGAC TTTATCTTCA TTTGGGGTAG AAAAATTATT TCTTTATGTA 1200
GTAGAGACAA ATTATTCTCA TTTTGCAAGT ACTTTCAATT TAAGCTACAA ATTGAGAAAA 1260
CCGTTATAAA TAAGAATAAA ATAGGCCAGG CACAGTGGCT CACACCTGTA ATCCCAGCAC 1320
TTTGGGAGGC CGAGGTGGGC GGATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
ACCCTGTCTC TACTAAAAAT ACAAAAGTTA GCTGGGGCTG GTGGTGGGCA TCTGTAGTCC 1440
CAGCTAATTG GAAGGGTGAG GCGGGAGGAT CGCTTGAACC TGGGAGGCGG AGGTTCCAGA 1500
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GAGCCAAGAT CGCACCACTG CACTACAGCC TGGGCGACAG AACGAGACCC TGTCTCCAAA   1560
GGAAAAACAA AAAAGAAGAA TAAAATAATT TGGATGAAAA TCATGTTTAT TTAAATAGTA   1620
ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCAATGA AAATCATTAA AGTAGGACAG   1680
CTAAGAAATT AATATTAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCCTTA   1740
ACGCACTCCA TTCTCCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA   1800
GGACTTGATG AAACTGAGTA CTAAGATTTG GTACAGAGTA TGTCAGGAAG ACAACTCAGA   1860
TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAAAAAA AAAAA                   1906
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Seq ID NO: C90 DNA Sequence
Nucleic Acid Accession #: NM_004994
Coding sequence: 20..2143

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AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCCTG GTCCTGGTGC TCCTGGTGCT   60
GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA   120
CCTGAGAACC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA   180
CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCCTGCGC TGCTGCTTCT   240
CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT   300
GCGAACCCCA CGGTGCGGGG TCCCAGACCT GGGCAGATTC CAAACCTTTG AGGGCGACCT   360
CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGCCGCG   420
GGCGGTGATT GACGACGCCT TTGCCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCCGCT   480
CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTCGCGGA   540
GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC   600
TGGCCCCGGC ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA   660
GGGCGTCGTG GTTCCAACTC GGTTTGGAAA CGCAGATGGC GCGGCCTGCC ACTTCCCCTT   720
CATCTTCGAG GGCCGCTCCT ACTCTGCCTG CACCACCGAC GGTCGCTCCG ACGGCTTGCC   780
CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA   840
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Seq ID NO: C91 Sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 188.5656

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Seq ID NO: C92 DNA Sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 250..1326

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Seq ID NO: C94 DNA Sequence
Nucleic Acid Accession #: NM_006875
Coding sequence: 186..1190

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Seq ID NO: C95 DNA Sequence
Nucleic Acid Accession #: NM_002510.1
Coding sequence: 92..1774

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Seq ID NO: C96 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1…4247

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Seq ID NO: C97 DNA Sequence
Nucleic Acid Accession #: XM_031379
Coding sequence: 148..7095

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Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3340

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Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..4480

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Coding sequence: 1..4220

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Seq ID NO: C110 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 939..2372

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Seq ID NO: C111 DNA Sequence
Nucleic Acid Accession #: NM_130830.1
Coding sequence: 1..1746

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CTCAACACGC ACATCACTGA ACTCAATGAG TCCCCGTTCC TCAATATCTC AGCCCTCATC  240
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Seq ID NO: C112 DNA Sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77..1372

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Seq ID NO: C113 DNA Sequence
Nucleic Acid Accession #: XM_087254.1
Coding sequence: 47..2332

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GAGGGCTGTA AGCCTGAAGA TAGTGGCAAG CACCAAGTCA GTTTCCAAAA TTGCCCCTCA 4920
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Seq ID NO: C114 DNA Sequence
Nucleic Acid Accession #: XM_087461.1
Coding sequence: 236..1138

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CCGCTCGCCA TGCAACCGCC GCCGGCCTCG CGCGCGTAGG CGCCCGCCGC AGGCCATGCT  240
GCCCCTGCTC GCCGCGCTCC TGGCCGCCGC CTGCCCGCTG CCGCCCGTCC GCGGCGGGGC  300
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GGCGAGCCCA TCGCCCCGCG GCTGCTGGCC TCGGCGGCCC CCGGGCCCCC CGAGCGCCCG  420
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CGCCGCCGCC GCTGCCGCCG CCGCCGCGGC CGTCACTTCG GGGGTGGCGA CCAAGTGACC 1140
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Seq ID NO: C115 DNA Sequence
Nucleic Acid Accession #: XM_051522.4
Coding sequence: 127..1215

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Seq ID NO: C116 DNA Sequence
Nucleic Acid Accession #: NM_000350.1
Coding sequence: 82..6903

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Seq ID NO: C117 DNA Sequence
Nucleic Acid Accession #: NM_006671.2
Coding sequence: 138..1820

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AGCTGGAGAC CAATGTCTGA GCCTGCGGAG CTGCAGGGGC AGGCGAGGCC TCCAGGGGCA   1860
GGGTCCTGAG GCAGGAACTC GACTCTCCAA CCCTCCTGAG CAGCCGGCAG GGGCCAGGAT   1920
CACACATTCT TCTCACCCTT GAGAGGCTGG AATTAACCCC GCTTGACGGA AAATGTATCT   1980
CAGAGAAGGG AAAGGCTGCA TGGGGGAGCC CCATCCAGGG AGTGATGGGC CCGGCATTGC   2040
CTGAGGCCCC GCTGTGACAG TTTCCCCGGT GTGAGCCCGG TGAGGGCGGC AGGCAGGGGT   2100
TATCCGGCCC CACTTTCTGG ATGACAGACT TGAGGCTCTG AGAGCTGAAA ACACTTGTCC   2160
AAGGTCTCAC GTTAAGGTCA AGACACTAAC TCAAATCTTT CAAGCCCCGC CTCTCCTCTT   2220
GGAGGACAGG GCAGCCTGCA GCTGTGTCCA GGCCCAGGCC CCACCCCATA ACAGGTGGCC   2280
TCAGCCACAC AGTTCTCCCC AAGGGGAGCA GCCCAGGGCC AAGCCCCGCT GCCTTCCCCA   2340
GGCCACAGTG CGTCCAGTCT CCTGTCCTGC CACGTGTCTT TTGCAAAGCT CCTTGGATGT   2400
GGAGACAGAT GTCTTTACTA GAGCTGAAAG GCCCCCTTGA CACATCCAGG CCAACCTCCC   2460
ATGGAATAGG TAGGCAAGCC AGGACTCCGG GAAGGAGGTG CAGCCAGGAT GCTCTGGTGG   2520
AGCTGCCGAT GGGGCCCTGG TGTCAGAACT CCCCAAAGGC CTGTGCGTCC AAGTGGAGTC   2580
AGGTTTTCTA TTCCTTTCTG TGTTTGCAAA TTCAGTGTTA ACTAAATAAA GGTATTTTGT   2640
TTTTCAAAAA AAAAAAAAAA AAA                                           2663
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Seq ID NO: C118 DNA Sequence
Nucleic Acid Accession #: NM_005689
Coding sequence: 278..2806

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GTACGTGCCC TGCGTGAGTG CGTGGCGGCG GCGCGTGCGC TAGGGGAGTG GGCGGTGAGG   120
CCTGGTCCAC GTGCGTCCCT TCCCGGGACC CCCGCAGCTT GGCGCCCAGC GGCTACGTGA   180
GCCAAGGCAC CCGGATGTCC GCGCCCCTCT CCGAGTGACA AGTCCCGGCC TCCGGTCCCG   240
CAGTGCCCGC AGCCTCGGCC GGCGTCCACG CATTGCCATG GTGACTGTGG GCAACTACTG   300
CGAGGCCGAA GGGCCCGTGG GTCCGGCCTG GATGCAGGAT GGCCTGAGTC CCTGCTTCTT   360
CTTCACGCTC GTGCCCTCGA CGCGGATGGC TCTAGGGACT CTGGCCTTGG TGCTGGCTCT   420
TCCCTGCAGA CGCCGGGAGC GGCCCGCTGG TGCTGATTCG CTGTCTTGGG GGGCCGGCCC   480
TCGCATCTCT CCCTACGTGC TGCAGCTGCT TCTGGCCACA CTTCAGGCGG CGCTGCCCCT   540
GGCCGGCCTG GCTGGCCGGG TGGGCACTGC CCGGGGGGCC CCACTGCCAA GCTATCTACT   600
TCTGGCCTCC GTGCTGGAGA GTCTGGCCGG CGCCTGTGGC CTGTGGCTGC TTGTCGTGGA   660
GCGGAGCCAG GCACGGCAGC GTCTGGCAAT GGGCATCTGG ATCAAGTTCA GGCACAGCCC   720
TGGTCTCCTG CTCCTCTGGA CTGTGGCGTT TGCAGCTGAG AACTTGGCCC TGGTGTCTTG   780
GAACAGCCCA CAGTGGTGGT GGGCAAGGGC AGACTTGGGC CAACAGGTTC AGTTTAGCCT   840
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CCAGGTTCGG TCAGCAGCCC AACAGTCTAC CTGGCGAGAT TTTGGCAGGA AGCTCCGCCT   1020
CCTGAGTGGC TACCTGTGGC CTCGAGGGAG TCCAGCTCTG CAGCTGGTGG TGCTCATCTG   1080
CCTGGGGCTC ATGGGTTTGG AACGGGCACT CAATGTGTTG GTGCCTATAT TCTATAGGAA   1140
CATTGTGAAC TTGCTGACTG AGAAGGCACC TTGGAACTCT CTGGCCTGGA CTGTTACCAG   1200
TTACGTCTTC CTCAAGTTCC TCCAGGGGGG TGGCACTGGC AGTACAGGCT TCGTGAGCAA   1260
CCTGCGCACC TTCCTGTGGA TCCGGGTGCA GCAGTTCACG TCTCGGCGGG TGGAGCTGCT   1320
CATCTTCTCC CACCTGCACG AGCTCTCACT GCGCTGGCAC CTGGGGCGCC GCACAGGGGA   1380
GGTGCTGCGG ATCGCGGATC GGGGCACATC CAGTGTCACA GGGCTGCTCA GCTACCTGGT   1440
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CTTCAACGCC TGGTTTGGCC TCATTGTGTT CCTGTGCATG AGTCTTTACC TCACCCTGAC   1560
CATTGTGGTC ACTGAGTGGA GAACCAAGTT TCGTCGTGCT ATGAACACAC AGGAGAACGC   1620
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CGAGAGTTAC GAAGTGGAAC GCTATCGAGA GGCCATCATC AAATATCAGG GTTTGGAGTG   1740
GAAGTCGAGC GCTTCACTGG TTTTACTAAA TCAGACCCAG AACCTGGTGA TTGGGCTCGG   1800
GCTCCTCGCC GGCTCCCTGC TTTGCGCATA CTTTGTCACT GAGCAGAAGC TACAGGTTGG   1860
GGACTATGTG CTCTTTGGCA CCTACATTAT CCAGCTGTAC ATGCCCCTCA ATTGGTTTGG   1920
CACCTACTAC AGGATGATCC AGACCAACTT CATTGACATG GAGAACATGT TTGACTTGCT   1980
GAAAGAGGAG ACAGAAGTGA AGGACCTTCC TGGAGCAGGG CCCCTTCGCT TTCAGAAGGG   2040
CCGTATTGAG TTTGAGAACG TGCACTTCAG CTATGCCGAT GGGCGGGAGA CTCTGCAGGA   2100
CGTGTCTTTC ACTGTGATGC CTGGACAGAC ACTTGCCCTG GTGGGCCCAT CTGGGGCAGG   2160
GAAGAGCACA ATTTTGCGCC TGCTGTTTCG CTTCTACGAC ATCAGCTCTG GCTGCATCCG   2220
AATAGATGGG CAGGACATTT CACAGGTGAC CCAGGCCTCT CTCCGGTCTC ACATTGGAGT   2280
TGTGCCCCAA GACACTGTCC TCTTTAATGA CACCATCGCC GACAATATCC GTTACGGCCG   2340
TGTCACAGCT GGGAATGATG AGGTGGAGGC TGCTGCTCAG GCTGCAGGCA TCCATGATGC   2400
CATTATGGCT TTCCCTGAAG GGTACAGGAC ACAGGTGGGC GAGCGGGGAC TGAAGCTGAG   2460
CGGCGGGGAG AAGCAGCGCG TCGCCATTGC CCGCACCATC CTCAAGGCTC CGGGCATCAT   2520
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GGTCAATGCT GACCAGATCC TCGTCATCAA GGATGGCTGC ATCGTGGAGA GGGGACGACA   2700
CGAGGCTCTG TTGTCCCGAG GTGGGGTGTA TGCTGACATG TGGCAGCTGC AGCAGGGACA   2760
GGAAGAAACC TCTGAAGACA CTAAGCCTCA GACCATGGAA CGGTGACAAA AGTTTGGCCA   2820
CTTCCCTCTC AAAGACTAAC CCAGAAGGGA ATAAGATGTG TCTCCTTTCC CTGGCTTATT   2880
TCATCCTGGT CTTGGGGTAT GGTGCTAGCT ATGGTAAGGG AAAGGGACCT TTCCGAAAAA   2940
CATCTTTTGG GGAAATAAAA ATGTGGACTG TGAAAAAAAA AAAAAAAAAA AAA           2993
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Seq ID NO: C119 DNA Sequence
Nucleic Acid Accession #: NM_000676
Coding sequence: 333..1331

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CCCCGCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA  120
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GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG  240
GGCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG  300
TAGGGGGCGC CCGGGGCCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT  360
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CCGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCCACCAA CTACTTCCTG GTGTCCCTGG  480
CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCCTT TGCCATCACC ATCAGCCTGG  540
GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC  600
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CGCTCAGGTA TAAAAGTTTG GTCACGGGGA CCCGAGCAAG AGGGGTCATT GCTGTCCTCT  720
GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG  780
CCACCAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCTTGTGA  840
AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCAAT TTCTTTGGGT  900
GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT  960
GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCCTC CAGCGGGAGA 1020
TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG 1080
TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT 1140
GGGCAATGAA TATGGCCATT CTTCTGTCAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT 1200
ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC 1260
TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG 1320
TGGGCCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA 1380
AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATGGACTGC 1440
CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAGTAGT 1500
AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTCAG CTGCTTTTAC TGTGTGGATT 1560
ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGTT TTTAAAAGTC TGCCTTGTTT 1620
ATGGTGGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACTATT ATAATGCAAA 1680
TACTTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAA ATG         1733
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Seq ID NO: C120 DNA Sequence
Nucleic Acid Accession #: NM_052932
Coding sequence: 217..786

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CGCCCTATTT GGTCATTCGG GGGGCAAGCG GCGGGAGGGG AAACGTGCGC GGCCGAAGGG  120
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GAGCCCACGA GGCTGCCGCA TCCTGCCCTC GGAACAATGG GACTCGGCGC GCGAGGTGCT  240
TGGGCCGCGC TGCTCCTGGG GACGCTGCAG GTGCTAGCGC TGCTGGGGGC CGCCCATGAA  300
AGCGCAGCCA TGGCGGAGAC TCTCCAACAT GTGCCTTCTG ACCATACAAA TGAAACTTCC  360
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ACCATGAAAC CTACAGCGGC ATCTAATACA ACAACACCAG GGATGGTCTC AACAAATATG  480
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ATATCAACAT CCACAATGAC CGTAACCCAC AATAGTTCAG TGACATCTGC TGCTTCATCA  600
GTAACAATCA CAACAACTAT GCATTCTGAA GCAAAGAAAG GATCAAAATT TGATACTGGG  660
AGCTTTGTTG GTGGTATTGT ATTAACGCTG GGAGTTTTAT CTATTCTTTA CATTGGATGC  720
AAAATGTATT ACTCAAGAAG AGGCATTCGG TATCGAACCA TAGATGAACA TGATGCCATC  780
ATTTAAGGAA ATCCATGGAC CAAGGATGGA ATACAGATTG ATGCTGCCCT ATCAATTAAT  840
TTTGGTTTAT TAATAGTTTA AAACAATATT CTCTTTTTGA AAATAGTATA AACAGGCCAT  900
GCATATAATG TACAGTGTAT TACGTAAATA TGTAAAGATT CTTCAAGGTA ACAAGGGTTT  960
GGGTTTTGAA ATAAACATCT GGATCTTATA GACCGTTCAT ACAATGGTTT TAGCAAGTTC 1020
ATAGTAAGAC AAACAAGTCC TATCTTTTTT TTTTTGGCTG GGGTGGGGGC ATTGGTCACA 1080
TATGACCAGT AATTGAAAGA CGTCATCACT GAAAGACAGA ATGCCATCTG GGCATACAAA 1140
TAAGAAGTTT GTCACAGCAC TCAGGATTTT GGGTATCTTT TGTAGCTCAC ATAAAGAACT 1200
TCAGTGCTTT TCAGAGCTGG ATATATCTTA ATTACTAATG CCACACAGAA ATTATACAAT 1260
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ACCACTGGAA GTTACTTTAG TTCATTTAAT TTTAATTTTA TATTTTGTGA ATATTTTAAG 1680
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ACTATAGCGT AATGCTGTGT TTATTAAGCC AGGGATTGTG GGACTTCCCC CAGGCAACTA 1860
AACCTGCAGG ATGAAAATGC TATATTTTCT TTCATGCACT GTCGATATTA CTCAGATTTG 1920
GGGAAATGAC ATTTTTATAC TAAAACAAAC ACCAAAATAT TTTAGAATAA ATTCTTAGAA 1980
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CATTTTACAG TTTATATTCC AGCACTCAAA ACTCAGGGTC AAGTTTTAAC AAAAGAGGTA 2220
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CAGTTTCTGA AGGTCCTAAA AATAGCTCAG ATGTCCTAAT GAACATGCAC CTACATTTAA 2340
TAGGAGTACA ATAAAACTGT TGTCAGCTTT TGTTTTACAG AGAACGCTAG ATATTAAGAA 2400
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AAAAAATGAT CCAAAATATG GATATGATTG GATGTATGTA ACACATACAT GGAGTATGGA 2520
GGAAATTTTC TGAAAAATAC ATTTAGATTA GTTTAGTTTG AAGGAGAGGT GGGCTGATGC 2580
CTGAGTTGTA TGTTACTAAC TTGGCCCTGA CTGGTTGTGC AACCATTGCT TCATTTCTTT 2640
GCAAAATGTA GTTAAGATAT ACTTTATTCT AATGAAGGCC TTTTAAATTT GTCCACTGCA 2700
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TTCTTGGTAT TTCACTACTT CAAGTCAGTC AGAACTTCGT AGACCGACCT GAAGTTTCTT   2760
TTTGAATACT TGTTTCTTTA GCACTTTGAA GATAGAAAAA CCACTTTTTA AGTACTAAGT   2820
CATCATTTGC CTTGAAAGTT TCCTCTGCAT TGGGTTTGAA GTAGTTTAGT TATGTCTTTT   2880
TCTCTGTATG TAAGTAGTAT AATTTGTTAC TTTCAAATAC CCGTACTTTG AATGTAGGTT   2940
TTTTTGTTGT TGTTATCTAT AAAAATTGAG GGAAATGGTT ATGCAAAAAA ATATTTTGCT   3000
TTGGACCATA TTTCTTAAGC ATAAAAAAAT GCTCAGTTTT GCTTGCATTC CTTGAGAATG   3060
TATTTATCTG AAGATCAAAA CAAACAATCC AGATGTATAA GTACTAGGCA GAAGCCAATT   3120
TTAAAATTTC CTTGAATAAT CCATGAAAGG AATAATTCAA ATACAGATAA ACAGAGTTGG   3180
CAGTATATTA TAGTGATAAT TTTGTATTTT CAAMAAAAAA AAAGTTAAAC TCTTCTTTTC   3240
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Seq ID NO: C121 DNA Sequence
Nucleic Acid Accession #: NM_004195
Coding sequence: 1..726

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GCGCTCAGCC TGGGTCAGCG CCCCACCGGG GGTCCCGGGT GCGGCCCTGG GCGCCTCCTG  120
CTTGGGACGG GAACGGACGC GCGCTGCTGC CGGGTTCACA CGACGCGCTG CTGCCGCGAT  180
TACCCGGGCG AGGAGTGCTG TTCCGAGTGG GACTGCATGT GTGTCCAGCC TGAATTCCAC  240
TGCGGAGACC CTTGCTGCAC GACCTGCCGG CACCACCCTT GTCCCCCAGG CCAGGGGGTA  300
CAGTCCCAGG GGAAATTCAG TTTTGGCTTC CAGTGTATCG ACTGTGCCTC GGGGACCTTC  360
TCCGGGGGCC ACGAAGGCCA CTGCAAACCT TGGACAGACT GCACCCAGTT CGGGTTTCTC  420
ACTGTGTTCC CTGGGAACAA GACCCACAAC GCTGTGTGCG TCCCAGGGTC CCCGCCGGCA  480
GAGCCGCTTG GGTGGCTGAC CGTCGTCCTC CTGGCCGTGG CCGCCTGCGT CCTCCTCCTG  540
ACCTCGGCCC AGCTTGGACT GCACATCTGG CAGCTGAGGA GTCAGTGCAT GTGGCCCCGA  600
GAGACCCAGC TGCTGCTGGA GGTGCCGCCG TCGACCGAAG ACGCCAGAAG CTGCCAGTTC  660
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Seq ID NO: C122 DNA Sequence
Nucleic Acid Accession #: AK091896.1
Coding sequence: 28..1572

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CAGATCTCCT GGGTCTTCTT CTCGCAGCAG CTCTGCCTCC TGCTGGGCAG CGCCCTCGGG  240
GGCGTCTTCA AAAGGACCCT GGCCCAGTCA CTATGGGCCC TGTTCACCTC CTCTCTGGCC  300
ATCTCCCTGG TGTTTGCCGT CATCCCCTTC TGCCGCGACG TGAAGGTGCT GGCCTCAGTC  360
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GCCAATAGCA CGGCCAACAC CACCTCCCGA GGCCACCTGT TCCATGTCTC CAGGGTGCTG  600
GGCCAGCACC ACGTAGATGC CAAGCCTTGG TCCAACCAGA CGTTCCCAGG GCTGACTCCA  660
AAGGACGGGG CAGGGACCCG AGTGTCCTAT GCCTTCTGGA TCATGGCCCT CATCGATCTT  720
CCAGTGCCCA TGGCTGTGCT GATGCTGCTG TCCAAGGAGC GGCTGCTGAC CTGCTGTCCC  780
CAGAGGAGGC CCCTGCTTCT GTCTGCTGAT GAGCTTGCCT TGGAGACACA GCCTCCTGAG  840
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TTCAGCTGCT GCCAAAGGAA GAACCTCAGA GGAGCCCCTT ATTCCTTCTT TGCCATCCAC  960
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GTGTACAGCT ATGCTGTGGA GAAGCCCCTG TCTGTGGGAC ACAAGGTGGC TGGCTACCTC 1080
CCCAGCCTCT TCTGGGGCTT CATCACACTG GGCCGGCTCC TCTCCATTCC CATATCCTCA 1140
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GTGCTGCTTA TTTTCTCCTA CAACGTCGTC TTCCTGTTCG TGGGGACGGC AAGCCTGGGC 1260
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ATGCTGGTTG GTTCGATATT CCAGGCTCAG GGCAGCTATA GTTTCCTGGT CTGTGGCGTG 1440
ATCTTTGGTT GTCTGGCTTT TACCTTCTAT ATCTTGCTCC TGTTTTTCCA CAGGATGCAC 1500
CCTGGACTCC CATCAGTTCC TACCCAAGAC AGATCAATTG GAATGGAAAA CTCTGAGTGC 1560
TACCAGAGGT AAAACTGGGT GAAGAAGGCA AGAGAAGACT TTCAGCCTCT TGATCACCAG 1620
CACGACCATA CTGTTTCAGA AAGCTGGGTG GTGGTGGAGG CGCTCTCTCA ATGGCTATTC 1680
AAGTCTTCTC CACTAAAACT TGGTTGGGTA GAGGAAATTA AATTGAGTCC TGGTACCTGG 1740
TCAAAATCAT TAGAAGTTTA CCTGGCTTCT CAAGTTATCT TCTTCCCTGG TTCAGACTGT 1800
TGGTAAGAGC TGTCCAGATA CCCAGATGGG AAGGAAGGAG ACAGCCGCGC GCTTCACTCC 1860
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TATTAAATGC AGCCATTATT AAAAATCAAA TCATACAAAC TTATAATTAA ATCAATTACA 2280
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Seq ID NO: C123 DNA Sequence
Nucleic Acid Accession #: NM_002203.2
Coding sequence: 43..3588

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TGTTTGGCCT ACAATGTTGG TCTCCCAGAA GCAAAAATAT TTTCCGGTCC TTCAAGTGAA  180
CAGTTTGGGT ATGCAGTGCA GCAGTTTATA AATCCAAAAG GCAACTGGTT ACTGGTTGGT  240
TCACCCTGGA GTGGCTTTCC TGAGAACCGA ATGGGAGATG TGTATAAATG TCCTGTTGAC  300
CTATCCACTG CCACATGTGA AAAACTAAAT TTGCAAACTT CAACAAGCAT TCCAAATGTT  360
ACTGAGATGA AAACCAACAT GAGCCTCGGC TTGATCCTCA CCAGGAACAT GGGAACTGGA  420
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GGTGTGTGTT CTGACATCAG TCCTGATTTT CAGCTCTCAG CCAGCTTCTC ACCTGCAACT  540
CAGCCCTGCC CTTCCCTCAT AGATGTTGTG GTTGTGTGTG ATGAATCAAA TAGTATTTAT  600
CCTTGGGATG CAGTAAAGAA TTTTTTGGAA AAATTTGTAC AAGGCCTTGA TATAGGCCCC  660
ACAAAGACAC AGGTGGGGTT AATTCAGTAT GCCAATAATC CAAGAGTTGT GTTTAACTTG  720
AACACATATA AAACCAAAGA AGAAATGATT GTAGCAACAT CCCAGACATC CCAATATGGT  780
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GCTTCTGGTG GGCGACGAAG TGCTACGAAA GTAATGGTAG TTGTAACTGA CGGTGAATCA  900
CATGATGGTT CAATGTTGAA AGCTGTGATT GATCAATGCA ACCATGACAA TATACTGAGG  960
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GAAGCAGCTC TACTAGAAAA GGCTGGGACA TTAGGAGAAC AAATTTTCAG CATTGAAGGT 1140
ACTGTTCAAG GAGGAGACAA CTTTCAGATG GAAATGTCAC AAGTGGGATT CAGTGCAGAT 1200
TACTCTTCTC AAAATGATAT TCTGATGCTG GGTGCAGTGG GAGCTTTTGG CTGGAGTGGG 1260
ACCATTGTCC AGAAGACATC TCATGGCCAT TTGATCTTTC CTAAACAAGC CTTTGACCAA 1320
ATTCTGCAGG ACAGAAATCA CAGTTCATAT TTAGGTTACT CTGTGGCTGC AATTTCTACT 1380
GGAGAAAGCA CTCACTTTGT TGCTGGTGCT CCTCGGGCAA ATTATACCGG CCAGATAGTG 1440
CTATATAGTG TGAATGAGAA TGGCAATATC ACGGTTATTC AGGCTCACCG AGGTGACCAG 1500
ATTGGCTCCT ATTTTGGTAG TGTGCTGTGT TCAGTTGATG TGGATAAAGA CACCATTACA 1560
GACGTGCTCT TGGTAGGTGC ACCAATGTAC ATGAGTGACC TAAAGAAAGA GGAAGGAAGA 1620
GTCTACCTGT TTACTATCAA AAAGGGCATT TTGGGTCAGC ACCAATTTCT TGAAGGCCCC 1680
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Seq ID NO: C124 DNA Sequence
Nucleic Acid Accession #: NM_031460
Coding sequence: 103..1101

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Seq ID NO: C125 DNA Sequence
Nucleic Acid Accession #: NM_004154
Coding sequence: 309..1295

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CCTGTCATCT GGATAGTGTC TAAAAATTTG CAAACTGCCT TCTTGTCAGT GTCTTGCTCA  240
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TGCCAGAACA TTGCACGCGA CAGTTTCAGG CACAGAACTG ACTGGCAGCA GGGGCTGCTC  360
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Seq ID NO: C126 DNA Sequence
Nucleic Acid Accession #: NM_007197
Coding sequence: 18..1763

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Seq ID NO: C127 DNA Sequence
Nucleic Acid Accession #: NM_005761.1
Coding sequence: 250..4956

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GACCACTGCC ATTTGATTTT ACCAGATTCG GAAGCATTCC AAGATGTGCA AGGAAAGAGA   4260
CATCGAGGGA AGCACAAGTT CAAAGTAAAA GAAATGTATC TGACAAAGCT GCTGTCGACC   4320
AAGGTGGCAA TTCATTCTGT GCTTGAAAAA CTTTTTAGAA GCATTTGGAG TTTACCCAAC   4380
AGCAGAGCTC CATTTGCTAT AAAATACTTT TTTGACTTTT TGGACGCCCA GGCTGAAAAC   4440
AAAAAAATCA CAGATCCTGA CGTCGTACAT ATTTGGAAAA CAAACAGCCT TCCTCTTCGC   4500
TTCTGGGTAA ACATCCTGAA GAACCCTCAG TTTGTCTTTG ACATTAAGAA GACACCACAT   4560
ATAGACGGCT GTTTGTCAGT GATTGCCCAG GCATTCATGG ATGCATTTTC TCTCACAGAG   4620
CAGCAACTAG GGAAGGAAGC ACCAACTAAT AAGCTTCTCT ATGCCAAGGA TATCCCAACC   4680
TACAAAGAAG AAGTAAAATC TTATTACAAA GCAATCAGGG ATTTGCCTCC ATTGTCATCC   4740
TCAGAAATGG AAGAATTTTT AACTCAGGAA TCTAAGAAAC ATGAAAATGA ATTTAATGAA   4800
GAAGTGGCCT TGACAGAAAT TTACAAATAC ATCGTAAAAT ATTTTGATGA GATTCTAAAT   4860
AAACTAGAAA GAGAACGAGG GCTGGAAGAA GCTCAGAAAC AACTCTTGCA TGTAAAAGTC   4920
TTATTTGATG AAAAGAAGAA ATGCAAGTGG ATGTAAGCAC TCTGGGGCCT GGCTTAATCT   4980
GGCAAAGTTC TTCAGACGAC TTGGGAGCAA AATGGCTGCT TGAGCTACTC TGTGTCGTTA   5040
ATTGTTGTT TGCACATAGG TTCCACTTTG GGCACTGTCT TTTTAAGAGA CCAAGGCACA   5100
TGCACAGCTT TTAGAAAGCA A                                             5121
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Seq ID NO: C128 DNA Sequence
Nucleic Acid Accession #: NM_002185.1
Coding sequence: 23..1402

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CTCTCTCTCT ATCTCTCTCA GAATGACAAT TCTAGGTACA ACTTTTGGCA TGGTTTTTTC   60
TTTACTTCAA GTCGTTTCTG GAGAAAGTGG CTATGCTCAA AATGGAGACT TGGAAGATGC  120
AGAACTGGAT GACTACTCAT TCTCATGCTA TAGCCAGTTG GAAGTGAATG GATCGCAGCA  180
TTCACTGACC TGTGCTTTTG AGGACCCAGA TGTCAACACC ACCAATCTGG AATTTGAAAT  240
ATGTGGGGCC CTCGTGGAGG TAAAGTGCCT GAATTTCAGG AAACTACAAG AGATATATTT  300
CATCGAGACA AAGAAATTCT TACTGATTGG AAAGAGCAAT ATATGTGTGA AGGTTGGAGA  360
AAAGAGTCTA ACCTGCAAAA AAATAGACCT AACCACTATA GTTAAACCTG AGGCTCCTTT  420
TGACCTGAGT GTCATCTATC GGGAAGGAGC CAATGACTTT GTGGTGACAT TTAATACATC  480
ACACTTGCAA AAGAAGTATG TAAAAGTTTT AATGCATGAT GTAGCTTACC GCCAGGAAAA  540
GGATGAAAAC AAATGGACGC ATGTGAATTT ATCCAGCACA AAGCTGACAC TCCTGCAGAG  600
AAAGCTCCAA CCGGCAGCAA TGTATGAGAT TAAAGTTCGA TCCATCCCTG ATCACTATTT  660
TAAAGGCTTC TGGAGTGAAT GGAGTCCAAG TTATTACTTC AGAACTCCAG AGATCAATAA  720
TAGCTCAGGG GAGATGGATC CTATCTTACT AACCATCAGC ATTTTGAGTT TTTTCTCTGT  780
CGCTCTGTTG GTCATCTTGG CCTGTGTGTT ATGGAAAAAA AGGATTAAGC CTATCGTATG  840
GCCCAGTCTC CCCGATCATA AGAAGACTCT GGAACATCTT TGTAAGAAAC CAAGAAAAAA  900
TTTAAATGTG AGTTTCAATC CTGAAAGTTT CCTGGACTGC CAGATTCATA GGGTGGATGA  960
CATTCAAGCT AGAGATGAAG TGGAAGGTTT TCTGCAAGAT ACGTTTCCTC AGCAACTAGA 1020
AGAATCTGAG AAGCAGAGGC TTGGAGGGGA TGTGCAGAGC CCCAACTGCC CATCTGAGGA 1080
TGTAGTCGTC ACTCCAGAAA GCTTTGGAAG AGATTCATCC CTCACATGCC TGGCTGGGAA 1140
TGTCAGTGCA TGTGACGCCC CTATTCTCTC CTCTTCCAGG TCCCTAGACT GCAGGGAGAG 1200
TGGCAAGAAT GGGCCTCATG TGTACCAGGA CCTCCTGCTT AGCCTTGGGA CTACAAACAG 1260
```

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CACGCTGCCC CCTCCATTTT CTCTCCAATC TGGAATCCTG ACATTGAACC CAGTTGCTCA   1320
GGGTCAGCCC ATTCTTACTT CCCTGGGATC AAATCAAGAA GAAGCATATG TCACCATGTC   1380
CAGCTTCTAC CAAAACCAGT GAAGTGTAAG AAACCCAGAC TGAACTTACC GTGAGCGACA   1440
AAGATGATTT AAAAGGGAAG TCTAGAGTTC CTAGTCTCCC TCACAGCACA GAGAAGACAA   1500
AATTAGCAAA ACCCCACTAC ACAGTCTGCA AGATTCTGAA ACATTGCTTT GACCACTCTT   1560
CCTGAGTTCA GTGGCACTCA ACATGAGTCA AGAGCATCCT GCTTCTACCA TGTGGATTTG   1620
GTCACAAGGT TTAAGGTGAC CCAATGATTC AGCTATTT                           1658
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Seq ID NO: C129 DNA Sequence
Nucleic Acid Accession #: NM_002722.1
Coding sequence: 15..302

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ACTCTGGACT CCGGATGGCT GCCGCACGCC TCTGCCTCTC CCTGCTGCTC CTGTCCACCT   60
GCGTGGCTCT GTTACTACAG CCACTGCTGG GTGCCCAGGG AGCCCCACTG GAGCCAGTGT   120
ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCCAGTA TGCAGCTGAT CTCCGTAGAT   180
ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAAGACA CAAAGAGGAC ACGCTGGCCT   240
TCTCGGAGTG GGGGTCCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT   300
AATGCCACCT TCTGTCTCCT ACGACTCCAT GAGCAGCGCC AGCCCAGCTC TCCCCTCTGC   360
ACCCTTGGCT CTGGCCAAAG CTTGCTCCCT GCTCCCACAC AGGCTCAATA AAGCAAGTCA   420
AAGCC                                                              425
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Seq ID NO: C130 DNA Sequence
Nucleic Acid Accession #: NM_032545.1
Coding sequence: 47..718

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1          11         21         31         41         51
|          |          |          |          |          |
AAACTGATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CCTGGAGGCA   60
CCATGTCAGG CTTCTGTTTA CGGTCAGTTT GGCATTACAG ATCATCAATT TGGGAAACAG   120
CTATCAAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA   180
GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC   240
CGAGGGCTGG GGGCCGGAGG AGCCGCTCCC CTACTCCCGG GCTTTCGGAG AGGGTGCGTC   300
CGCGCGGCCG CGCTGCTGCA GGAACGGCGG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG   360
CCCGGCCCAC TTCACCGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC   420
CCTGGAGCAC GGAGCCTGGA CCCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGGC   480
CCTGCACTGC CTCCCCCTCC AGACGCCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC   540
CCACGCTCAC GGGCCGAGCG CCGGGGGCGC GCCCAGCCTG CTACTCTTGC TGCCCTGCGC   600
ACTCCTGCAC CGCCTCCTGC GCCCGGATGC GCCCGCGCAC CCTCGGTCCC TGGTCCCTTC   660
CGTCCTCCAG CGGGAGCGGC GCCCCTGCGG AAGGCCGGGA CTTGGGCATC GCCTTTAATT   720
TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA   780
TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA   840
AAAAAA                                                             846
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Seq ID NO: C131 DNA Sequence
Nucleic Acid Accession #: NM_006533.1
Coding sequence: 72..467

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CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT   120
TCTCCGGACC TGGTGTCAGG GGTGGTCCTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG   180
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC   240
CCGACTGCCG ATTCCTGACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA   300
AGGGCCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG   360
CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG   420
GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG   480
CTGGCCCTGC CGTTTCCCCT CCTTGGGTTT ATGCAAATAC AATCAGCCCA GTGCAAAC     538
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Seq ID NO: C132 DNA Sequence
Nucleic Acid Accession #: AB064272
Coding sequence: 1..708

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AAAACCACAA GAACCCCAGA AAAGCCTACG CTATACTCAG AGAAGACCAT ATGCACCAAA   120
GGGAAAAACA CACCAGTCCC AGAAAAGCCT ACAGAAAACC TGGGGAACAC CACACTGACC   180
ACTGAGACCA TAAAAGCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC   240
ACAAAGACTA TAAAACCTTC AGTCAAGGTC ACAGGAGACA AATCTCTCAC TACTACCTCT   300
TCTCATCTAA ATAAAACTGA AGTTACTCAT CAGGTGCCCA CTGGTTCTTT CACCCTCATT   360
ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAAGCCA CAGGAAACGA GAGCCATCCA   420
TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCACGCTG GACAGATGGG AGAGAATGAT   480
TCATTCCCTG CATGGGCCAT AGTTATTGTG GTCCTGGTGG CTGTGATTCT CCTCCTGGTG   540
TTCCTTGGCC TGATCTTCTT GGTCTCCTAT ATGATGCGGA CACGCCGCAC ACTAACCCAG   600
AACACCCAGT ACAATGATGC AGAGGATGAG GGTGGCCCCA ATTCCTACCC GGTCTACCTG   660
ATGGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGGTGA                708
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Seq ID NO: C133 DNA Sequence
Nucleic Acid Accession #: NM_080870.1
Coding sequence: 3..710

WO03042661 [file:///E:/WO03042661.epc]


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AGAAAACCAC AAGAACCCCA GAAAAGCCTA CGCTATACTC AGAGAAGACC ATATGCACCA  120
AAGGGAAAAA CACACCAGTC CCAGAAAAGC CTACAGAAAA CCTGGGGAAC ACCACACTGA  180
CCACTGAGAC CATAAAAGCC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG  240
TCACAAAGAC TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT  300
CTTCTCATCT AAATAAAACT GAAGTTACTC ATCAGGTGCC CACTGGTTCT TTCACCCTCA  360
TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAAGC CACAGGAAAC GAGAGCCATC  420
CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAATG  480
ATTCATTCCC TGCATGGGCC ATAGTTATTG TGGTCCTGGT GGCTGTGATT CTCCTCCTGG  540
TGTTCCTTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACACGCCGC ACACTAACCC  600
AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAATTCCTAC CCGGTCTACC  660
TGATGGAGCA GCAGAATCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGGAGTA  720
GGCGCCCAGC CCTGGCTCTT CCATGCTCTG CCCCTTTCCT GGATGAGGAA CCGGACTCAC  780
AATTTCTATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAACC  840
CTTCATCTGT TCTTGAAACT GGTTGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT  900
AGGGGACAAA GAAGAAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGGT  960
CTGAGAATGA AAAGGTGTTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC 1020
TGAGTCCTAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080
GGTTTATGGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTTCAGGA CAGCATTATG 1140
TTATTTCCAT TCACTATTAC TTAAGAGTTT GTGTGTAAAC AGGCTCATCT CTGAGTTCTC 1200
AGGACCCTTG CCCCCACCCC CATTTTTTTA ATGAAAAAAA AAAACAAAAA AAACGGATCC 1260
AAGAAGAAAA GAGAATTTAT TTCCTTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAAGT 1320
CCAGAAGAAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTTCCT CCCAAATCCC 1380
TTAGTTTTCC TAAATGTCTA CAGTGGACGC CCTGTTGGTT TGGCTTGCTG GGTTGTGGGT 1440
GGACACGCAA GGAGGGGATT TTTATTTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500
GACCTTCCCT GATTGGTGTC TCAGCATTTA TTTTCCTGTC TCTTCCACCA AAAGCCAGCT 1560
GTAGCTTTAT CTCGTAAAAG TTACCCATCT TCTCTACTGT CCCCATTCTC TCTCCTCCCA 1620
CCTTCACCCC AGATTCAAGT TTTCCTCCTT GTAGGCATTT CATCTGTGTG TGTTTTCTGG 1680
ATTTTCTCTC TCTCTTCTTA TGGCCATTTC ACCTTATTAC TGATTGGGTA GAGGGGGAAA 1740
AGGAGAATGA TGATGATAGT TTCCTTCTGT CTATTGACCT TTTTTATAAT AAAGTATAAC 1800
ATGTT                                                             1805
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Seq ID NO: C134 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..10674

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GGGGCCCCCG GGAGTATCCC CGCGCCGCCC GCTCCTGGCG ACGAAGCGGC GGGGAGCAGA  180
GTGGAGCGGC TGGGCCAGGC GTTCCGGCGA CGCGTGCGGC TGCTGCGGGA GCTCAGCGAG  240
CGCCTGGAGC TTGTCTTCCT GGTGGATGAT TCGTCCAGCG TGGGCGAAGT CAACTTCCGC  300
AGCGAGCTCA TGTTCGTCCG CAAGCTGCTG TCCGACTTCC CCGTGGTGCC CACGGCCACG  360
CGCGTGGCCA TCGTGACCTT CTCGTCCAAG AACTACGTGG TGCCGCGCGT CGATTACATC  420
TCCACCCGCC GCGCGCGCCA GCACAAGTGC GCGCTGCTCC TCCAAGAGAT CCCTGCCATC  480
TCCTACCGAG GTGGCGGCAC CTACACCAAG GGCGCCTTCC AGCAAGCCGC GCAAATTCTT  540
CTTCATGCTA GAGAAAACTC AACAAAAGTT GTATTTCTCA TCACTGATGG ATATTCCAAT  600
GGGGGAGACC CTAGACCAAT TGCAGCGTCA CTGCGAGATT CAGGAGTGGA GATCTTCACT  660
TTTGGCATAT GGCAAGGGAA CATTCGAGAG CTGAATGACA TGGCTTCCAC CCCAAAGGAG  720
GAGCACTGTT ACCTGCTACA CAGTTTTGAA GAATTTGAGG CTTTAGCTCG CCGGGCATTG  780
CATGAAGATC TACCTTCTGG GAGTTTTATT CAAGATGATA TGGTCCACTG CTCATATCTT  840
TGTGATGAAG GCAAGGACTG CTGTGACCGA ATGGGAAGCT GCAAATGTGG GACACACACA  900
GGCCATTTTG AGTGCATCTG TGAAAAGGGG TATTACGGGA AAGGTCTGCA GTATGAATGC  960
ACAGCTTGCC CATCGGGGAC ATACAAACCT GAAGGCTCAC CAGGAGGAAT CAGCAGTTGC 1020
ATTCCATGTC CTGATGAAAA TCACACCTCT CCACCTGGAA GCACATCCCC TGAAGACTGT 1080
GTCTGCAGAG AGGGATACAG GGCATCTGGC CAGACCTGTG AACTTGTCCA CTGCCCTGCC 1140
CTGAAGCCTC CCGAAAATGG TTACTTTATC CAAAACACTT GCAACAACCA CTTCAATGCA 1200
GCCTGTGGGG TCCGATGTCA CCCTGGATTT GATCTTGTGG GAAGCAGCAT CATCTTATGT 1260
CTACCCAATG GTTTGTGGTC CGGTTCAGAG AGCTACTGCA GAGTAAGAAC ATGTCCTCAT 1320
CTCCGCCAGC CGAAACATGG CCACATCAGC TGTTCTACAA GGGAAATGTT ATATAAGACA 1380
ACATGTTTGG TTGCCTGTGA TGAAGGGTAC AGACTAGAAG GCAGTGATAA GCTTACTTGT 1440
CAAGGAAACA GCCAGTGGGA TGGGCCAGAA CCCCGGTGTG TGGAGCGCCA CTGTTCCACC 1500
TTTCAGATGC CCAAAGATGT CATCATATCC CCCCACAACT GTGGCAAGCA GCCAGCCAAA 1560
TTTGGGACGA TCTGCTATGT AAGTTGCCGC CAAGGGTTCA TTTTATCTGG AGTCAAAGAA 1620
ATGCTGAGAT GTACCACTTC TGGAAAATGG AATGTCGGAG TTCAGGCAGC TGTGTGTAAA 1680
GACGTGGAGG CTCCTCAAAT CAACTGTCCT AAGGACATAG AGGCTAAGAC TCTGGAACAG 1740
CAAGATTCTG CCAATGTTAC CTGGCAGATT CCAACAGCTA AAGACAACTC TGGTGAAAAG 1800
GTGTCAGTCC ACGTTCATCC AGCTTTCACC CCACCTTACC TTTTCCCAAT TGGAGATGTT 1860
GCTATCGTAT ACACGGCAAC TGACCTATCC GGCAACCAGG CCAGCTGCAT TTTCCATATC 1920
AAGGTTATTG ATGCAGAACC ACCTGTCATA GACTGGTGCA GATCTCCACC TCCCGTCCAG 1980
GTCTCGGAGA AGGTACATGC CGCAAGCTGG GATGAGCCTC AGTTCTCAGA CAACTCAGGG 2040
GCTGAATTGG TCATTACCAG AAGTCATACA CAAGGAGACC TTTTCCCTCA AGGGGAGACT 2100
ATAGTACAGT ATACAGCCAC TGACCCCTCA GGCAATAACA GGACATGTGA TATCCATATT 2160
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ACTCCAGATA ATACTGGAGT CAACTGTACA TTAACTTGCT TGGAGGGCTA TGATTTCACA 2280
GAAGGGTCTA CTGACAAGTA TTATTGTGCT TATGAAGATG GCGTCTGGAA ACCAACATAT 2340
ACCACTGAAT GGCCAGACTG TGCCAAAAAA CGTTTTGCAA ACCACGGGTT CAAGTCCTTT 2400
GAGATGTTCT ACAAAGCAGC TCGTTGTGAT GACACAGATC TGATGAAGAA GTTTTCTGAA 2460
GCATTTGAGA CGACCCTGGG AAAAATGGTC CCATCATTTT GTAGTGATGC AGAGGACATT 2520
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GACTGCAGAC TGGAGGAGAA CCTGACCAAA AAATATTGCC TAGAATATAA TTATGACTAT 2580
GAAAATGGCT TTGCAATTGG ACCAGGTGGC TGGGGTGCAG CTAATAGGCT GGATTACTCT 2640
TACGATGACT TCCTGGACAC TGTGCAAGAA ACAGCCACAA GCATCGGCAA TGCCAAGTCC 2700
TCACGGATTA AAAGAAGTGC CCCATTATCT GACTATAAAA TTAAGTTAAT TTTTAACATC 2760
ACAGCTAGTG TGCCATTACC CGATGAAAGA AATGATACCC TTGAATGGGA AAATCAGCAA 2820
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CCCATGTATT CCTTTCAGCT TGCATCAGAA ATACTTATAG CCGACAGCAA TTCATTAGAA 2940
ACAAAAAAGG CTTCCCCCTT CTGCAGACCA GGCTCAGTGC TGAGAGGGCG TATGTGTGTC 3000
AATTGCCCTT TGGGAACCTA TTATAATCTG GAACATTTCA CCTGTGAAAG CTGCCGGATC 3060
GGATCCTATC AAGATGAAGA AGGGCAACTT GAGTGCAAGC TTTGCCCCTC TGGGATGTAC 3120
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TACTCATACA GTGGACTTGA GACTTGTGAA TCGTGTCCAC TGGGCACTTA TCAGCCAAAA 3240
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GTGAACATTT CTGCATGTGG AGTTCCTTGT CCAGAAGGAA AATTCTCGCG TTCTGGGTTA 3360
ATGCCCTGTC ACCCATGTCC TCGTGACTAT TACCAACCTA ATGCAGGGAA GGCCTTCTGC 3420
CTGGCCTGTC CCTTTTATGG AACTACCCCA TTCGCTGGTT CCAGATCCAT CACAGAATGT 3480
TCAACTTCAG TTCTGAATAT TACTATTTTC GGTGGATTTG GGCATCTGGA GTTGTTAAAT 3540
TGTCCTTCTG AGGTTTTCCA TGAATGCTTC TTTAACCCTT GCCACAATAG TGGAACCTGC 3600
CAGCAACTTG GGCGTGGTTA TGTTTGTCTC TGTCCACTTG GATATACAGG CTTAAAGTGT 3660
GAAACAGACA TCGATGAGTG CAGCCCACTG CCTTGCCTCA ACAATGGAGT TTGTAAAGAC 3720
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TCTGATTGCC CACGCTTAGG AGGGTCAGTG CCTCATCTGA GAACTGCATC TGAAGATTTA 4920
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ATATGTTCAT GTGTCCCACC GTACACAGGA GATGGGAAAA ACTGTGCAGA ACCTATAAAA 5340
TGTAAGGCTC CAGGAAATCC GGAAAATGGC CACTCCTCAG GTGAGATTTA TACAGTAGGT 5400
GCCGGAGTCA CATTTTCGTG TCAGGAAGGA TACCAGTTGA TGGGAGTAAC CAAAATCACA 5460
TGTTTGGAGT CTGGAGAATG GAATCATCTA ATACCATATT GTAAAGCTGT TTCATGTGGT 5520
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GCTAACAGTT CTTGGAGTCA TTCCCCTCCT GTGTGTGAAC CAGTGAAGTG TTCTAGTCCG 5700
GAAAATATAA ATAATGGAAA ATATATTTTG AGTGGGCTTA CCTACCTTTC TACTGCATCA 5760
TATTCATGCG ATACAGGATA CAGCTTACAG GGCCCTTCCA TTATTGAATG CACGGCTTCT 5820
GGCATCTGGG ACAGAGCGCC ACCTGCCTGT CACCTCGTCT TCTGTGGAGA ACCACCTGCC 5880
ATCAAAGATG CTGTCATTAC GGGGAATAAC TTCACTTTCA GGAACACCGT CACTTACACT 5940
TGCAAAGAAG GCTATACTCT TGCTGGTCTT GACACCATTG AATGCCTGGC CGACGGCAAG 6000
TGGAGTAGAA GTGACCAGCA GTGCCTGGCT GTCTCCTGTG ATGAGCCACC CATTGTGGAC 6060
CACGCCTCTC CAGAGACTGC CCATCGGCTC TTTGGAGACA TTGCATTCTA CTACTGCTCT 6120
GATGGTTACA GCCTAGCAGA CAATTCCCAG CTTCTCTGCA ATGCCCAGGG CAAGTGGGTA 6180
CCCCCAGAAG GTCAAGACAT GCCCCGTTGT ATAGCTCATT TCTGTGAAAA ACCTCCATCG 6240
GTTTCCTATA GCATCTTGGA ATCTGTGAGC AAAGCAAAAT TTGCAGCTGG CTCAGTTGTG 6300
AGCTTTAAAT GCATGGAAGG CTTTGTACTG AACACCTCAG CAAAGATTGA ATGTATGAGA 6360
GGTGGGCAGT GGAACCCTTC CCCCATGTCC ATCCAGTGCA TCCCTGTGCG GTGTGGAGAG 6420
CCACCAAGCA TCATGAATGG CTATGCAAGT GGATCAAACT ACAGTTTTGG AGCCATGGTG 6480
GCTTACAGCT GCAACAAGGG GTTCTACATC AAAGGGGAAA AGAAGAGCAC CTGCGAAGCC 6540
ACAGGGCAGT GGAGTAGTCC TATACCGACG TGCCACCCGG TATCTTGTGG TGAACCACCT 6600
AAGGTTGAGA ATGGCTTTCT GGAGCATACA ACTGGCAGGA TCTTTGAGAG TGAAGTGAGG 6660
TATCAGTGTA ACCCGGGCTA TAAGTCAGTC GGAAGTCCTG TATTTGTCTG CCAAGCCAAT 6720
CGCCACTGGC ACAGTGAATC CCCTCTGATG TGTGTTCCTC TCGACTGTGG AAAACCTCCC 6780
CCGATCCAGA ATGGCTTCAT GAAAGGAGAA AACTTTGAAG TAGGGTCCAA GGTTCAGTTT 6840
TTCTGTAATG AGGGTTATGA GCTTGTTGGT GACAGTTCTT GGACATGTCA GAAATCTGGC 6900
AAATGGAATA AGAAGTCAAA TCCAAAGTGC ATGCCTGCCA AGTGCCCAGA GCCGCCCCTC 6960
TTGGAAAACC AGCTAGTATT AAAGGAGTTG ACCACCGAGG TAGGAGTTGT GACATTTTCC 7020
TGTAAAGAAG GGCATGTCCT GCAAGGCCCC TCTGTCCTGA AATGCTTGCC ATCCCAGCAA 7080
TGGAATGACT CTTTCCCTGT TTGTAAGATT GTTCTTTGTA CCCCACCTCC CCTAATTTCC 7140
TTTGGTGTCC CCATTCCTTC TTCTGCTCTT CATTTTGGAA GTACTGTCAA GTATTCTTGT 7200
GTAGGTGGGT TTTTCCTAAG AGGAAATTCT ACCACCCTCT GCCAACCTGA TGGCACCTGG 7260
AGCTCTCCAC TGCCAGAATG TGTTCCAGTA GAATGTCCCC AACCTGAGGA AATCCCCAAT 7320
GGAATCATTG ATGTGCAAGG CCTTGCCTAT CTCAGCACAG CTCTCTATAC CTGCAAGCCA 7380
GGCTTTGAAT TGGTGGGAAA TACTACCACC CTTTGTGGAG AAAATGGTCA CTGGCTTGGA 7440
GGAAAACCAA CATGTAAAGC CATTGAGTGC CTGAAACCCA AGGAGATTTT GAATGGCAAA 7500
TTCTCTTACA CGGACCTACA CTATGGACAG ACCGTTACCT ACTCTTGCAA CCGAGGCTTT 7560

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CGGCTCGAAG GTCCCAGTGC CTTGACCTGT TTAGAGACAG GTGATTGGGA TGTAGATGCC   7620
CCATCTTGCA ATGCCATCCA CTGTGATTCC CCACAACCCA TTGAAAATGG TTTTGTAGAA   7680
GGTGCAGATT ACAGCTATGG TGCCATAATC ATCTACAGTT GCTTCCCTGG GTTTCAGGTG   7740
GCTGGTCATG CCATGCAGAC CTGTGAAGAG TCAGGATGGT CAAGTTCCAT CCCAACATGT   7800
ATGCCAATAG ACTGTGGCCT CCCTCCTCAT ATAGATTTTG GAGACTGTAC TAAACTCAAA   7860
GATGACCAGG GATATTTTGA GCAAGAAGAC GACATGATGG AAGTTCCATA TGTGACTCCT   7920
CACCCTCCTT ATCATTTGGG AGCAGTGGCT AAAACCTGGG AAAATACAAA GGAGTCTCCT   7980
GCTACACATT CATCAAACTT TCTGTATGGT ACCATGGTTT CATACACCTG TAATCCAGGA   8040
TATGAACTTC TGGGGAACCC TGTGCTGATC TGCCAGGAAG ATGGAACTTG GAATGGCAGT   8100
GCACCATCCT GCATTTCAAT TGAATGTGAC TTGCCTACTG CTCCTGAAAA TGGCTTTTTG   8160
CGTTTTACAG AGACTAGCAT GGGAAGTGCT GTGCAGTATA GCTGTAAACC TGGACACATT   8220
CTAGCAGGCT CTGACTTAAG GCTTTGTCTA GAGAATAGAA AGTGGAGTGG TGCCTCCCCA   8280
CGCTGTGAAG CCATTTCATG CAAAAAGCCA AATCCAGTCA TGAATGGATC CATCAAAGGA   8340
AGCAACTACA CATACCTGAG CACGTTGTAC TATGAGTGTG ACCCCGGATA TGTGCTGAAT   8400
GGCACTGAGA GGAGAACATG CCAGGATGAC AAAAACTGGG ATGAGGATGA GCCCATTTGC   8460
ATTCCTGTGG ACTGCAGTTC ACCCCCAGTC TCAGCCAATG GCCAGGTGAG AGGAGACGAG   8520
TACACATTCC AAAAAGAGAT TGAATACACT TGCAATGAAG GGTTCTTGCT TGAGGGAGCC   8580
AGGAGTCGGG TTTGTCTTGC CAATGGAAGT TGGAGTGGAG CCACTCCCGA CTGTGTGCCT   8640
GTCAGATGTG CCACCCCGCC ACAACTGGCC AATGGGGTGA CGGAAGGCCT GGACTATGGC   8700
TTCATGAAGG AAGTAACATT CCACTGTCAC GAGGGCTACA TCTTGCACGG TGCTCCAAAA   8760
CTCACCTGTC AGTCAGATGG CAACTGGGAT GCAGAGATTC CTCTCTGTAA ACCAGTCAAC   8820
TGTGGACCTC CTGAAGATCT TGCCCATGGT TTCCCTAATG GTTTTTCCTT TATTCATGGG   8880
GGCCATATAC AGTATCAGTG CTTTCCTGGT TATAAGCTCC ATGGAAATTC ATCAAGAAGG   8940
TGCCTCTCCA ATGGCTCCTG GAGTGGCAGC TCACCTTCCT GCCTGCCTTG CAGATGTTCC   9000
ACACCAGTAA TTGAATATGG AACTGTCAAT GGGACAGATT TTGACTGTGG AAAGGCAGCC   9060
CGGATTCAGT GCTTCAAAGG CTTCAAGCTC CTAGGACTTT CTGAAATCAC CTGTGAAGCC   9120
GATGGCCAGT GGAGCTCTGG GTTCCCCCAC TGTGAACACA CTTCTTGTGG TTCTCTTCCA   9180
ATGATACCAA ATGCGTTCAT CAGTGAGACC AGCTCTTGGA AGGAAAATGT GATAACTTAC   9240
AGCTGCAGGT CTGGATATGT CATACAAGGC AGTTCAGATC TGATTTGTAC AGAGAAAGGG   9300
GTATGGAGCC AGCCTTATCC AGTCTGTGAG CCCTTGTCCT GTGGGTCCCC ACCGTCTGTC   9360
GCCAATGCAG TGGCAACTGG AGAGGCACAC ACCTATGAAA GTGAAGTGAA ACTCAGATGT   9420
CTGGAAGGTT ATACGATGGA TACAGATACA GATACATTCA CCTGTCAGAA AGATGGTCGC   9480
TGGTTCCCTG AGAGAATCTC CTGCAGTCCT AAAAAATGTC CTCTCCCGGA AAACATAACA   9540
CATATACTTG TACATGGGGA CGATTTCAGT GTGAATAGGC AAGTTTCTGT GTCATGTGCA   9600
GAAGGGTATA CCTTTGAGGG AGTTAACATA TCAGTATGTC AGCTTGATGG AACCTGGGAG   9660
CCACCATTCT CCGATGAATC TTGCAGTCCA GTTTCTTGTG GGAAACCTGA AAGTCCAGAA   9720
CATGGATTTG TGGTTGGCAG TAAATACACC TTTGAAAGCA CAATTATTTA TCAGTGTGAG   9780
CCTGGCTATG AACTAGAGGG GAACAGGGAA CGTGTCTGCC AGGAGAACAG ACAGTGGAGT   9840
GGAGGGGTGG CAATATGCAA AGAGACCAGG TGTGAAACTC CACTTGAATT TCTCAATGGG   9900
AAAGCTGACA TTGAAAACAG GACGACTGGA CCCAACGTGG TATATTCCTG CAACAGAGGC   9960
TACAGTCTTG AAGGGCCATC TGAGGCACAC TGCACAGAAA ATGGAACCTG GAGCCACCCA  10020
GTCCCTCTCT GCAAACCAAA TCCATGCCCT GTTCCTTTTG TGATTCCCGA GAATGCTCTG  10080
CTGTCTGAAA AGGAGTTTTA TGTTGATCAG AATGTGTCCA TCAAATGTAG GGAAGGTTTT  10140
CTGCTGCAGG GCCACCGCAT CATTACCTGC AACCCCGACG AGACGTGGAC ACAGACAAGC  10200
GCCAAATGTG AAAAAATCTC ATGTGGTCCA CCAGCTCACG TAGAAAATGC AATTGCTCGA  10260
GGCGTACATT ATCAATATGG AGACATGATC ACCTACTCAT GTTACAGTGG ATACATGTTG  10320
GAGGGTTTCC TGAGGAGTGT TTGTTTAGAA AATGGAACAT GGACATCACC TCCTATTTGC  10380
AGAGCTGTCT GTCGATTTCC ATGTCAGAAT GGGGGCATCT GCCAACGCCC AAATGCTTGT  10440
TCCTGTCCAG AGGGCTGGAT GGGGCGCCTC TGTGAAGAAC CAATCTGCAT TCTTCCCTGT  10500
CTGAACGGAG GTCGCTGTGT GGCCCCTTAC CAGTGTGACT GCCCGCCTGG CTGGACGGGG  10560
TCTCGCTGTC ATACAGCTGT TTGCCAGTCT CCCTGCTTAA ATGGTGGAAA ATGTGTAAGA  10620
CCAAACCGAT GTCACTGTCT TTCTTCTTGG ACGGGACATA ACTGTTCCAG GTAA        10674
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Seq ID NO: C135 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..390

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1          11         21         31         41         51
|          |          |          |          |          |
ATGAGGTTCA GTGTCTCAGG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT   60
TATGTGTCAG TCTGTCTCCT CCTCTTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA  120
GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTTGGAG  180
CAGTGCTGTT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCCGCCAATG TGGTCCCCCC  240
TGCACCTTCT GGCCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT  300
TTTGTTGTGA AGCTGAAGGT TCAGGGTGTG AATTCCCAGT GCCACTCATC TCCCATCTCC  360
AGTAAATGTG AAAGAGGCCG GATATGTTAG                                   390
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Seq ID NO: C136 DNA Sequence
Nucleic Acid Accession #: BC035671.1
Coding sequence: 126..1745

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GGCAGCGACT GCGCCCCGTC CCGGCGCCGC GCTCGTCCGC AGAGGAGGCG GCCCGGCCCG   60
GGCAGCTGCG GCTCGGGATC CGTCGAGGGG AGGCCGAGCT TGCCAAGCTG GCGCCCAGCG  120
GGGTCATGGT GCCCGGCGCC CGCGGCGGCG GCGCACTGGC GCGGGCTGCC GGGCGGGGCC  180
TCCTGGCTTT GCTGCTCGCG GTCTCCGCCC CGCTCCGGCT GCAGGCGGAG GAGCTGGGTG  240
ATGGCTGTGG ACACCTAGTG ACTTATCAGG ATAGTGGCAC AATGACATCT AAGAATTATC  300
CCGGGACCTA CCCCAATCAC ACTGTTTGCG AAAAGACAAT TACAGTACCA AAGGGGAAAA  360
GACTGATTCT GAGGTTGGGA GATTTGGATA TCGAATCCCA GACCTGTGCT TCTGACTATC  420
TTCTCTTCAC CAGCTCTTCA GATCAATATG GTCCATACTG TGGAAGTATG ACTGTTCCCA  480
AAGAACTCTE GTTGAACACA AGTGAAGTAA CCGTCCGCTT TGAGAGTGGA TCCCACATTT  540
CTGGCCGGGG TTTTTTGCTG ACCTATGCGA GCAGCGACCA TCCAGATTTA ATAACATGTT  600
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TGGAACGAGC TAGCCATTAT TTGAAGACAG AATACAGCAA ATTCTGCCCA GCTGGTTGTA   660
GAGACGTAGC AGGAGACATT TCTGGGAATA TGGTAGATGG ATATAGAGAT ACCTCTTTAT   720
TGTGCAAAGC TGCCATCCAT GCAGGAATAA TTGCTGATGA ACTAGGTGGC CAGATCAGTG   780
TGCTTCAGCG CAAAGGGATC AGTCGATATG AAGGGATTCT GGCCAATGGT GTTCTTTCGA   840
GGGATGGTTC CCTGTCAGAC AAGCGATTTC TGTTTACCTC CAATGGTTGC AGCAGATCCT   900
TGAGTTTTGA ACCTGACGGG CAAATCAGAG CTTCTTCCTC ATGGCAGTCG GTCAATGAGA   960
GTGGAGACCA AGTTCACTGG TCTCCTGGCC AAGCCCGACT TCAGGACCAA GGCCCATCAT  1020
GGGCTTCGGG CGACAGTAGC AACAACCACA AACCACGAGA GTGGCTGGAG ATCGATTTGG  1080
GGGAGAAAAA GAAAATAACA GGAATTAGGA CCACAGGATC TACACAGTCG AACTTCAACT  1140
TTTATGTTAA GAGTTTTGTG ATGAACTTCA AAAACAATAA TTCTAAGTGG AAGACCTATA  1200
AAGGAATTGT GAATAATGAA GAAAAGGTGT TTCAGGGTAA CTCTAACTTT CGGGACCCAG  1260
TGCAAAACAA TTTCATCCCT CCCATCGTGG CCAGATATGT GCGGGTTGTC CCCCAGACAT  1320
GGCACCAGAG GATAGCCTTG AAGGTGGAGC TCATTGGTTG CCAGATTACA CAAGGTAATG  1380
ATTCATTGGT GTGGCGCAAG ACAAGTCAAA GCACCAGTGT TTCAACTAAG AAAGAAGATG  1440
AGACAATCAC AAGGCCCATC CCCTCGGAAG AAACATCCAC AGGAATAAAC ATTACAACGG  1500
TGGCTATTCC ATTGGTGCTC CTTGTTGTCC TGGTGTTTGC TGGAATGGGG ATCTTTGCAG  1560
CCTTTAGAAA GAAGAAGAAG AAAGGAAGTC CGTATGGATC AGCAGAGGCT CAGAAAACAG  1620
ACTGTTGGAA GCAGATTAAA TATCCCTTTG CCAGACATCA GTCAGCTGAG TTTACCATCA  1680
GCTATGATAA TGAGAAGGAG ATGACACAAA AGTTAGATCT CATCACAAGT GATATGGCAG  1740
GTTAACTCCG TTGACTGCCA AAATAGCATC CCCAACGTGC AGCCCTCCGC ATCTATCAGC  1800
AGGTTGCCCC GGATGGATCT CAGAGATGAG GATCGGAACA CCATGTTCTT TCCCACCCTA  1860
ACAACAACAA AGGGCAGTAA ATTAAAGTAC TCTTTGTAAG GTACAGTTAC CGATTAATCT  1920
AGAGATAAAA TATTTTCTTA AAAATATATT TCATTAAACA CCTATGCTGT CTCTATAAAA  1980
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA                                   2010
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Seq ID NO: C137 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1761

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ATGGGATTCG GTGCGGGGCA GCGACTGCGC CCCGTCCCGG CGCCGCGCTC GTCCGCAGAG   60
GAGGCGGCCC GGCCCGGGCA GCTGCGGCTC GGGATCCGTC GAGGGGAGGC CGAGCTTGCC  120
AAGCTGGCGC CCAGCGGGGT CATGGTGCCC GGCGCCCGCG GCGGCGGCGC ACTGGCGCGG  180
GCTGCCGGGC GGGGCCTCCT GGCTTTGCTG CTCGCGGTCT CCGCCCCGCT CCGGCTGCAG  240
GCGGAGGAGC TGGGTGATGG CTGTGGACAC CTAGTGACTT ATCAGGATAG TGGCACAATG  300
ACATCTAAGA ATTATCCCGG GACCTACCCC AATCACACTG TTTGCGAAAA GACAATTACA  360
GTACCAAAGG GGAAAAGACT GATTCTGAGG TTGGGAGATT TGGATATCGA ATCCCAGACC  420
TGTGCTTCTG ACTATCTTCT CTTCACCAGC TCTTCAGATC AATATGGTCC ATACTGTGGA  480
AGTATGACTG TTCCCAAAGA ACTCTTGTTG AACACAAGTG AAGTAACCGT CCGCTTTGAG  540
AGTGGATCCC ACATTTCTGG CCGGGGTTTT TTGCTGACCT ATGCGAGCAG CGACCATCCA  600
GATTTAATAA CATGTTTGGA ACGAGCTAGC CATTATTTGA AGACAGAATA CAGCAAATTC  660
TGCCCAGCTG GTTGTAGAGA CGTAGCAGGA GACATTTCTG GGAATATGGT AGATGGATAT  720
AGAGATACCT CTTTATTGTG CAAAGCTGCC ATCCATGCAG GAATAATTGC TGATGAACTA  780
GGTGGCCAGA TCAGTGTGCT TCAGCGCAAA GGGATCAGTC GATATGAAGG GATTCTGGCC  840
AATGGTGTTC TTTCGAGGGA TGGTTCCCTG TCAGACAAGC GATTTCTGTT TACCTCCAAT  900
GGTTGCAGCA GATCCTTGAG TTTTGAACCT GACGGGCAAA TCAGAGCTTC TTCCTCATGG  960
CAGTCGGTCA ATGAGAGTGG AGACCAAGTT CACTGGTCTC CTGGCCAAGC CCGACTTCAG 1020
GACCAAGGCC CATCATGGGC TTCGGGCGAC AGTAGCAACA ACCACAAACC ACGAGAGTGG 1080
CTGGAGATCG ATTTGGGGGA GAAAAAGAAA ATAACAGGAA TTAGGACCAC AGGATCTACA 1140
CAGTCGAACT TCAACTTTTA TGTTAAGAGT TTTGTGATGA ACTTCAAAAA CAATAATTCT 1200
AAGTGGAAGA CCTATAAAGG AATTGTGAAT AATGAAGAAA AGGTGTTTCA GGGTAACTCT 1260
AACTTTCGGG ACCCAGTGCA AAACAATTTC ATCCCTCCCA TCGTGGCCAG ATATGTGCGG 1320
GTTGTCCCCC AGACATGGCA CCAGAGGATA GCCTTGAAGG TGGAGCTCAT TGGTTGCCAG 1380
ATTACACAAG GTAATGATTC ATTGGTGTGG CGCAAGACAA GTCAAAGCAC CAGTGTTTCA 1440
ACTAAGAAAG AAGATGAGAC AATCACAAGG CCCATCCCCT CGGAAGAAAC ATCCACAGGA 1500
ATAAACATTA CAACGGTGGC TATTCCATTG GTGCTCCTTG TTGTCCTGGT GTTTGCTGGA 1560
ATGGGGATCT TTGCAGCCTT TAGAAAGAAG AAGAAGAAAG GAAGTCCGTA TGGATCAGCA 1620
GAGGCTCAGA AAACAGACTG TTGGAAGCAG ATTAAATATC CCTTTGCCAG ACATCAGTCA 1680
GCTGAGTTTA CCATCAGCTA TGATAATGAG AAGGAGATGA CACAAAAGTT AGATCTCATC 1740
ACAAGTGATA TGGCAGGTTA A                                            1761
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Seq ID NO: C138 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2310

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ATGTTCCAGC GGCAGGAAAG ATTTCTTGAC TTATCTTCAG CTGAAGCAGT GGCAGCTTGG   60
ATATTACATC AACATCCTGA CATTATTAAC AAAGGTGATG GCTGTGGACA CCTAGTGACT  120
TATCAGGATA GTGGCACAAT GACATCTAAG AATTATCCCG GGACCTACCC CAATCACACT  180
GTTTGCGAAA AGACAATTAC AGTACCAAAG GGGAAAAGAC TGATTCTGAG GTTGGGAGAT  240
TTGGATATCG AATCCCAGAC CTGTGCTTCT GACTATCTTC TCTTCACCAG CTCTTCAGAT  300
CAATATGGAA TGCAGAAGGA GGAGGAGACA GAAGTGCTTT GTCTTTCAGT GGCTGGCGCT  360
CAGAGAGTGG ACATTCCTGT GCAGCTGTTG CCCAGCTTCC TGGAAGGGTG GAAGGGTCAT  420
GCTGATGCAA GAGGTCCATA CTGTGGAAGT ATGACTGTTC CCAAAGAACT CTTGTTGAAC  480
ACAAGTGAAG TAACCGTCCG CTTTGAGAGT GGATCCCACA TTTCTGGCCG GGGTTTTTTG  540
CTGACCTATG CGAGCAGCGA CCATCCAGAT TTAATAACAT GTTTGGAACG AGCTAGCCAT  600
TATTTGAAGA CAGAATACAG CAAATTCTGC CCAGCTGGTT GTAGAGACGT AGCAGGAGAC  660
ATTTCTGGGA ATATGGTAGA TGGATATAGA GATACCTCTT TATTGTGCAA AGCTGCCATC  720
CATGCAGGAA TAATTGCTGA TGAACTAGGT GGCCAGATCA GTGTGCTTCA GCGCAAAGGG  780
ATCAGTCGAT ATGAAGGGAT TCTGGCCAAT GGTGTTCTTT CGAGGGATGG TTCCCTGTCA  840
GACAAGCGAT TTCTGTTTAC CTCCAATGGT TGCAGCAGAT CCTTGAGTTT TGAACCTGAC  900
GGGCAAATCA GAGCTTCTTC CTCATGGCAG TCGGTCAATG AGAGTGGAGA CCAAGTTCAC  960
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TGGTCTCCTG GCCAAGCCCG ACTTCAGGAC CAAGGCCCAT CATGGGCTTC GGGCGACAGT   1020
AGCAACAACC ACAAACCACG AGAGTGGCTG GAGATCGATT TGGGGGAGAA AAAGAAAATA   1080
ACAGGAATTA GGACCACAGG ATCTACACAG TCGAACTTCA ACTTTTATGT TAAGAGTTTT   1140
GTGATGAACT TCAAAAACAA TAATTCTAAG TGGAAGACCT ATAAAGGAAT TGTGAATAAT   1200
GAAGAAAAGG TGTTTCAGGG TAACTCTAAC TTTCGGGACC CAGTGCAAAA CAATTTCATC   1260
CCTCCCATCG TGGCCAGATA TGTGCGGGTT GTCCCCCAGA CATGGCACCA GAGGATAGCC   1320
TTGAAGGTGG AGCTCATTGG TTGCCAGATT ACACAAGGTA ATGATTCATT GGTGTGGCGC   1380
AAGACAAGTC AAAGCACCAG TGTTTCAACT AAGAAAGAAG ATGAGACAAT CACAAGGCCC   1440
ATCCCCTCGG AAGAAACATC CACAGATGCC ATGCCAGTGC AGATTGTCGG AGACCATACC   1500
CAGATGATCT CACAAAGGGA GAATCTGGGA CCTGATGAGG GCAAAATACC TTTTAAAGGC   1560
ACAGCGGAAA GCATGGTTAG AGTAGTGTTT GCTGTTGTGG TTAATGACCT TGGCATGCTG   1620
TTCTTAGCAC ACACACCTGA GGAGGACATT GATCACTACT GTTGGAAGCA GATTAAATAT   1680
CCCTTTGCCA GACATCAGTC AGCTGAGTTT ACCATCAGCT ATGATAATGA GAAGGAGATG   1740
ACACAAAAGT TAGATCTCAT CACAAGTGAT ATGGCAGATT ACCAGCAGCC CCTCATGATT   1800
GGCACCGGGA CAGTCACGAG GAAGGGCTCC ACCTTCCGGC CCATGGACAC GGATGCCGAG   1860
GAGGCAGGGG TGAGCACCGA TGCCGGCGGC CACTATGACT GCCCGCAGCG GGCCGGCCGC   1920
CACGAGTACG CGCTGCCCCT GGCGCCCCCG GAGCCCGAGT ACGCCACGCC CATCGTGGAG   1980
CGGCACGTGC TGCGCGCCCA CACGTTCTCT GCGCAGAGCG GCTACCGCGT CCCAGGGCCC   2040
CAGCCCGGCC ACAAACACTC CCTCTCCTCG GGCGGCTTCT CCCCCGTAGC GGGTGTGGGC   2100
GCCCAGGACG GAGACTATCA AAGGCCACAC AGCGCACAGC CTGCGGACAG GGGCTACGAC   2160
CGGCCCAAAG CTGTCAGCGC CCTCGCCACC GAAAGCGGGC ACCCTGACTC TCAGAAGCCC   2220
CCAACGCATC CCGGGACGAG TGACAGCTAT TCTGCCCCCA GAGACTGCCT CACACCCCTC   2280
AACCAGACGG CCATGACTGC CCTTTTGTGA                                    2310
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Seq ID NO: C139 DNA Sequence
Nucleic Acid Accession #: NM_004616.2
Coding sequence: 180..893

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AGTGCCCCAG GAGCTATGAC AAGCAAAGGA ACATACTTGC CTGGAGATAG CCTTTGCGAT   60
ATTTAAATGT CCGTGGATAC AGAAATCTCT GCAGGCAAGT TGCTCCAGAG CATATTGCAG   120
GACAAGCCTG TAACGAATAG TTAAATTCAC GGCATCTGGA TTCCTAATCC TTTTCCGAAA   180
TGGCAGGTGT GAGTGCCTGT ATAAAATATT CTATGTTTAC CTTCAACTTC TTGTTCTGGC   240
TATGTGGTAT CTTGATCCTA GCATTAGCAA TATGGGTACG AGTAAGCAAT GACTCTCAAG   300
CAATTTTTGG TTCTGAAGAT GTAGGCTCTA GCTCCTACGT TGCTGTGGAC ATATTGATTG   360
CTGTAGGTGC CATCATCATG ATTCTGGGCT TCCTGGGATG CTGCGGTGCT ATAAAAGAAA   420
GTCGCTGCAT GCTTCTGTTG TTTTTCATAG GCTTGCTTCT GATCCTGCTC CTGCAGGTGG   480
CGACAGGTAT CCTAGGAGCT GTTTTCAAAT CTAAGTCTGA TCGCATTGTG AATGAAACTC   540
TCTATGAAAA CACAAAGCTT TTGAGCGCCA CAGGGGAAAG TGAAAAACAA TTCCAGGAAG   600
CCATAATTGT GTTTCAAGAA GAGTTTAAAT GCTGCGGTTT GGTCAATGGA GCTGCTGATT   660
GGGGAAATAA TTTTCAACAC TATCCTGAAT TATGTGCCTG TCTAGATAAG CAGAGACCAT   720
GCCAAAGCTA TAATGGAAAA CAAGTTTACA AAGAGACCTG TATTTCTTTC ATAAAAGACT   780
TCTTGGCAAA AAATTTGATT ATAGTTATTG GAATATCATT TGGACTGGCA GTTATTGAGA   840
TACTGGGTTT GGTGTTTTCT ATGGTCCTGT ATTGCCAGAT CGGGAACAAA TGAATCTGTG   900
GATGCATCAA CCTATCGTCA GTCAAACCCC TTTAAAATGT TGCTTTGGCT TTGTAAATTT   960
AAATATGTAA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TTAAAATGTC TCGGCTAGCT   1020
AGACCACAGA TATCTTCTAG ACATATTGAA CACATTTAAG ATTTGAGGGA TATAAGGGAA   1080
AATGATATGA ATGTGTATTT TTACTCAAAA TAAAAGTAAC TGTTTACGTT AAAAAAAAAA   1140
AAAAAAAAAA AAAAAAAAA                                                1159
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Seq ID NO: C140 DNA Sequence
Nucleic Acid Accession #: NM_004617.2
Coding sequence: 232..840

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AGCTGAAGCA ACTCCAAGGA CACAGTTCAC AGAAATTTGG TTCTCAGCCC CAAAATACTG   120
ATTGAATTGG AGACAATTAC AAGGACTCTC TGGCCAAAAA CCCTTGAAGA GGCCCCGTGA   180
AGGAGGCAGT GAGGAGCTTT TGATTGCTGA CCTGTGTCGT ACCACCCCAG AATGTGCACT   240
GGGGGCTGTG CCAGATGCCT GGGGGGGACC CTCATTCCCC TTGCTTTTTT TGGCTTCCTG   300
GCTAACATCC TGTTATTTTT TCCTGGAGGA AAAGTGATAG ATGACAACGA CCACCTTTCC   360
CAAGAGATCT GGTTTTTCGG AGGAATATTA GGAAGCGGTG TCTTGATGAT CTTCCCTGCG   420
CTGGTGTTCT TGGGCCTGAA GAACAATGAC TGCTGTGGGT GCTGCGGCAA CGAGGGCTGT   480
GGGAAGCGAT TTGCGATGTT CACCTCCACG ATATTTGCTG TGGTTGGATT CTTGGGAGCT   540
GGATACTCGT TTATCATCTC AGCCATTTCA ATCAACAAGG GTCCTAAATG CCTCATGGCC   600
AATAGTACAT GGGGCTACCC CTTCCACGAC GGGGATTATC TCAATGATGA GGCCTTATGG   660
AACAAGTGCC GAGAGCCTCT CAATGTGGTT CCCTGGAATC TGACCCTCTT CTCCATCCTG   720
CTGGTCGTAG GAGGAATCCA GATGGTTCTC TGCGCCATCC AGGTGGTCAA TGGCCTCCTG   780
GGGACCCTCT GTGGGGACTG CCAGTGTTGT GGCTGCTGTG GGGGAGATGG ACCCGTTTAA   840
ACCTCCGAGA TGAGCTGCTC AGACTCTACA GCATGACGAC TACAATTTCT TTTCATAAAA   900
CTTCTTCTCT TCTTGGAATT ATTAATTCCT ATCTGCTTCC TAGCTGATAA AGCTTAGAAA   960
AGGCAGTTAT TCCTTCTTTC CAACCAGCTT TGCTCGAGTT AGAATTTTGT TATTTTCAAA   1020
TAAAAAATAG TTTGGCCACT TAACAAATTT GATTTATAAA TCTTTCAAAT TAGTTCCTTT   1080
TTAGAATTTA CCAACAGGTT CAAAGCATAC TTTTCATGAT TTTTTTATTA CAAATGTAAA   1140
ATGTATAAAG TCACATGTAC TGCCATACTA CTTCTTTGTA TATAAAGATG TTTATATCTT   1200
TGGAAGTTTT ACATAAATCA AAGGAAGAAA GCACATTTAA AATGAGAAAC TAAGACCAAT   1260
TTCTGTTTTT AAGAGGAAAA AGAATGATTG ATGTATCCTA AGTATTGTTA TTTGTTGTCT   1320
TTTTTTGCTG CCTTGCTTGA GTTGCTTGTG ACTGATCTTT TGAGGCTGTC ATCATGGCTA   1380
GGGTTCTTTT ATGTATGTTA AATTAAAACC TGAATTCAGA GGTAACGT                1428
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Seq ID NO: C141 DNA Sequence
Nucleic Acid Accession #: NM_002381.2

Coding sequence: 64..1524

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AAATCCGAGC CTCGCGTGGG CTCCTGGCCC CCGACGGACA CCACCAGGCC CACGGAGCCC   60
ACCATGCCGC GCCCGGCCCC CGCGCGCCGC CTCCCGGGAC TCCTCCTGCT GCTCTGGCCG  120
CTGCTGCTGC TGCCCTCCGC CGCCCCCGAC CCCGTGGCCC GCCCGGGCTT CCGGAGGCTG  180
GAGACCCGAG GTCCCGGGGG CAGCCCTGGA CGCCGCCCCT CTCCTGCGGC TCCCGACGGC  240
GCGCCCGCTT CCGGGACCAG CGAGCCTGGC CGCGCCCGCG GTGCAGGTGT TTGCAAGAGC  300
AGACCCTTGG ACCTGGTGTT TATCATTGAT AGTTCTCGTA GCGTACGGCC CCTGGAATTC  360
ACCAAAGTGA AAACTTTTGT CTCCCGGATA ATCGACACTC TGGACATTGG GCCAGCCGAC  420
ACGCGGGTGG CAGTGGTGAA CTATGCTAGC ACTGTGAAGA TCGAGTTCCA ACTCCAGGCC  480
TACACAGATA AGCAGTCCCT GAAGCAGGCT GTGGGTCGAA TCACACCCTT GTCAACAGGC  540
ACCATGTCAG GCCTAGCCAT CCAGACAGCA ATGGACGAAG CCTTCACAGT GGAGGCAGGG  600
GCTCGAGAGC CCTCTTCTAA CATCCCTAAG GTGGCCATCA TTGTTACAGA TGGGAGGCCC  660
CAGGACCAGG TGAATGAAGT GGCGGCTCGG GCCCAAGCAT CTGGTATTGA GCTCTATGCT  720
GTGGGCGTGG ACCGGGCAGA CATGGCGTCC CTCAAGATGA TGGCCAGTGA GCCCCTAGAG  780
GAGCATGTTT TCTACGTGGA GACCTATGGG GTCATTGAGA AACTTTCCTC TAGATTCCAG  840
GAAACCTTCT GTGCGCTGGA CCCCTGTGTG CTTGGAACAC ACCAGTGCCA GCACGTCTGC  900
ATCAGTGATG GGGAAGGCAA GCACCACTGT GAGTGTAGCC AAGGATACAC CTTGAATGCC  960
GACAAGAAAA CGTGTTCAGC TCTTGATAGG TGTGCTCTTA ACACCCACGG ATGTGAGCAC 1020
ATCTGTGTGA ATGACAGAAG TGGCTCTTAT CATTGTGAGT GCTATGAAGG TTATACCTTG 1080
AATGAAGACA GGAAAACTTG TTCAGCTCAA GATAAATGTG CTTTGGGTAC CCATGGGTGT 1140
CAGCACATTT GTGTGAATGA CAGAACAGGG TCCCATCATT GTGAATGCTA TGAGGGCTAC 1200
ACTCTGAATG CAGATAAAAA AACATGTTCA GTCCGTGACA AGTGTGCCCT AGGCTCTCAT 1260
GGTTGCCAGC ACATTTGTGT GAGTGATGGG GCCGCATCCT ACCACTGTGA TTGCTATCCT 1320
GGCTACACCT TAAATGAGGA CAAGAAAACA TGTTCAGCCA CTGAGGAAGC ACGAAGACTT 1380
GTTTCCACTG AAGATGCTTG TGGATGTGAA GCTACACTGG CATTCCAGGA CAAGGTCAGC 1440
TCGTATCTTC AAAGACTGAA CACTAAACTT GATGACATTT TGGAGAAGTT GAAAATAAAT 1500
GAATATGGAC AAATACATCG TTAAATTGCT CCAATTTCTC ACCTGAAAAT GTGGACAGCT 1560
TGGTGTACTT AATACTCATG CATTCTTTTG CACACCTGTT ATTGCCAATG TTCCTGCTAA 1620
TAATTTGCCA TTATCTGTAT TAATGCTTGA ATATTACTGG ATAAATTGTA TGAAGATCTT 1680
CTGCAGAATC AGCATGATTT TTCCAAGGAA ATACATATGC AGATACTTAT TAAGAGCAAA 1740
CTTTAGTGTC TCTAAGTTAT GACTGTGAAA TGATTGGTAG GAAATAGAAT GAAAAGTTTA 1800
GTGTTTCTTT ATCTACTAAT TGAGCCATTT AATTTTTAAA TGTTTATATT AGATAACCAT 1860
ATTCACAATG GAAACTTTAG GTCTAGTTTC TTTTGATAGT ATTTATAATA TAAATCAATC 1920
TTATTACTGA GAGTGCAAAT TGTACAAGGT ATTTACACAT ACAACTTCAT ATAACTGAGA 1980
TGAATGTAAT TTTGAACTGT TTAACACTTT TTGTTTTTTG CTTATTTTGT TGGAGTATTA 2040
TTGAAGATGT GATCAATAGA TTGTAATACA CATATCTAAA AATAGTTAAC ACAGATCAAG 2100
TGAACATTAC ATTGCCATTT TTAATTCATT CTGGTCTTTG AAAGAAATGT ACTACTAAAG 2160
AGCACTAGTT GTGAATTTAG GGTGTTAAAC TTTTTACCAA GTACAAAAAT CCCAAATTCA 2220
CTTTATTATT TTGCTTCAGG ATCCAAGTGA CAAAGTTATA TATTTATAAA ATTGCTATAA 2280
ATCGACAAAA TCTAATGTTG TCTTTTTAAT GTTAGTGATC CACCTGCCTC AGCCTCCCAA 2340
AGTGCTGGGA TTACAGGCTT GAAAGTCTAA CTTTTTTTTA CTTATATATT TGATACATAT 2400
AATTCTTTTG GCTTTGAAAC TTGCAACTTT GAGAACAAAA CAGTCCTTTA AATTTTGCAC 2460
TGCTCAATTC TGTTTTTCGT TTGCATTGTC TTTAATATAA TAAAAGTTAT TACCTTTACA 2520
TATTATCATG TCTATTTTTG ATGACTCATC AATTTTGTCT ATTAAAGATA TTTCTTTAAA 2580
TTAAAAAAAA AAAAAAAAA                                              2599
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Seq ID NO: C142 DNA Sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

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1          11         21         31         41         51
|          |          |          |          |          |
GCGGCGGGCG CAGACAGCGG CGGGCGCAGG ACGTGCACTA TGGCTCGGGG CTCGCTGCGC   60
CGGTTGCTGC GGCTCCTCGT GCTGGGGCTC TGGCTGGCGT TGCTGCGCTC CGTGGCCGGG  120
GAGCAAGCGC CAGGCACCGC CCCCTGCTCC CGCGGCAGCT CCTGGAGCGC GGACCTGGAC  180
AAGTGCATGG ACTGCGCGTC TTGCAGGGCG CGACCGCACA GCGACTTCTG CCTGGGCTGC  240
GCTGCAGCAC CTCCTGCCCC CTTCCGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC  300
CTGACCTTCG TGCTGGGGCT GCTTTCTGGC TTTTTGGTCT GGAGACGATG CCGCAGGAGA  360
GAGAAGTTCA CCACCCCCAT AGAGGAGACC GGCGGAGAGG GCTGCCCAGC TGTGGCGCTG  420
ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTCATCCA  480
TTCTAGAGCC AGTCTCTGCC TCCCAGACGC GGCGGGAGCC AAGCTCCTCC AACCACAAGG  540
GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA  600
AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC  660
ACAAAACAGC TGACACTGAC TAAGGAACTG CAGCATTTGC ACAGGGGAGG GGGGTGCCCT  720
CCTTCCTTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC  780
TCACTCAGAT GTCCTGAAAT TCCACCACGG GGGTCACCCT GGGGGGTTAG GGACCTATTT  840
TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCCAACTC  900
CCCAAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT  960
AATAAAAGAA TCTTTAACTT TAAAAAAAAA AAAAAAAA                         998
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Seq ID NO: C143 DNA Sequence
Nucleic Acid Accession #: NM_001819
Coding sequence: 113..2146

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1          11         21         31         41         51
|          |          |          |          |          |
CCAGGAGGCA CGCTGGTTTT CCGGGGCCGC TCCATCGCGC CTTCCTCCTG CGCCTCGCTT   60
CTCCGGTCCA GCCGCCATCT TCCTTTCCGC ACAGGGGCCG CCGAGCGGGG CCATGCAGCC  120
AACGCTGCTT CTCAGCCTCC TGGGAGCCGT GGGGCTGGCG GCTGTCAATT CCATGCCAGT  180
GGATAACAGG AACCACAATG AAGGAATGGT GACTCGCTGC ATCATTGAGG TCCTCTCAAA  240
```

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TGCCTTGTCG AAGTCCAGCG CTCCACCCAT CACCCCTGAG TGCCGCCAAG TCCTGAAGAC   300
GAGTAGAAAA GACGTCAAAG ACAAAGAGAC AACTGAAAAT GAAAACACAA AGTTTGAAGT   360
AAGATTGTTA AGAGACCCAG CTGATGCCTC GGAAGCCCAC GAGTCCTCCA GCAGGGGAGA   420
GGCAGGAGCC CCAGGGGAGG AGGACATCCA AGGCCCAACA AAGGCAGACA CAGAGAAATG   480
GGCAGAGGGA GGCGGGCACA GCCGAGAGCG AGCGGATGAG CCCCAGTGGA GCCTCTATCC   540
CTCCGACAGC CAAGTCTCTG AAGAAGTGAA GACACGCCAT TCTGAGAAGA GCCAGAGAGA   600
GGATGAGGAG GAGGAGGAGG GAGAGAACTA TCAAAAAGGG GAGCGAGGGG AAGATAGCAG   660
TGAAGAGAAA CACCTTGAAG AGCCAGGAGA GACACAAAAC GCTTTTCTCA ATGAAAGAAA   720
GCAGGCTTCA GCTATAAAAA AAGAGGAGTT AGTGGCCAGA TCGGAAACAC ATGCTGCCGG   780
GCATTCTCAG GAGAAGACAC ATAGCCGAGA GAAGAGTAGC CAGGAGAGTG GAGAGGAGGC   840
AGGGAGCCAG GAGAATCACC CCCAGGAGTC TAAAGGCCAA CCCCGAAGCC AGGAAGAATC   900
TGAGGAAGGT GAGGAAGATG CCACCTCTGA GGTGGACAAA CGACGCACGA GGCCCAGACA   960
CCACCACGGG AGGAGCAGGC CCGACAGGTC CTCTCAAGGA GGGAGTCTTC CCTCTGAGGA  1020
AAAGGGACAC CCCCAGGAGG AATCTGAGGA GTCAAACGTC AGCATGGCCA GTTTAGGGGA  1080
AAAGAGGGAC CACCATTCAA CCCACTACAG GGCTTCAGAG GAAGAACCTG AATATGGAGA  1140
AGAAATAAAG GGTTATCCAG GCGTCCAGGC CCCTGAGGAC CTGGAGTGGG AGCGCTATAG  1200
GGGCAGAGGA AGTGAAGAAT ACAGGGCTCC AAGACCTCAG AGTGAGGAGA GTTGGGATGA  1260
GGAGGACAAG AGAAACTACC CCAGCTTAGA GCTTGATAAG ATGGCACATG GATATGGTGA  1320
AGAAAGTGAG GAAGAGAGGG GCCTTGAGCC GGGAAAGGGA CGCCATCACA GAGGCAGGGG  1380
AGGGGAGCCA CGTGCCTATT TCATGTCTGA CACCAGAGAA GAGAAAAGGT TCTTGGGTGA  1440
AGGACACCAC CGTGTCCAAG AAAACCAGAT GGACAAGGCA AGGAGGCATC CACAAGGTGC  1500
GTGGAAAGAG CTGGACAGAA ATTATCTCAA CTACGGTGAG GAAGGAGCCC CAGGGAAGTG  1560
GCAGCAGCAG GGAGACCTGC AGGACACTAA AGAAAACAGG GAGGAAGCTA GGTTTCAAGA  1620
TAAACAATAT AGCTCCCATC ACACAGCTGA AAAGAGGAAG AGATTAGGGG AACTGTTCAA  1680
CCCATACTAC GACCCTCTCC AGTGGAAGAG CAGCCATTTT GAAAGAAGAG ACAACATGAA  1740
TGACAATTTT CTCGAGGGTG AGGAGGAAAA TGAGCTGACC TTGAACGAGA AGAATTTCTT  1800
CCCAGAATAC AACTATGACT GGTGGGAGAA AAAGCCCTTC TCTGAGGATG TGAACTGGGG  1860
GTATGAGAAG AGAAACCTCG CCAGGGTCCC CAAGCTGGAC CTGAAAAGGC AATATGACAG  1920
GGTGGCCCAA CTGGACCAGC TCCTTCACTA CAGGAAGAAG TCAGCTGAGT TTCCAGACTT  1980
CTATGATTCT GAGGAGCCGG TGAGCACCCA CCAGGAGGCA GAAAATGAAA AGGACAGGGC  2040
TGACCAGACA GTCCTGACAG AGGACGAGAA AAAAGAACTC GAAAACTTGG CTGCAATGGA  2100
TTTGGAACTA CAGAAGATAG CTGAGAAATT CAGCCAAAGG GGCTGACTGT CATTGGAGCG  2160
GTGGGCACTG TTAAGAAGCA GCCATCACAT GATCTGTTTT TCACCACTTC ACTGAAAGAC  2220
ACCATTTATA TACCCAAGGG CAGAAAGTAG AACTTACTAT TCATTAAATG TTTGACACAA  2280
TTGGAATTGT CTTTAATTTC TGTCAGAATG CTATTGAAAA TGTGAATTGC ATGACTTGTA  2340
GCATATTCTT TTCTGCAAAA TAGACATATT AACATGCTTA TGACAATGAC TGTGCTACTG  2400
TCTTTGGAAA AATGTTTGTC TCAGTTGGAA ATAATAAAAG ATTCACCTGA GACC        2454
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Seq ID NO: C144 DNA Sequence
Nucleic Acid Accession #: XM_093082.1
Coding sequence: 93..1988

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1          11         21         31         41         51
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CTTCTTGTGG TAGGGACCTC TCCTCAGTAT TTGAAACTAA CCAGCATCTG ACAGATTTCG   60
AATTTGTAAA AAATACCCTC GAAGATTCAG GAATGAAGCT TCTGTGTGAA GGATTAAAAC  120
AGCCCAACTG TGTATTACAG ACATTGAGGT GGTACCGGTG CCTTATCTCT TCTGCTTCTT  180
GTGGGGCTCT AGCAGCTGTT CTTAGCACCA GTCAGTGGCT CACTGAACTG GAATTTAGTG  240
AGACAAAACT GGAAGCTTCA GCTTTGAAAT TGCTCTATGG AGGCTTAAAA GATCCAAATT  300
GCAAATTACA GAAGCTCAAC TTGCAGTTTT CTTTATCTGT AACCGCTGCA AAACTTCCAG  360
TTGGAATGGT TGGAAATTGT TCTGGTTTCT CGGGATCATT GGTGCAATCT CATTTTGGCT  420
ACTGTCAGGA CAGTTCTTTC AAATGTGATC TTTGTAAGCT GCTCTGGCCT TCCACCAGAG  480
TTGCTGCTGC AAAGGATTGT GGGAGTCCTA AGTCCTTCCT ATCAGAAGGG CTGAACTGGG  540
CAGGAAGACT TGAGGCAGTG GAGGAGGTTT TGGGGTTGGG GGTGCTTGTA CAGCCCGGTG  600
ACCCAGCATC TCAGGGTGGG GGGCATTGTG AAAACTATGG GTCTTTTAGA GACTTGGTGG  660
ACTTAGAAGT CAAGGCAGAA CCAAGCCTGA GAAAAGGTGG TATGGATCTC CAGAGACCCA  720
CCCTACAAGT TGTCCTCCTT TGCAAAATCT TCTCCCTCAA ACTATTTCTC TTTATTGCAT  780
TGCCTAATTC TCCTGGTCAG GTTAGTGTGG TGCAAGTGAC CATCCCAGAC GGTTTCGTGA  840
ACGTGACTGT TGGATCTAAT GTCACTCTCA TCTGCATCTA CACCACCACT GTGGCCTCCC  900
GAGAACAGCT TTCCATCCAG TGGTCTTTCT TCCATAAGAA GGAGATGGAG CCAATTTCTT  960
CTCCTTGGGA GGAGGGGAAG TGGCCAGATG TTGAGGCTGT GAAGGGCACT CTTGATGGAC 1020
AGCAGGCTGA ACTCCAGATT TACTTTTCTC AAGGTGGACA AGCTGTAGCC ATCGGGCAAT 1080
TTAAAGATCG AATTACAGGG TCCAACGATC CAGGTAATGC ATCTATCACT ATCTCGCATA 1140
TGCAGCCAGC AGACAGTGGA ATTTACATCT GCGATGTTAA CAACCCCCCA GACTTTCTCG 1200
GCCAAAACCA AGGCATCCTC AACGTCAGTG TGTTAGTGAA ACCTTCTAAG CCCCTTTGTA 1260
GCGTTCAAGG AAGACCAGAA ACTGGCCACA CTATTTCCCT TTCCTGTCTC TCTGCGCTTG 1320
GAACACCTTC CCCTGTGTAC TACTGGCATA AACTTGAGGG AAGAGACATC GTGCCAGTGA 1380
AAGAAAACTT CAACCCAACC ACCGGGATTT TGGTCATTGG AAATCTGACA AATTTTGAAC 1440
AAGGTTATTA CCAGTGTACT GCCATCAACA GACTTGGCAA TAGTTCCTGC GAAATCGATC 1500
TCACTTCTTC ACATCCAGAA GTTGGAATCA TTGTTGGGGC CTTGATTGGT AGCCTGGTAG 1560
GTGCCGCCAT CATCATCTCT GTTGTGTGCT TCGCAAGGAA TAAGGCAAAA GCAAAGGCAA 1620
AAGAAAGAAA TTCTAAGACC ATCGCGGAAC TTGAGCCAAT GACAAAGATA AACCCAAGGG 1680
GAGAAAGCGA AGCAATGCCA AGAGAAGACG CTACCCAACT AGAAGTAACT CTACCATCTT 1740
CCATTCATGA GACTGGCCCT GATACCATCC AAGAACCAGA CTATGAGCCA AAGCCTACTC 1800
AGGAGCCTGC CCCAGAGCCT GCCCCAGGAT CAGAGCCTAT GGCAGTGCCT GACCTTGACA 1860
TCGAGCTGGA GCTGGAGCCA GAAACGCAGT CGGAATTGGA GCCAGAGCCA GAGCCAGAGC 1920
CAGAGTCAGA GCCTGGGGTT GTAGTTGAGC CCTTAAGTGA AGATGAAAAG GGAGTGGTTA 1980
AGGCATAG                                                          1988
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Seq ID NO: C145 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1242

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1          11         21         31         41         51
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ATGGTGTTCG CATTTTGGAA GGTCTTTCTG ATCCTAAGCT GCCTTGCAGG TCAGGTTAGT   60
GTGGTGCAAG TGACCATCCC AGACGGTTTC GTGAACGTGA CTGTTGGATC TAATGTCACT   120
CTCATCTGCA TCTACACCAC CACTGTGGCC TCCCGAGAAC AGCTTTCCAT CCAGTGGTCT   180
TTCTTCCATA AGAAGGAGAT GGAGCCAATT TCTTCTCCTT GGGAGGAGGG GAAGTGGCCA   240
GATGTTGAGG CTGTGAAGGG CACTCTTGAT GGACAGCAGG CTGAACTCCA GATTTACTTT   300
TCTCAAGGTG GACAAGCTGT AGCCATCGGG CAATTTAAAG ATCGAATTAC AGGGTCCAAC   360
GATCCAGGTA ATGCATCTAT CACTATCTCG CATATGCAGC CAGCAGACAG TGGAATTTAC   420
ATCTGCGATG TTAACAACCC CCCAGACTTT CTCGGCCAAA ACCAAGGCAT CCTCAACGTC   480
AGTGTGTTAG TGAAACCTTC TAAGCCCCTT TGTAGCGTTC AAGGAAGACC AGAAACTGGC   540
CACACTATTT CCCTTTCCTG TCTCTCTGCG CTTGGAACAC CTTCCCCTGT GTACTACTGG   600
CATAAACTTG AGGGAAGAGA CATCGTGCCA GTGAAAGAAA ACTTCAACCC AACCACCGGG   660
ATTTTGGTCA TTGGAAATCT GACAAATTTT GAACAAGGTT ATTACCAGTG TACTGCCATC   720
AACAGACTTG GCAATAGTTC CTGCGAAATC GATCTCACTT CTTCACATCC AGAAGTTGGA   780
ATCATTGTTG GGGCCTTGAT TGGTAGCCTG GTAGGTGCCG CCATCATCAT CTCTGTTGTG   840
TGCTTCGCAA GGAATAAGGC AAAAGCAAAG GCAAAAGAAA GAAATTCTAA GACCATCGCG   900
GAACTTGAGC CAATGACAAA GATAAACCCA AGGGGAGAAA GCGAAGCAAT GCCAAGAGAA   960
GACGCTACCC AACTAGAAGT AACTCTACCA TCTTCCATTC ATGAGACTGG CCCTGATACC   1020
ATCCAAGAAC CAGACTATGA GCCAAAGCCT ACTCAGGAGC CTGCCCCAGA GCCTGCCCCA   1080
GGATCAGAGC CTATGGCAGT GCCTGACCTT GACATCGAGC TGGAGCTGGA GCCAGAAACG   1140
CAGTCGGAAT TGGAGCCAGA GCCAGAGCCA GAGCCAGAGT CAGAGCCTGG GGTTGTAGTT   1200
GAGCCCTTAA GTGAAGATGA AAAGGGAGTG GTTAAGGCAT AG                       1242
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Seq ID NO: C146 DNA Sequence
Nucleic Acid Accession #: NM_003020.1
Coding sequence: 29..664

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1          11         21         31         41         51
|          |          |          |          |          |
CGCTCCTCGG GCTGCCCCTC GGTTGACAAT GGTCTCCAGG ATGGTCTCTA CCATGCTATC   60
TGGCCTACTG TTTTGGCTGG CATCTGGATG GACTCCAGCA TTTGCTTACA GCCCCCGGAC   120
CCCTGACCGG GTCTCAGAAG CAGATATCCA GAGGCTGCTT CATGGTGTTA TGGAGCAATT   180
GGGCATTGCC AGGCCCCGAG TGGAATATCC AGCTCACCAG GCCATGAATC TTGTGGGCCC   240
CCAGAGCATT GAAGGTGGAG CTCATGAAGG ACTTCAGCAT TTGGGTCCTT TTGGCAACAT   300
CCCCAACATC GTGGCAGAGT TGACTGGAGA CAACATTCCT AAGGACTTTA GTGAGGATCA   360
GGGGTACCCA GACCCTCCAA ATCCCTGTCC TGTTGGAAAA ACAGATGATG GATGTCTAGA   420
AAACACCCCT GACACTGCAG AGTTCAGTCG AGAGTTCCAG TTGCACCAGC ATCTCTTTGA   480
TCCGGAACAT GACTATCCAG GCTTGGGCAA GTGGAACAAG AAACTCCTTT ACGAGAAGAT   540
GAAGGGAGGA GAGAGACGAA AGCGGAGGAG TGTCAATCCA TATCTACAAG GACAGAGACT   600
GGATAATGTT GTTGCAAAGA AGTCTGTCCC CCATTTTTCA GATGAGGATA AGGATCCAGA   660
GTAAAGAGAA GATGCTAGAC GAAAACCCAC ATTACCTGTT AGGCCTCAGC ATGGCTTATG   720
TGCACGTGTA AATGGAGTCC CTGTGAATGA CAGCATGTTT CTTACATAGA TAATTATGGA   780
TACAAAGCAG CTGTATGTAG ATAGTGTATT GTCTTCACAC CGATGATTCT GCTTTTTGCT   840
AAATTAGAAT AAGAGCTTTT TTGTTTCTTG GGTTTTTAAA ATGTGAATCT GCAATGATCA   900
TAAAAATTAA AATGTGAATG TCAACAATAA AAAGCAAGAC TATGAAAGGC TCAGATTTCT   960
TGCAGTTTAA AATGGTGTCT GAGGTTGTAC TATTTTGGCC AAGTCTGTAG AAAGCTGTCA   1020
TTTGATTTTG ATTATGTAGT TCATCCAGCC CTTGGGCATT GTTATACACC AGTAAAGAAG   1080
GCTGTACTCA AGAGGAGGAG CTGACACATT TCACTTGGCT GCGTCTTAAT AAACATGAAT   1140
GCAAGCATTG GC                                                       1152
```

Seq ID NO: C147 DNA Sequence
Nucleic Acid Accession #: NM_024021.2
Coding sequence: 144..806

```
1          11         21         31         41         51
|          |          |          |          |          |
AACATTCCTG CAAATGGTTT CAATATATGC AGATGTCTCG ATATAGGAAT GAAATTACGT   60
CTTTGGAACA ACTTAAATAA GTCAAATATA CTTGGAGCTT TAAAAATTAA AAGGAGAGAG   120
ATTCGAGCAC CTTTTCTGCT GCCATGACAA CCATGCAAGG AATGGAACAG GCCATGCCAG   180
GGGCTGGCCC TGGTGTGCCC CAGCTGGGAA ACATGGCTGT CATACATTCA CATCTGTGGA   240
AAGGATTGCA AGAGAAGTTC TTGAAGGGAG AACCCAAAGT CCTTGGGGTT GTGCAGATTC   300
TGACTGCCCT GATGAGCCTT AGCATGGGAA TAACAATGAT GTGTATGGCA TCTAATACTT   360
ATGGAAGTAA CCCTATTTCC GTGTATATCG GGTACACAAT TTGGGGGTCA GTAATGTTTA   420
TTATTTCAGG ATCCTTGTCA ATTGCAGCAG GAATTAGAAC TACAAAAGGC CTGGTCCGAG   480
GTAGTCTAGG AATGAATATC ACCAGCTCTG TACTGGCTGC ATCAGGGATC TTAATCAACA   540
CATTTAGCTT GGCGTTTTAT TCATTCCATC ACCCTTACTG TAACTACTAT GGCAACTCAA   600
ATAATTGTCA TGGGACTATG TCCATCTTAA TGGGTCTGGA TGGCATGGTG CTCCTCTTAA   660
GTGTGCTGGA ATTCTGCATT GCTGTGTCCC TCTCTGCCTT TGGATGTAAA GTGCTCTGTT   720
GTACCCCTGG TGGGGTTGTG TTAATTCTGC CATCACATTC TCACATGGCA GAAACAGCAT   780
CTCCCACACC ACTTAATGAG GTTTGAGGCC ACCAAAAGAT CAACAGACAA ATGCTCCAGA   840
AATCTATGCT GACTGTGACA CAAGAGCCTC ACATGAGAAA TTACCAGTAT CCAACTTCGA   900
TACTGATAGA CTTGTTGATA TTATTATTAT ATGTAATCCA ATTATGAACT GTGTGTGTAT   960
AGAGAGATAA TAAATTCAAA ATTATGTTCT CATTTTTTTC CCTGGAACTC AATAACTCAT   1020
TTCACTGGCT CTTTATCGAG AGTACTAGAA GTTAAATTAA TAAATAATGC ATTTAATGAG   1080
GCAACAGCAC TTGAAAGTTT TTCATTCATC ATAAGAACTT TATATAAAGG CATTACATTG   1140
GCAAATAAGG TTTGGAAGCA GAAGAGCAAA AAAAAGATAT TGTTAAAATG AGGCCTCCAT   1200
GCAAAACACA TACTTCCCTC CCATTTATTT AACTTTTTTT TTCTCCTACC TATGGGGACC   1260
AAAGTGCTTT TTCCTTCAGG AAGTGGAGAT GCATGGCCAT CTCCCCCTCC CTTTTTCCTT   1320
CTCCTGCTTT TCTTTCCCCA TAGAAAGTAC CTTGAAGTAG CACAGTCCGT CCTTGCATGT   1380
GCACGAGCTA TCATTTGAGT AAAAGTATAC ATGGAGTAAA AATCATATTA AGCATCAGAT   1440
TCAACTTATA TTTTCTATTT CATCTTCTTC CTTTCCCTTC TCCCACCTTC TACTGGGCAT   1500
AATTATATCT TAATCATATA TGGAAATGTG CAACATATGG TATTTGTTAA ATACGTTTGT   1560
TTTTATTGCA GAGCAAAAAT AAATCAAATT AGAAGCAATA AAAAAAAAAA AAAAAAAAA   1619
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Seq ID NO: C148 DNA Sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..502

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1          11         21         31         41         51
|          |          |          |          |          |
AGTCTCTGCT CTTCCCAGCC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GGACCATGCG   60
CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCCTC TGCCTAGCGC CCCGGGGCG   120
AGCGGTCCCG CTGCCTGCGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCAA   180
CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC   240
TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG   300
GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA   360
GGCCTTGGGC AATCAGCAGC CTTCGTGGGA TTCAGAGGAT AGCAGCAACT TCAAAGATGT   420
AGGTTCAAAA GGCAAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA   480
CCCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC   540
TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA   600
AAATATTTGA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT   660
CTTCTGGTTT AAACTTGTTT GCTGTGAACA ATTGTCGAAA AGAGTCTTCC AATTAATGCT   720
TTTTTATATC TAGGCTACCT GTTGGTTAGA TTCAAGGCCC CGAGCTGTTA CCATTCACAA   780
TAAAAGCTTA AACACAT                                                  797
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Seq ID NO: C149 DNA Sequence
Nucleic Acid Accession #: NM_012261.1
Coding sequence: 203..1045

```
1          11         21         31         41         51
|          |          |          |          |          |
GATTTGCTCT GCCAGCAGCT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC   60
ACAGAATACG CGCTCCCTCC CTCCCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC   120
CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG   180
CCTCATTCGG GGCACTGCGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG   240
ACTTCGAGTT CTCCTGATGT TGTTCCATAC AATGGCTCAA ATCATGGCAG AACAAGAAGT   300
GGAAAATCTC TCAGGCCTTT CCACTAACCC TGAAAAAGAT ATATTTGTGG TGCGGGAAAA   360
TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG   420
GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCCGAT ATCGCATTGA CCCGGGGAGC   480
TGAGGTGAAG GGCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTTCT GGGTGGATCG   540
CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA   600
GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT   660
CAAAGACGCA GTCAGTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT   720
CACCCCCGCT GGGAAGTCCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG   780
TGATCCGCAG AAGACGGTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTTGACAT   840
TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT   900
GGAAGAAACC TTGCCCCTGA TTTTGGGGCT CATCTTGGGC CTCGTCATCA TGGTAACACT   960
CGCGATTTAC CACGTCCACC ACAAAATGAC TGCCAACCAG GTGCAGATCC CTCGGGACAG   1020
ATCCCAGTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCCTAT TCCTGCTCCC   1080
CCAACTGGAT CAGGTAGAAC AACAAAAGCA CTTTTCCATC TTGTACACGA GATACACCAA   1140
CATAGCTACA ATCAAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA   1200
AACCCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC   1260
ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT   1320
TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA   1380
TTGAAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCTT   1440
TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC   1500
TCATGCTCCC TGCAGCAAGA CCCCTGAAAG TGATTCATGC TTCTGGCTGG CATTCTGCAT   1560
GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG   1620
AAAACGACTA ATGTAACTAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC   1680
GGGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AAACACACTA   1740
TTCTCTGGC                                                           1749
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Seq ID NO: C150 DNA Sequence
Nucleic Acid Accession #: NM_003226.1
Coding sequence: 2..226

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1          11         21         31         41         51
|          |          |          |          |          |
GATGCTGGGG CTGGTCCTGG CCTTGCTGTC CTCCAGCTCT GCTGAGGAGT ACGTGGGCCT   60
GTCTGCAAAC CAGTGTGCCG TGCCGGCCAA GGACAGGGTG GACTGCGGCT ACCCCCATGT   120
CACCCCCAAG GAGTGCAACA ACCGGGGCTG CTGCTTTGAC TCCAGGATCC CTGGAGTGCC   180
TTGGTGTTTC AAGCCCCTGA CTAGGAAGAC AGAATGCACC TTCTGAGGCA CCTCCAGCTG   240
CCCCTGGGAT GCAGGCTGAG CACCCTTGCC CGGCTGTGAT TGCTGCCAGG CACTGTTCAT   300
CTCAGTTTTT CTGTCCCTTT GCTCCCGGCA AGCTTTCTGC TGAAAGTTCA TATCTGGAGC   360
CTGATGTCTT AACGAATAAA GGTCCCATGC TCCACCCG                           398
```

Seq ID NO: C151 DNA Sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

```
1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGCC AGTCTCCGCG CCTCCACCCA GCTCAGGAAC CCGCGAACCC TCTCTTGACC   60
ACTATGAGCC TCCCGTCCAG CCGCGCGGCC CGTGTCCCGG GTCCTTCGGG CTCCTTGTGC   120
GCGCTGCTCG CGCTGCTGCT CCTGCTGACG CCGCCGGGGC CCCTCGCCAG CGCTGGTCCT   180
GTCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTTTAC GCGTTACGCT GAGAGTAAAC   240
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CCCAAAACGA TTGGTAAACT GCAGGTGTTC CCCGCAGGCC CGCAGTGCTC CAAGGTGGAA   300
GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA   360
AAGAAAGTCA TCCAGAAAAT TTTGGACAGT GGAAACAAGA AAAACTGAGT AACAAAAAAG   420
ACCATGCATC ATAAAATTGC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGACC   480
CAGTAAGAAT AAGAAGGAAG GGTTGGTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT   540
GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA   600
CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCTTTGG   660
CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT   720
TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCTTACCGAA AAGGCTGTGG   780
ATTTCGTATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTTGTTCTT   840
ACTCACTCTT CTCATAAAAT AGGAAATATT TTAGTTCTGT TTTCTTGGGG AATATGTTAC   900
TCTTTACCCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACTGGGTG TGTCATACCG   960
TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG   1020
CTAATATATT CTCTTCCTAT GGTTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT   1080
CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCACTATAG GATGACTATA   1140
ATTCTGGTCA CTAAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC   1200
TGATTGCTAA TTTACATAGA AATGTATTCT CTTGGTTTTT TAAATAAAAG CAAAATTAAC   1260
AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTTGAAT ATAAATTCAT   1320
CATTTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT   1380
TTTAAAGGTT TTGACCATTT TGTTATGAGG AATTATACAT GTATCACATT CACTATATTA   1440
AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCATT   1500
TGGAGAAACA ATAAAAGATT TCTAAACCAA AAAAAAAAAA AAAAAAA                 1547
```

Seq ID NO: C152 DNA Sequence
Nucleic Acid Accession #: NM_005242.2
Coding sequence: 148..1341

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1          11         21         31         41         51
|          |          |          |          |          |
CGGCCCGCCC TGGGGAGGCG CGCAGCAGAG GCTCCGATTC GGGGCAGGTG AGAGGCTGAC   60
TTTCTCTCGG TGCGTCCAGT GGAGCTCTGA GTTTCGAATC GGTGGCGGCG GATTCCCCGC   120
GCGCCCGGCG TCGGGGCTTC CAGGAGGATG CGGAGCCCCA GCGCGGCGTG GCTGCTGGGG   180
GCCGCCATCC TGCTAGCAGC CTCTCTCTCC TGCAGTGGCA CCATCCAAGG AACCAATAGA   240
TCCTCTAAAG GAAGAAGCCT TATTGGTAAG GTTGATGGCA CATCCCACGT CACTGGAAAA   300
GGAGTTACAG TTGAAACAGT CTTTTCTGTG GATGAGTTTT CTGCATCTGT CCTCACTGGA   360
AAACTGACCA CGGTCTTCCT TCCAATTGTC TACACAATTG TGTTTGTGGT GGGTTTGCCA   420
AGTAACGGCA TGGCCCTGTG GGTCTTTCTT TTCCGAACTA AGAAGAAGCA CCCTGCTGTG   480
ATTTACATGG CCAATCTGGC CTTGGCTGAC CTCCTCTCTG TCATCTGGTT CCCCTTGAAG   540
ATTGCCTATC ACATACATGC CAACAACTGG ATTTATGGGG AAGCTCTTTG TAATGTGCTT   600
ATTGGCTTTT TCTATGGCAA CATGTACTGT TCCATTCTCT TCATGACCTG CCTCAGTGTG   660
CAGAGGTATT GGGTCATCGT GAACCCCATG GGGCACTCCA GGAAGAAGGC AAACATTGCC   720
ATTGGCATCT CCCTGGCAAT ATGGCTGCTG ATTCTGCTGG TCACCATCCC TTTGTATGTC   780
GTGAAGCAGA CCATCTTCAT TCCTGCCCTG AACATCACGA CCTGTCATGA TGTTTTGCCT   840
GAGCAGCTCT TGGTGGGAGA CATGTTCAAT TACTTCCTCT CTCTGGCCAT TGGGGTCTTT   900
CTGTTCCCAG CCTTCCTCAC AGCCTCTGCC TATGTGCTGA TGATCAGAAT GCTGCGATCT   960
TCTGCCATGG ATGAAAACTC AGAGAAGAAA AGGAAGAGGG CCATCAAACT CATTGTCACT   1020
GTCCTGGCCA TGTACCTGAT CTGCTTCACT CCTAGTAACC TTCTGCTTGT GGTGCATTAT   1080
TTTCTGATTA AGAGCCAGGG CCAGAGCCAT GTCTATGCCC TGTACATTGT AGCCCTCTGC   1140
CTCTCTACCC TTAACAGCTG CATCGACCCC TTTGTCTATT ACTTTGTTTC ACATGATTTC   1200
AGGGATCATG CAAAGAACGC TCTCCTTTGC CGAAGTGTCC GCACTGTAAA GCAGATGCAA   1260
GTATCCCTCA CCTCAAAGAA ACACTCCAGG AAATCCAGCT CTTACTCTTC AAGTTCAACC   1320
ACTGTTAAGA CCTCCTATTG AGTTTTCCAG GTCCTCAGAT GGGAATTGCA CAGTAGGATG   1380
TGGAACCTGT TTAATGTTAT GAGGACGTGT CTGTTATTTC CTAATCAAAA AGGTCTCACC   1440
ACATACCACC G                                                        1451
```

Seq ID NO: C153 DNA Sequence
Nucleic Acid Accession #: NM_003469.2
Coding sequence: 92..1945

```
1          11         21         31         41         51
|          |          |          |          |          |
GAAACGGCCC GAGAAGCTCG CCCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC   60
CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG   120
AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT   180
TCAGAGAAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAAAATG TCCAAAAGTT   240
TCCCAGTCCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAAGCTCA   300
TAAGGAAGAA AGCAGCCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA   360
AAAAGAAAAT GGCGATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG   420
GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCACCAAA   480
AGAAAATAAG CCCTATGCCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA   540
TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA   600
TGAAGAGAAT TCCAGGGATA ACCCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA   660
TACTCCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG   720
ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACTTTATA CGGATGATGA   780
AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG   840
GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAAGA   900
GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT   960
CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT   1020
AATTGCCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA   1080
AAATGGGGAA AGGGCCACCA GGCTTTTTGA GAAACCTCTT GATTCTCAGT CTATTTATCA   1140
GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCCAGAA GACTTAATTG AGATGCTCAA   1200
AACTGGGGAG AAGCCGAATG GATCAGTGGA ACCGGAGCGG GAGCTTGACC TTCCTGTTGA   1260
CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT   1320
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CTCCAAGAGT GGCTACCCTA AAACACCTGG TCGTGCTGGG ACTGAGGCCC TACCAGACGG   1380
GCTCAGTGTT GAGGATATTT TAAATCTTTT AGGGATGGAG AGTGCAGCAA ATCAGAAAAC   1440
GTCGTATTTT CCCAATCCAT ATAACCAGGA GAAAGTTCTG CCAAGGCTCC CTTATGGTGC   1500
TGGAAGATCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCCACATG TTGAAAACAG   1560
ACAGATGGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG   1620
GATGCTAGTT AAATACCCTG AGATCATTAA TTCAAACCAA GTGAAGCGAG TTCCTGGTCA   1680
AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAAGAGCA   1740
TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC   1800
TGTGGGGCCC CCGAAGAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT   1860
AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC   1920
TAAGAGAGCA ATGGAAAATA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCCTCC   1980
CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTTGA CTTCTATCCT GTTAACACTG   2040
TAATATCTTT AAATGATGTA CAGGCAGATG AAACCAGGTC ACTGGGGAGT CTGCTTCATT   2100
TCCTCTGAGC TGTTATCTTG TGTATGGATA TGTGTAAATG TTATGACTCC TTGATAAAAA   2160
ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT   2220
GGCTGTGGCA TTGTTGATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG   2280
TTTTTAATAT TTATTGAATT ATTTTGTTAC TGTCTGTAGC GTTTTGTGGA GTACTGGACC   2340
AAAAAAATAA AGCATTATAA ATATA                                         2365
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Seq ID NO: C154 DNA Sequence
Nucleic Acid Accession #: NM_030955
Coding sequence: 327..5108

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1          11         21         31         41         51
|          |          |          |          |          |
GAATTCCGGG AGCGGGCGGG CTGCGAGGCC GCGGGGCATG CGGGAGGCGG AGGGGTGGGA   60
CCGGGTGGCT GCGCCCATTC CACACCCGCC GAAAGCGGAC ACTGTCAGCT GAATCACTCC   120
CCTTTTAGGA GGAGGGAGGG GGAAAAGGTG TCTAGCTAAT TTCTGCTTAA AAAACCACAG   180
GAGATCGCGG GTCAGCTTTG CAGTCGCTGC CTTCTCGCGC CTGACCATGC ACCCCTGCAT   240
CTTCCTGCTG GGCACAGGCG AGCGCTTTAT TTCTGGAGCT GAGGGCTAAA ACTTTTTTCA   300
CTTTTCTTCT CCTCAACATC TGAATCATGC CATGTGCCCA GAGGAGCTGG CTTGCAAACC   360
TTTCCGTGGT GGCTCAGCTC CTTAACTTTG GGGCGCTTTG CTATGGGAGA CAGCCTCAGC   420
CAGGCCCGGT TCGCTTCCCG GACAGGAGGC AAGAGCATTT TATCAAGGGC CTGCCAGAAT   480
ACCACGTGGT GGGTCCAGTC CGAGTAGATG CCAGTGGGCA TTTTTTGTCA TATGGCTTGC   540
ACTATCCCAT CACGAGCAGC AGGAGGAAGA GAGATTTGGA TGGCTCAGAG GACTGGGTGT   600
ACTACAGAAT TTCTCACGAG GAGAAGGACC TGTTTTTTAA CTTGACGGTC AATCAAGGAT   660
TTCTTTCCAA TAGCTACATC ATGGAGAAGA GATATGGGAA CCTCTCCCAT GTTAAGATGA   720
TGGCTTCCTC TGCCCCCCTC TGCCATCTCA GTGGCACGGT TCTACAGCAG GGCACCAGAG   780
TTGGGACGGC AGCCCTCAGT GCCTGCCATG GACTGACTGG ATTTTTCCAA CTACCACATG   840
GAGACTTTTT CATTGAACCC GTGAAGAAGC ATCCACTGGT TGAGGGAGGG TACCACCCGC   900
ACATCGTTTA CAGGAGGCAG AAAGTTCCAG AAACCAAGGA GCCAACCTGT GGATTAAAGG   960
ACAGTGTTAA CATCTCCCAG AAGCAAGAGC TATGGCGGGA GAAGTGGGAG AGGCACAACT   1020
TGCCAAGCAG AAGCCTCTCT CGGCGTTCCA TCAGCAAGGA GAGATGGGTG GAGACACTGG   1080
TGGTGGCCGA CACAAAGATG ATTGAATACC ATGGGAGTGA GAATGTGGAG TCCTACATCC   1140
TCACCATCAT GAACATGGTC ACTGGGTTGT TCCATAACCC AAGCATTGGC AATGCAATTC   1200
ACATTGTTGT GGTTCGGCTC ATTCTACTCG AAGAAGAAGA GCAAGGACTG AAAATAGTTC   1260
ACCATGCAGA AAAGACACTG TCTAGCTTCT GCAAGTGGCA GAAGAGTATC AATCCCAAGA   1320
GTGACCTCAA TCCTGTTCAT CACGACGTGG CTGTCCTTCT CACCAGAAAG GACATCTGTG   1380
CTGGTTTCAA TCGCCCCTGC GAGACCCTGG GCCTGTCTCA CCTTTCAGGA ATGTGTCAGC   1440
CTCACCGCAG TTGTAACATC AATGAAGATT CGGGACTCCC TCTGGCTTTC ACAATTGCCC   1500
ATGAGCTAGG ACACAGCTTC GGCATCCAGC ATGATGGGAA AGAAAATGAC TGTGAGCCTG   1560
TGGGCAGACA TCCGTACATC ATGTCCCGCC AGCTCCAGTA CGATCCCACT CCGCTGACAT   1620
GGTCCAAGTG CAGCGAGGAG TACATCACCC GCTTCTTGGA CCGAGGCTGG GGGTTCTGTC   1680
TTGATGACAT ACCTAAAAAG AAAGGCTTGA AGTCCAAGGT CATTGCCCCC GGAGTGATCT   1740
ATGATGTTCA CCACCAGTGC CAGCTACAAT ATGGACCCAA TGCTACCTTC TGCCAGGAAG   1800
TAGAAAACGT CTGCCAGACA CTGTGGTGCT CCGTGAAGGG CTTTTGTCGC TCTAAGCTGG   1860
ACGCTGCTGC AGATGGAACT CAATGTGGTG AGAAGAAGTG GTGTATGGCA GGCAAGTGCA   1920
TCACAGTGGG GAAGAAACCA GAGAGCATTC CTGGAGGCTG GGGCCGCTGG TCACCCTGGT   1980
CCCACTGTTC CAGGACCTGT GGGGCTGGAG TCCAGAGCGC AGAGAGGCTC TGCAACAACC   2040
CCGAGCCAAA GTTTGGAGGG AAATATTGCA CTGGAGAAAG AAAACGCTAT CGCTTGTGCA   2100
ACGTCCACCC CTGTCGCTCA GAGGCACCAA CATTTCGGCA GATGCAGTGC AGTGAATTTG   2160
ACACTGTTCC CTACAAGAAT GAACTCTACC ACTGGTTTCC CATTTTTAAC CCAGCACATC   2220
CTTGTGAGCT CTACTGCCGA CCCATAGATG GCCAGTTTTC TGAGAAAATG CTGGATGCTG   2280
TCATTGATGG TACCCCTTGC TTTGAAGGCG GCAACAGCAG AAATGTCTGT ATTAATGGCA   2340
TATGTAAGAT GGTTGGCTGT GACTATGAGA TCGATTCCAA TGCCACCGAG GATCGCTGCG   2400
GTGTGTGCCT GGGAGATGGC TCTTCCTGCC AGACTGTGAG AAAGATGTTT AAGCAGAAGG   2460
AAGGATCTGG TTATGTTGAC ATTGGGCTCA TTCCAAAAGG AGCAAGGGAC ATAAGAGTGA   2520
TGGAAATTGA GGGAGCTGGA AACTTCCTGG CCATCAGGAG TGAAGATCCT GAAAAATATT   2580
ACCTGAATGG AGGGTTTATT ATCCAGTGGA ACGGGAACTA TAAGCTGGCA GGGACTGTCT   2640
TTCAGTATGA CAGGAAAGGA GACCTGGAAA AGCTGATGGC CACAGGTCCC ACCAATGAGT   2700
CTGTGTGGAT CCAGCTTCTA TTCCAGGTGA CTAACCCTGG CATCAAGTAT GAGTACACAA   2760
TCCAGAAAGA TGGCCTTGAC AATGATGTTG AGCAGATGTA CTTCTGGCAG TACGGCCACT   2820
GGACAGAGTG CAGTGTGACC TGCGGGACAG GTATCCGCCG CCAAACTGCC CATTGCATAA   2880
AGAAGGGCCG CGGGATGGTG AAAGCTACAT TCTGTGACCC AGAAACACAG CCCAATGGGA   2940
GACAGAAGAA GTGCCATGAA AAGGCTTGTC CACCCAGGTG GTGGGCAGGG GAGTGGGAAG   3000
CATGCTCGGC GACATGCGGG CCCCACGGGG AGAAGAAGCG AACCGTGCTG TGCATCCAGA   3060
CCATGGTCTC TGACGAGCAG GCTCTCCCGC CCACAGACTG CCAGCACCTG CTGAAGCCCA   3120
AGACCCTCCT TTCCTGCAAC AGAGACATCC TGTGCCCCTC GGACTGGACA GTGGGCAACT   3180
GGAGTGAGTG TTCTGTTTCC TGTGGTGGTG GAGTGCGGAT TCGCAGTGTC ACATGTGCCA   3240
AGAACCATGA TGAACCTTGC GATGTGACAA GGAAACCCAA CAGCCGAGCT CTGTGTGGCC   3300
TCCAGCAATG CCCTTCTAGC CGGAGAGTTC TGAAACCAAA CAAAGGCACT ATTTCCAATG   3360
GAAAAAACCC ACCAACACTA AAGCCCGTCC CTCCACCTAC ATCCAGGCCC AGAATGCTGA   3420
CCACACCCAC AGGGCCTGAG TCTATGAGCA CAAGCACTCC AGCAATCAGC AGCCCTAGTC   3480
CTACCACAGC CTCCAAAGAA GGAGACCTGG GTGGGAAACA GTGGCAAGAT AGCTCAACCC   3540
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AACCTGAGCT GAGCTCTCGC TATCTCATTT CCACTGGAAG CACTTCCCAG CCCATCCTCA   3600
CTTCCCAATC CTTGAGCATT CAGCCAAGTG AGGAAAATGT TTCCAGTTCA GATACTGGTC   3660
CTACCTCGGA GGGAGGCCTT GTAGCTACAA CAACAAGTGG TTCTGGCTTG TCATCTTCCC   3720
GCAACCCTAT CACTTGGCCT GTGACTCCAT TTTACAATAC CTTGACCAAA GGTCCAGAAA   3780
TGGAGATTCA CAGTGGCTCA GGGGAAGAAA GAGAACAGCC TGAGGACAAA GATGAAAGCA   3840
ATCCTGTAAT ATGGACCAAG ATCAGAGTAC CTGGAAATGA CGCTCCAGTG GAAAGTACAG   3900
AAATGCCACT TGCACCTCCA CTAACACCAG ATCTCAGCAG GGAGTCCTGG TGGCCACCCT   3960
TCAGCACAGT AATGGAAGGA CTGCTCCCCA GCCAAAGGCC CACTACTTCC GAAACTGGGA   4020
CACCCAGAGT TGAGGGGATG GTTACTGAAA AGCCAGCCAA CACTCTGCTC CCTCTGGGAG   4080
GAGACCACCA GCCAGAACCC TCAGGAAAGA CGGCAAACCG TAACCACCTG AAACTTCCAA   4140
ACAACATGAA CCAAACAAAA AGTTCTGAAC CAGTCCTGAC TGAGGAGGAT GCAACAAGTC   4200
TGATTACTGA GGGCTTTTTG CTAAATGCCT CCAATTACAA GCAGCTCACA AACGGCCACG   4260
GCTCTGCACA CTGGATCGTC GGAAACTGGA GCGAGTGCTC CACCACATGT GGCCTGGGGG   4320
CCTACTGGAA AAGGGTGGAG TGCACCACCC AGATGGATTC TGACTGTGCG GCCATCCAGA   4380
GACCTGACCC TGCAAAAAGA TGCCACCTCC GTCCCTGTGC TGGCTGGAAA GTGGGAAACT   4440
GGAGCAAGTG CTCCAGAAAC TGCAGTGGGG GCTTCAAGAT ACGCGAGATT CAGTGCGTGG   4500
ACAGCCGGGA CCACCGGAAC CTGAGGCCAT TTCACTGCCA GTTCCTGGCC GGCATTCCTC   4560
CCCCATTGAG CATGAGCTGT AACCCGGAGC CCTGTGAGGC GTGGCAGGTG GAGCCTTGGA   4620
GCCAGTGCTC CAGGTCCTGT GGAGGTGGAG TTCAGGAGAG AGGAGTGTTC TGTCCAGGAG   4680
GCCTCTGTGA TTGGACAAAA AGACCCACAT CCACCATGTC TTGCAATGAG CACCTGTGCT   4740
GTCACTGGGC CACTGGGAAC TGGGACCTGT GTTCCACTTC CTGTGGAGGT GGCTTTCAGA   4800
AGAGGATTGT CCAATGTGTG CCCTCAGAGG GCAATAAAAC TGAAGACCAA GACCAATGTC   4860
TATGTGATCA CAAACCCAGA CCTCCAGAAT TCAAAAAATG CAACCAGCAG GCCTGCAAGA   4920
AAAGTGCCGA TTTACTTTGC ACTAAGGACA AACTGTCAGC CAGTTTCTGC CAGACACTGA   4980
AAGCCATGAA GAAATGTTCT GTGCCCACCG TGAGGGCTGA GTGCTGCTTC TCGTGTCCCC   5040
AGACACACAT CACACACACC CAAAGGCAAA GAAGGCAACG GTTGCTCCAA AAGTCAAAAG   5100
AACTCTAAGC CCAAA                                                   5115
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Seq ID NO: C155 DNA Sequence
Nucleic Acid Accession #: NM_001062.1
Coding sequence: 76..1380

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1          11         21         31         41         51
|          |          |          |          |          |
GCTCTCATTA CCTTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG   60
TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT   120
TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC   180
CTAAAACCTC TGTTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC   240
AATGTTGTGT TGTCCCTCAA ACTTGTTGGA ATCCAGATCC AAACCCTGAT GCAAAAGATG   300
ATCCAACAAA TCAAATACAA TGTGAAAAGC AGATTGTCAG ATGTAAGCTC GGGAGAGCTT   360
GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACTT AATATATGAT   420
TACCACCTGA CTGACAAGCT AGAAAATAAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA   480
CACAATGGCA CTCCCCTGAC TAACTACTAC CAGCTCAGCC TGGACGTTTT GGCCTTGTGT   540
CTGTTCAATG GGAACTACTC AACCGCCGAA GTTGTCAACC ACTTCACTCC TGAAAATAAA   600
AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG   660
ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG   720
AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAAT   780
GGTCTCATTG GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA   840
GACTATTATA ATGAAAATGA CTGGAATTGC CAACAAACTC TGAATACAGT GCTCACGGAA   900
ATTTCTCAAG GAGCATTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG   960
GGAAAGACCT TCTTGGATAT TAACAAAGAC TCTTCTTGCG TCTCTGCTTC AGGTAACTTC   1020
AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC   1080
GTCAATTACT CTGTGAGAAT CAATGAAACA TATTTCACCA ATGTCACTGT GCTAAATGGT   1140
TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC   1200
ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACCTGTA TTCAGGGCCT ATGTGCCAAC   1260
AATAATGACA GAACCTACTG GGAACTTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT   1320
GGTAGTTACG TTGTCCGCAA TGGAGAAAAC TTGGAGGTTC GCTGGAGCAA ATACTAATAA   1380
GCCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCCATG TTTATTGTCC   1440
TTATGCCTTC TTCTTCATTT ATCCCAGTAC GAGCAGGAGA GTTAATAACC TCCCCTTCTC   1500
TCTCTACATG TTCAATAAAA GTTGTTGAAA GATTAAC                            1537
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Seq ID NO: C156 DNA Sequence
Nucleic Acid Accession #: NM_004591
Coding sequence: 59..349

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1          11         21         31         41         51
|          |          |          |          |          |
CACTCCCAAA GAACTGGGTA CTCAACACTG AGCAGATCTG TTCTTTGAGC TAAAAACCAT   60
GTGCTGTACC AAGAGTTTGC TCCTGGCTGC TTTGATGTCA GTGCTGCTAC TCCACCTCTG   120
CGGCGAATCA GAAGCAGCAA GCAACTTTGA CTGCTGTCTT GGATACACAG ACCGTATTCT   180
TCATCCTAAA TTTATTGTGG GCTTCACACG GCAGCTGGCC AATGAAGGCT GTGACATCAA   240
TGCTATCATC TTTCACACAA AGAAAAAGTT GTCTGTGTGC GCAAATCCAA AACAGACTTG   300
GGTGAAATAT ATTGTGCGTC TCCTCAGTAA AAAAGTCAAG AACATGTAAA AACTGTGGCT   360
TTTCTGGAAT GGAATTGGAC ATAGCCCAAG AACAGAAAGA ACCTTGCTGG GGTTGGAGGT   420
TTCACTTGCA CATCATGGAG GGTTTAGTGC TTATCTAATT TGTGCCTCAC TGGACTTGTC   480
CAATTAATGA AGTTGATTCA TATTGCATCA TAGTTTGCTT TGTTTAAGCA TCACATTAAA   540
GTTAAACTGT ATTTTATGTT ATTTATAGCT GTAGGTTTTC TGTGTTTAGC TATTTAATAC   600
TAATTTTCCA TAAGCTATTT TGGTTTAGTG CAAAGTATAA AATTATATTT GGGGGGGAAT   660
AAGATTATAT GGACTTTCTT GCAAGCAACA AGCTATTTTT TAAAAAAACT ATTTAACATT   720
CTTTTGTTTA TATTGTTTTG TCTCCTAAAT TGTTGTAATT GCATTATAAA ATAAGAAAAA   780
CATTAATAAG ACAAATATT                                               799
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Seq ID NO: C157 DNA Sequence
Nucleic Acid Accession #: NM_013271.1

Coding sequence: 27..809

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1          11         21         31         41         51
|          |          |          |          |          |
TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTCGCC GCTGCTCTGG GGGCCGCGGG   60
CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCGCGC   120
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AGACTGGCGC TCCTCGCCGC TTCCGGCGGT CAGTGCCCCG AGGTGAGGCG GCGGGGGCGG   240
TGCAGGAGCT GGCGCGGGCG CTGGCGCATC TGCTGGAGGC CGAACGTCAG GAGCGGGCGC   300
GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG   360
TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCCGACGCGC   420
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CCCAGCTTGT CCCCGCGCCC GTCCCCGCCG CGGCGCTCCG ACCCCGGCCC CCGGTCTACG   540
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CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAAACGCCT AGAGACCCCG GCGCCCCAGG   780
TGCCTGCACG CCGCCTCTTG CCACCCTGAG CACTGCCCGG ATCCCGTGCA CCCTGGGACC   840
CAGAAGTGCC CCCGCCATCC CGCCACCAGG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC   900
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Seq ID NO: C158 DNA Sequence
Nucleic Acid Accession #: NM_002245.2
Coding sequence: 183..1193

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CAAACTCACT ATTTATAATG CATAGGTAAC CATTAACTAT GTACATATAA AGTATAAATA   1740
TGTTTATATT CTGTACATAT GGTTTAGGTC ACCAGATCCT AGTGTAGTTC TGAAACTAAG   1800
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Seq ID NO: C159 DNA Sequence
Nucleic Acid Accession #: NM_005472.1
Coding sequence: 93..404

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TGCATCAGGT CT                                                      492
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Seq ID NO: C160 DNA Sequence
Nucleic Acid Accession #: NM_005245.1
Coding sequence: 187..13959

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TACAACGTCA CCGTGCAGGA GAACTCTGCA GCTAAGACTT ATGTGGGGCA TCCTGTCAAG 360
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GTGCTGGATA CAAATGACTT GAGACCGTTA TTCTCACCCA CCTCATACAG CGTTTCTTTA 660
CCTGAAAACA CAGCTATAAG GACCAGTATC GCAAGAGTCA GCGCCACGGA TGCAGACATA 720
GGAACCAACG GGGAATTTTA CTACAGTTTT AAAGATCGAA CAGATATGTT TGCTATTCAC 780
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Nucleic Acid Accession #: NM_014220.1
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Seq ID NO: C162 DNA Sequence
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CATCGACTGG ACCACCAACG TGACGGCGCA CGCCGCCTAC TCCTACATGT ACGCGGGCTT  960
CAGCTCCTTC CTCATTCTCG CCACCGTCCT CTGCAACGTG CTTGTGTGCG GCGCGCTGCT 1020
CCGCATGCAC CGCCAGTTCA TGCGCCGCAC CTCGCTGGGC ACCGAGCAGC ACCACGCGGC 1080
CGCGGCCGCC TCGGTTGCCT CCCGGGGCCA CCCCGCTGCC TCCCCAGCCT TGCCGCGCCT 1140
CAGCGACTTT CGGCGCCGCC GGAGCTTCCG CCGCATCGCG GGCGCCGAGA TCCAGATGGT 1200
CATCTTACTC ATTGCCACCT CCCTGGTGGT GCTCATCTGC TCCATCCCGC TCGTGGTGCG 1260
AGTATTCGTC AACCAGTTAT ATCAGCCAAG TTTGGAGCGA GAAGTCAGTA AAAATCCAGA 1320
TTTGCAGGCC ATCCGAATTG CTTCTGTGAA CCCCATCCTA GACCCCTGGA TATATATCCT 1380
CCTGAGAAAG ACAGTGCTCA GTAAAGCAAT AGAGAAGATC AAATGCCTCT TCTGCCGCAT 1440
TGGCGGGTCC CGCAGGGAGC GCTCCGGACA GCACTGCTCA GACAGTCAAA GGACATCTTC 1500
TGCCATGTCA GGCCACTCTC GCTCCTTCAT CTCCCGGGAG CTGAAGGAGA TCAGCAGTAC 1560
ATCTCAGACC CTCCTGCCAG ACCTCTCACT GCCAGACCTC AGTGAAAATG GCCTTGGAGG 1620
CAGGAATTTG CTTCCAGGTG TGCCTGGCAT GGGCCTGGCC CAGGAAGACA CCACCTCACT 1680
GAGGACTTTG CGAATATCAG AGACCTCAGA CTCTTCACAG GGTCAGGACT CAGAGAGTGT 1740
CTTACTGGTG GATGAGGCTG GTGGGAGCGG CAGGGCTGGG CCTGCCCCTA AGGGGAGCTC 1800
CCTGCAAGTC ACATTTCCCA GTGAAACACT GAACTTATCA GAAAAATGTA TATAATAGGC 1860
AAGGAAAGAA ATACAGTACT GTTTCTGGAC CCTTATAAAA TCCTGTGCAA TAGACACATA 1920
CATGTCACAT TTAGCTGTGC TCAGAAGGGC TATCATCA                          1958
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Seq ID NO: C164 DNA Sequence
Nucleic Acid Accession #: NM_002659.1
Coding sequence: 427..1434

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1          11         21         31         41         51
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CAGTATCCCT CCTGACAAAA CTAACAAAAA TCCTGTTAGC CAAATAATCA GCCACATTCA   60
TATTTACCGT CAAAGTTTTT ATCCTCATTT TACAGCAGTG GAGAGCGATT GCCCCGGGTC  120
CCACGTTAGG AAGAGAGAGA ACTGGGATTT GCACCCAGGC AATCTGGGGA CAGAGCTGTG  180
ATCACAACTC CATGAGTCAG GGCCGAGCCA GCCCCTTCAC CACCAGCCGG CCGCGCCCCG  240
GGAAGGAAGT TTGTGGCGGA GGAGGTTCGT ACGGGAGGAG GGGGAGGCGC CCACGCATCT  300
GGGGCTGACT CGCTCTTTCG CAAAACGTCT GGGAGGAGTC CCTGGGGCCA CAAAACTGCC  360
TCCTTCCTGA GGCCAGAAGG AGAGAAGACG TGCAGGGACC CCGCGCACAG GAGCTGCCCT  420
CGCGACATGG GTCACCCGCC GCTGCTGCCG CTGCTGCTGC TGCTCCACAC CTGCGTCCCA  480
GCCTCTTGGG GCCTGCGGTG CATGCAGTGT AAGACCAACG GGGATTGCCG TGTGGAAGAG  540
TGCGCCCTGG GACAGGACCT CTGCAGGACC ACGATCGTGC GCTTGTGGGA AGAAGGAGAA  600
GAGCTGGAGC TGGTGGAGAA AAGCTGTACC CACTCAGAGA AGACCAACAG GACCCTGAGC  660
TATCGGACTG GCTTGAAGAT CACCAGCCTT ACCGAGGTTG TGTGTGGGTT AGACTTGTGC  720
AACCAGGGCA ACTCTGGCCG GGCTGTCACC TATTCCCGAA GCCGTTACCT CGAATGCATT  780
TCCTGTGGCT CATCAGACAT GAGCTGTGAG AGGGGCCGGC ACCAGAGCCT GCAGTGCCGC  840
AGCCCTGAAG AACAGTGCCT GGATGTGGTG ACCCACTGGA TCCAGGAAGG TGAAGAAGGG  900
CGTCCAAAGG ATGACCGCCA CCTCCGTGGC TGTGGCTACC TTCCCGGCTG CCCGGGCTCC  960
AATGGTTTCC ACAACAACGA CACCTTCCAC TTCCTGAAAT GCTGCAACAC CACCAAATGC 1020
AACGAGGGCC CAATCCTGGA GCTTGAAAAT CTGCCGCAGA ATGGCCGCCA GTGTTACAGC 1080
TGCAAGGGGA ACAGCACCCA TGGATGCTCC TCTGAAGAGA CTTTCCTCAT TGACTGCCGA 1140
GGCCCCATGA ATCAATGTCT GGTAGCCACC GGCACTCACG AACCGAAAAA CCAAAGCTAT 1200
ATGGTAAGAG GCTGTGCAAC CGCCTCAATG TGCCAACATG CCCACCTGGG TGACGCCTTC 1260
AGCATGAACC ACATTGATGT CTCCTGCTGT ACTAAAAGTG GCTGTAACCA CCCAGACCTG 1320
GATGTCCAGT ACCGCAGTGG GGCTGCTCCT CAGCCTGGCC CTGCCCATCT CAGCCTCACC 1380
ATCACCCTGC TAATGACTGC CAGACTGTGG GGAGGCACTC TCCTCTGGAC CTAAACCTGA 1440
AATCCCCCTC TCTGCCCTGG CTGGATCCGG GGGACCCCTT TGCCCTTCCC TCGGCTCCCA 1500
GCCCTACAGA CTTGCTGTGT GACCTCAGGC CAGTGTGCCG ACCTCTCTGG GCCTCAGTTT 1560
TCCCAGCTAT GAAAACAGCT ATCTCACAAA GTTGTGTGAA GCAGAAGAGA AAAGCTGGAG 1620
GAAGGCCGTG GGCAATGGGA GAGCTCTTGT TATTATTAAT ATTGTTGCCG CTGTTGTGTT 1680
GTTGTTATTA ATTAATATTC ATATTATTTA TTTTATACTT ACATAAAGAT TTTGTACCAG 1740
TGG                                                               1743
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Seq ID NO: C165 DNA Sequence
Nucleic Acid Accession #: AK027843.1
Coding sequence: 193..1731

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CTAAATAGCA CATCACATGT GAATATTACA ACTCGGAACT TGGCTCTCAG CGTATCATCC  120
CTGTTACCAG GGACAAATGC AATTTCAAAT TTTAGCATTG GTCTTCCAAG CAATAATGAA  180
TCGTATTTCC AGATGGATTT TGAGAGTGGA CAAGTGGATC CACTGGCATC TGTAATTTTG  240
CCTCCAAACT TACTTGAGAA TTTAAGTCCA GAAGATTCTG TATTAGTTAG AAGAGCACAG  300
TTTACTTTCT TCAACAAAAC TGGACTTTTC CAGGATGTAG GACCCCAAAG AAAAACTTTA  360
GTGAGTTATG TGATGGCGTG CAGTATTGGA AACATTACTA TCCAGAATCT GAAGGATCCT  420
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GTTCAAATAA AAATCAAACA TACAAGAACT CAGGAAGTGC ATCATCCCAT CTGTGCCTTC   480
TGGGATCTGA ACAAAAACAA AAGTTTTGGA GGATGGAACA CGTCAGGATG TGTTGCACAC   540
AGAGATTCAG ATGCAAGTGA GACAGTCTGC CTGTGTAACC ACTTCACACA CTTTGGAGTT   600
CTGATGGACC TTCCAAGAAG TGCCTCACAG TTAGATGCAA GAAACACTAA AGTCCTCACT   660
TTCATCAGCT ATATTGGGTG TGGAATATCT GCTATTTTTT CAGCAGCAAC TCTCCTGACA   720
TATGTTGCTT TTGAGAAATT GCGAAGGGAT TATCCCTCCA AAATCTTGAT GAACCTGAGC   780
ACAGCCCTGC TGTTCCTGAA TCTCCTCTTC CTCCTAGATG GCTGGATCAC CTCCTTCAAT   840
GTGGATGGAC TTTGCATTGC TGTTGCAGTC CTGTTGCATT TCTTCCTTCT GGCAACCTTT   900
ACCTGGATGG GGCTAGAAGC AATTCACATG TACATTGCTC TAGTTAAAGT ATTTAACACT   960
TACATTCGCC GATACATTCT AAAATTCTGC ATCATTGGCT GGGGTTTGCC TGCCTTAGTG  1020
GTGTCAGTTG TTCTAGCGAG CAGAAACAAC AATGAAGTCT ATGGAAAAGA AAGTTATGGG  1080
AAAGAAAAAG GTGATGAATT CTGTTGGATT CAAGATCCAG TCATATTTTA TGTGACCTGT  1140
GCTGGGTATT TTGGAGTCAT GTTTTTTCTG AACATTGCCA TGTTCATTGT GGTAATGGTG  1200
CAGATCTGTG GGAGGAATGG CAAGAGAAGC AACCGGACCC TGAGAGAAGA AGTGTTAAGG  1260
AACCTGCGCA GTGTGGTTAG CTTGACCTTT CTGTTGGGCA TGACATGGGG TTTTGCATTC  1320
TTTGCCTGGG GACCCTTAAA TATCCCCTTC ATGTACCTCT TCTCCATCTT CAATTCATTA  1380
CAAGGCTTAT TTATATTCAT CTTCCACTGT GCTATGAAGG AGAATGTTCA GAAACAGTGG  1440
CGGCGGCATC TCTGCTGTGG TAGATTTCGG TTAGCAGATA ACTCAGATTG GAGTAAGACA  1500
GCTACCAATA TCATCAAGAA AAGTTCTGAT AATCTAGGAA AATCTTTGTC TTCAAGCTCC  1560
ATTGGTTCCA ACTCAACCTA TCTTACATCC AAATCTAAAT CCAGCTCTAC CACCTATTTC  1620
AAAAGGAATA GCCACACAGA TAATGTCTCC TATGAGCATT CCTTCAACAA AAGTGGATCA  1680
CTCAGACAGT GCTTCCATGG ACAAGTCCTT GTCAAAACTG GCCCATGCTG ATGGAGATCA  1740
AACATCAATC ATCCCTGTCC ATCAGGTCAT TGATAAGGTC AAGGGTTATT GCAATGCTCA  1800
TTCAGACAAC TTCTATAAAA ATATTATCAT GTCAGACACC TTCAGCCACA GCACAAAGTT  1860
TTAATGTCTT TAAGAAAAAG AAATCAATCT GCAGAAATGT GAAGATTTGC AAGCAGTGTA  1920
AACTGCAACT AGTGATGTAA ATGTGCTATT ACCTAGGTAA CTGCATATAT ATAAGGAATG  1980
TATTTTGTTA AGAAGGCTTT TGTGAAATTC AGAATTTTTC TTTTTAATAT ATTTCTTCCA  2040
TGGAAGAGTT GTCATCACTA AAACTTCAGT ACTGAGAGTA ACATGACTCA GTAGCCACAG  2100
AAGCTATGAT TTGTAAAATA TATAATTGAA TCAGAGTAAT CATAATGCAG GGGAGACATT  2160
CAAATTAGAG ACAAGGGAGA AGCAATGCTG AGGAAGACCC TAGATAGAGC TCATTTTACT  2220
CCACCTAATC GTTATATCTG GATATACCCA TTTTCTGCAT CTTCTTTCTC AACAATAAAC  2280
TGTCCTTGCT TTGGAGACTT TAAGACATTT CCTAAAGCAC AAATAAAAGC CTCGTATTTC  2340
CCCATTGAGA GTTTTGTTCC AAGGAATATG AAGTGAGACA TATGGGTGAG TCATAATAAT  2400
CAAAATAATT TATGAAGAGC TGGGTCTGCA ATAGCTAGTC TAAAAACTAC TTGTGTGTCA  2460
GTCCTCTGGT TATAGTATAT AAGAGCCTGA GGAGGTCTGG CAAGATAGAT GGTGTATTAT  2520
TTATGGATCA GGCTGCTGCA TACAAACCTT GCATACTATT ATGCAGCTTA CCTAACTCTC  2580
AGACTATTCT GAGTAATGCT TGCTTGCTAA TGAATGTATA GGAGACCACA TTGTAATTGT  2640
TCTTAGATGA TGGAGTCCAT GCAGTTTCTT AGAAATCGGT CTCAGTGCAT GCTGTGCTTT  2700
TTCACATTTG CTCTGGGTTA TCTGGGAAGT ATCAGGTTCT GGGAGGCAAC AGCATTAAGT  2760
GATAAGAAAA GGAGACATTC TGGCAAAGCC AATCTGCTTA AAGGCAAAGT CCAGAACCTG  2820
GAACCTAGAG GCCTTTCTCT CTGCACGAAA AACAGGTAGT TTGCAGTCTG AGATATGGGA  2880
GAGCTTTTAG GCTACACAGC AACCCAAGGG ACCTCTCACC TTTTGCTGAG CTTCAATCAG  2940
GAAGCTATTT GCCTGGCTCC AGCAGATGAT GAGATAATGA GGTAGTGGGT TTTTTATTAC  3000
TGTTCCATTT TGCAACATCC TGCAACACCA TCCTGGGAGA CAAGAGCATT ACCCAGCTTG  3060
GCTTTCACGG GGGAGGGTTG TATTCAGT                                     3088
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Seq ID NO: C166 DNA Sequence
Nucleic Acid Accession #: NM_000574.1
Coding sequence: 66..1211

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CCCGGCTGCT GCTGCTGGTG CTGTTGTGCC TGCCGGCCGT GTGGGGTGAC TGTGGCCTTC  180
CCCCAGATGT ACCTAATGCC CAGCCAGCTT TGGAAGGCCG TACAAGTTTT CCCGAGGATA  240
CTGTAATAAC GTACAAATGT GAAGAAAGCT TTGTGAAAAT TCCTGGCGAG AAGGACTCAG  300
TGATCTGCCT TAAGGGCAGT CAATGGTCAG ATATTGAAGA GTTCTGCAAT CGTAGCTGCG  360
AGGTGCCAAC AAGGCTAAAT TCTGCATCCC TCAAACAGCC TTATATCACT CAGAATTATT  420
TTCCAGTCGG TACTGTTGTG GAATATGAGT GCCGTCCAGG TTACAGAAGA GAACCTTCTC  480
TATCACCAAA ACTAACTTGC CTTCAGAATT TAAAATGGTC CACAGCAGTC GAATTTTGTA  540
AAAAGAAATC ATGCCCTAAT CCGGGAGAAA TACGAAATGG TCAGATTGAT GTACCAGGTG  600
GCATATTATT TGGTGCAACC ATCTCCTTCT CATGTAACAC AGGGTACAAA TTATTTGGCT  660
CGACTTCTAG TTTTTGTCTT ATTTCAGGCA GCTCTGTCCA GTGGAGTGAC CCGTTGCCAG  720
AGTGCAGAGA AATTTATTGT CCAGCACCAC CACAAATTGA CAATGGAATA ATTCAAGGGG  780
AACGTGACCA TTATGGATAT AGACAGTCTG TAACGTATGC ATGTAATAAA GGATTCACCA  840
TGATTGGAGA GCACTCTATT TATTGTACTG TGAATAATGA TGAAGGAGAG TGGAGTGGCC  900
CACCACCTGA ATGCAGAGGA AAATCTCTAA CTTCCAAGGT CCCACCAACA GTTCAGAAAC  960
CTACCACAGT AAATGTTCCA ACTACAGAAG TCTCACCAAC TTCTCAGAAA ACCACCACAA 1020
AAACCACCAC ACCAAATGCT CAAGCAACAC GGAGTACACC TGTTTCCAGG ACAACCAAGC 1080
ATTTTCATGA AACAACCCCA AATAAAGGAA GTGGAACCAC TTCAGGTACT ACCCGTCTTC 1140
TATCTGGGCA CACGTGTTTC ACGTTGACAG GTTTGCTTGG GACGCTAGTA ACCATGGGCT 1200
TGCTGACTTA GCCAAAGAAG AGTTAAGAAG AAAATACACA CAAGTATACA GACTGTTCCT 1260
AGTTTCTTAG ACTTATCTGC ATATTGGATA AAATAAATGC AATTGTGCTC TTCATTTAGG 1320
ATGCTTTCAT TGTCTTTAAG ATGTGTTAGG AATGTCAACA GAGCAAGGAG AAAAAAGGCA 1380
GTCCTGGAAT CACATTCTTA GCACACCTAC ACCTCTTGAA AATAGAACAA CTTGCAGAAT 1440
TGAGAGTGAT TCCTTTCCTA AAAGTGTAAG AAAGCATAGA GATTTGTTCG TATTTAGAAT 1500
GGGATCACGA GGAAAAGAGA AGGAAAGTGA TTTTTTTCCA CAAGATCTGT AATGTTATTT 1560
CCACTTATAA AGGAAATAAA AAATGAAAAA CATTATTTGG ATATCAAAAG CAAATAAAAA 1620
CCCAATTCAG TCTCTTCTAA GCAAAATTGC TAAAGAGAGA TGAACCACAT TATAAAGTAA 1680
TCTTTGGCTG TAAGGCATTT TCATCTTTCC TTCGGGTTGG CAAAATATTT TAAAGGTAAA 1740
ACATGCTGGT GAACCAGGGG TGTTGATGGT GATAAGGGAG GAATATAGAA TGAAAGACTG 1800
AATCTTCCTT TGTTGCACAA ATAGAGTTTG GAAAAAGCCT GTGAAAGGTG TCTTCTTTGA 1860
CTTAATGTCT TTAAAAGTAT CCAGAGATAC TACAATATTA ACATAAGAAA AGATTATATA 1920
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TTATTTCTGA ATCGAGATGT CCATAGTCAA ATTTGTAAAT CTTATTCTTT TGTAATATTT   1980
ATTTATATTT ATTTATGACA GTGAACATTC TGATTTTACA TGTAAAACAA GAAAAGTTGA   2040
AGAAGATATG TGAAGAAAAA TGTATTTTTC CTAAATAGAA ATAAATGATC CCATTTTTTG   2100
GT                                                                  2102
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Seq ID NO: C167 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence:1..2651

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GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT GCCCCACACA CTGTCATTGC   120
GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTCGGAGCTG   180
CCTTCCAACC TCAGCGTCTT CACCTCCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG   240
CTGCTCCCGA ATCCCCTGCC CAGTCTCCGC TTCCTGGAGG AGTTACGTCT TGCGGGAAAC   300
GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCTTATG   360
CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC TGCAGAATTT GCGAAGCCTT   420
CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC CCCCAAGCTG TTTCAGTGGC   480
CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT TAACAGAAAT CCCCGTCCAG   540
GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCCTGAACAA AATACACCAC   600
ATACCAGACT ATGCCTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAAT   660
AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT   720
TTAAATTACA ATAACCTTGA TGAATTCCCC ACTGCAATTA GGACACTCTC CAACCTTAAA   780
GAACTACATT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA   840
CCTGAACTAA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAATT TCCTGATTTA   900
ACTGGAACTG CAAACCTGGA GACTCTGACT TTAACTGGAG CACAGATCTC ATCTCTTCCT   960
CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA   1020
GAAGATTTAC CCAGTTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT   1080
GAAATCTACG AAATTAAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGCTGAAT   1140
TTGGCTTGGA ACAAAATTGC TATTATTCAC CCCAATGCAT TTTCCACTTT GCCATCCCTA   1200
ATAAAGCTGG ACCTATCGTC CAACCTCCTG TCGTCTTTTC CTATAACTGG GTTACATGGT   1260
TTAACTCACT TAAAATTAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC   1320
TTTCCAGAAC TCAAGGTTAT AGAAATGCCT TATGCTTACC AGTGCTGTGC ATTTGGAGTG   1380
TGTGAGAATG CCTATAAGAT TTCTAATCAA TGGAATAAAG GTGACAACAG CAGTATGGAC   1440
GACCTTCATA AGAAAGATGC TGGAATGTTT CAGGCTCAAG ATGAACGTGA CCTTGAAGAT   1500
TTCCTGCTTG ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC   1560
CCAGGCCCCT TCAAACCCTG TGAACACCTG CTTGATGGCT GGCTGATCAG AATTGGAGTG   1620
TGGACCATAG CAGTTCTGGC ACTTACTTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA   1680
TCCCCTCTGT ACATTTCCCC CATTAAACTG TTAATTGGGG TCATCGCAGC AGTGAACATG   1740
CTCACGGGAG TCTCCAGTGC CGTGCTGGCT GGTGTGGATG CGTTCACTTT TGGCAGCTTT   1800
GCACGACATG GTGCCTGGTG GGAGAATGGG GTTGGTTGCC ATGTCATTGG TTTTTTGTCC   1860
ATTTTTGCTT CAGAATCATC TGTTTTCCTG CTTACTCTGG CAGCCCTGGA GCGTGGGTTC   1920
TCTGTGAAAT ATTCTGCAAA ATTTGAAACG AAAGCTCCAT TTTCTAGCCT GAAAGTAATC   1980
ATTTTGCTCT GTGCCCTGCT GGCCTTGACC ATGGCCGCAG TTCCCCTGCT GGGTGGCAGC   2040
AAGTATGGCG CCTCCCCTCT CTGCCTGCCT TTGCCTTTTG GGGAGCCCAG CACCATGGGC   2100
TACATGGTCG CTCTCATCTT GCTCAATTCC CTTTGCTTCC TCATGATGAC CATTGCCTAC   2160
ACCAAGCTCT ACTGCAATTT GGACAAGGGA GACCTGGAGA ATATTTGGGA CTGCTCTATG   2220
GTAAAACACA TTGCCCTGTT GCTCTTCACC AACTGCATCC TAAACTGCCC TGTGGCTTTC   2280
TTGTCCTTCT CCTCTTTAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC   2340
CTTCTGGTGG TAGTCCCACT TCCTGCATGT CTCAATCCCC TTCTCTACAT CTTGTTCAAT   2400
CCTCACTTTA AGGAGGATCT GGTGAGCCTG AGAAAGCAAA CCTACGTCTG GACAAGATCA   2460
AAACACCCAA GCTTGATGTC AATTAACTCT GATGATGTCG AAAAACAGTC CTGTGACTCA   2520
ACTCAAGCCT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCCAGTTCC   2580
GTGCCATCAC CAGCTTATCC AGTGACTGAG AGCTGCCATC TTTCCTCTGT GGCATTTGTC   2640
CCATGTCTTA A                                                        2651
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Seq ID NO: C168 DNA Sequence
Nucleic Acid Accession #: NM_003667.2
Coding sequence: 49..2772

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CGGCTCGGTG TGCTCCTGTC CTTGCCTGTG CTGCTGCAGC TGGCGACCGG GGGCAGCTCT   120
CCCAGGTCTG GTGTGTTGCT GAGGGGCTGC CCCACACACT GTCATTGCGA GCCCGACGGC   180
AGGATGTTGC TCAGGGTGGA CTGCTCCGAC CTGGGGCTCT CGGAGCTGCC TTCCAACCTC   240
AGCGTCTTCA CCTCCTACCT AGACCTCAGT ATGAACAACA TCAGTCAGCT GCTCCCGAAT   300
CCCCTGCCCA GTCTCCGCTT CCTGGAGGAG TTACGTCTTG CGGGAAACGC TCTGACATAC   360
ATTCCCAAGG GAGCATTCAC TGGCCTTTAC AGTCTTAAAG TTCTTATGCT GCAGAATAAT   420
CAGCTAAGAC ACGTACCCAC AGAAGCTCTG CAGAATTTGC GAAGCCTTCA ATCCCTGCGT   480
CTGGATGCTA ACCACATCAG CTATGTGCCC CCAAGCTGTT TCAGTGGCCT GCATTCCCTG   540
AGGCACCTGT GGCTGGATGA CAATGCGTTA ACAGAAATCC CCGTCCAGGC TTTTAGAAGT   600
TTATCGGCAT TGCAAGCCAT GACCTTGGCC CTGAACAAAA TACACCACAT ACCAGACTAT   660
GCCTTTGGAA ACCTCTCCAG CTTGGTAGTT CTACATCTCC ATAACAATAG AATCCACTCC   720
CTGGGAAAGA AATGCTTTGA TGGGCTCCAC AGCCTAGAGA CTTTAGATTT AAATTACAAT   780
AACCTTGATG AATTCCCCAC TGCAATTAGG ACACTCTCCA ACCTTAAAGA ACTAGGATTT   840
CATAGCAACA ATATCAGGTC GATACCTGAG AAAGCATTTG TAGGCAACCC TTCTCTTATT   900
ACAATACATT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA   960
CCTGAACTAA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAATT TCCTGATTTA   1020
ACTGGAACTG CAAACCTGGA GAGTCTGACT TTAACTGGAG CACAGATCTC ATCTCTTCCT   1080
CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA   1140
GAAGATTTAC CCAGTTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT   1200
GAAATCTACG AAATTAAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGCTGAAT   1260
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TTGGCTTGGA ACAAAATTGC TATTATTCAC CCCAATGCAT TTTCCACTTT GCCATCCCTA   1320
ATAAAGCTGG ACCTATCGTC CAACCTCCTG TCGTCTTTTC CTATAACTGG GTTACATGGT   1380
TTAACTCACT TAAAATTAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC   1440
TTTCCAGAAC TCAAGGTTAT AGAAATGCCT TATGCTTACC AGTGCTGTGC ATTTGGAGTG   1500
TGTGAGAATG CCTATAAGAT TTCTAATCAA TGGAATAAAG GTGACAACAG CAGTATGGAC   1560
GACCTTCATA AGAAAGATGC TGGAATGTTT CAGGCTCAAG ATGAACGTGA CCTTGAAGAT   1620
TTCCTGCTTG ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC   1680
CCAGGCCCCT TCAAACCCTG TGAACACCTG CTTGATGGCT GGCTGATCAG AATTGGAGTG   1740
TGGACCATAG CAGTTCTGGC ACTTACTTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA   1800
TCCCCTCTGT ACATTTCCCC CATTAAACTG TTAATTGGGG TCATCGCAGC AGTGAACATG   1860
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GCACGACATG GTGCCTGGTG GGAGAATGGG GTTGGTTGCC ATGTCATTGG TTTTTGTCCC   1980
ATTTTTGCTT CAGAATCATC TGTTTTCCTG CTTACTCTGG CAGCCCTGGA GCGTGGGTTC   2040
TCTGTGAAAT ATTCTGCAAA ATTTGAAACG AAAGCTCCAT TTTCTAGCCT GAAAGTAATC   2100
ATTTTGCTCT GTGCCCTGCT GGCCTTGACC ATGGCCGCAG TTCCCCTGCT GGGTGGCAGC   2160
AAGTATGGCG CCTCCCCTCT CTGCCTGCCT TTGCCTTTTG GGGAGCCCAG CACCATGGGC   2220
TACATGGTCG CTCTCATCTT GCTCAATTCC CTTTGCTTCC TCATGATGAC CATTGCCTAC   2280
ACCAAGCTCT ACTGCAATTT GGACAAGGGA GACCTGGAGA ATATTTGGGA CTGCTCTATG   2340
GTAAAACACA TTGCCCTGTT GCTCTTCACC AACTGCATCC TAAACTGCCC TGTGGCTTTC   2400
TTGTCCTTCT CCTCTTTAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC   2460
CTTCTGGTGG TAGTCCCACT TCCTGCATGT CTCAATCCCC TTCTCTACAT CTTGTTCAAT   2520
CCTCACTTTA AGGAGGATCT GGTGAGCCTG AGAAAGCAAA CCTACGTCTG GACAAGATCA   2580
AAACACCCAA GCTTGATGTC AATTAACTCT GATGATGTCG AAAAACAGTC CTGTGACTCA   2640
ACTCAAGCCT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCCAGTTCC   2700
GTGCCATCAC CAGCTTATCC AGTGACTGAG AGCTGCCATC TTTCCTCTGT GGCATTTGTC   2760
CCATGTCTCT AATTAATATG TGAAGGAAAA TGTTTTCAAA GGTTGAGAAC CTGAAAATGT   2820
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Seq ID NO: C169 DNA Sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

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TTAGACGGGG ACGGGAAGGG ACAGCGGCCT TCGACCGCCC CCCGAGTAAT TGACCCAGGA   120
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ATCTTTGGAT GGGGATCTTC TGAGGATGCA AAGAGTGATT CATCCAAGCC ATGTGGTAAA   240
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Seq ID NO: C170 DNA Sequence
Nucleic Acid Accession #: NM_000582
Coding sequence: 88...990

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Seq ID NO: C171 DNA Sequence
Nucleic Acid Accession #: NM_002821
Coding sequence: 150..3362

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Seq ID NO: C172 DNA Sequence
Nucleic Acid Accession #: NM_002309.2
Coding sequence: 65..673

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Seq ID NO: C173 DNA Sequence
Nucleic Acid Accession #: XM_097508
Coding sequence: 44..2788

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Seq ID NO: C174 DNA Sequence
Nucleic Acid Accession #: NM_130849

Coding sequence: 101..2044

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Seq ID NO: C175 DNA Sequence
Nucleic Acid Accession #: NM_018971
Coding sequence: 1..1128

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Seq ID NO: C176 DNA Sequence
Nucleic Acid Accession #: NM_005631
Coding sequence: 290..2653

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Seq ID NO: C177 DNA Sequence
Nucleic Acid Accession #: AK094595
Coding sequence: 1..2853

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Seq ID NO: C178 DNA Sequence
Nucleic Acid Accession #: NM_004625
Coding sequence: 310..1359

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TACGCCCGCG TGTGGCAGTG CAACTGTAAG TTCCACTGGT GCTGCTATGT CAAGTGCAAC   1320
ACGTGCAGCG AGCGCACGGA GATGTACACG TGCAAGTGAG CCCCGTGTGC ACACCACCCT   1380
CCCGCTGCAA GTCAGATTGC TGGGAGGACT GGACCGTTTC CAAGCTGCGG GCTCCCTGGC   1440
AGGATGCTGA GCTTGTCTTT TCTGCTGAGG AGGGTACTTT TCCTGGGTTT CCTGCAGGCA   1500
TCCGTGGGGG AAAAAAAATC TCTCAGAGCC CTCAACTATT CTGTTCCACA CCCAATGCTG   1560
CTCCACCCTC CCCCAGACAC AGCCCAGGTC CCTCCGCGGC TGGAGCGAAG CCTTCTGCAG   1620
CAGGAACTCT GGACCCCTGG GCCTCATCAC AGCAATATTT AACAATTTAT TCTGATAAAA   1680
ATAATATTAA TTTATTTAAT TAAAAAGAAT TCTTCCACAA AAAAAAAAAA AAAAAA       1736
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Seq ID NO: C179 DNA Sequence OBR3
Nucleic Acid Accession #: NM_003786
Coding sequence: 71..4654

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CCTCGGCCCC ATGGACGCCC TGTGCGGTTC CGGGGAGCTC GGCTCCAAGT TCTGGGACTC   120
CAACCTGTCT GTGCACACAG AAAACCCGGA CCTCACTCCC TGCTTCCAGA ACTCCCTGCT   180
GGCCTGGGTG CCCTGCATCT ACCTGTGGGT CGCCCTGCCC TGCTACTTGC TCTACCTGCG   240
GCACCATTGT CGTGGCTACA TCATCCTCTC CCACCTGTCC AAGCTCAAGA TGGTCCTGGG   300
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WO03042661 [file:///E:/WO03042661.pcp] Page 1313 of 1385


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TGTCCTGCTG TGGTGCGTCT CCTGGGCGGA CCTTTTTTAC TCCTTCCATG GCCTGGTCCA   360
TGGCCGGGCC CCTGCCCCTG TTTTCTTTGT CACCCCCTTG GTGGTGGGGG TCACCATGCT   420
GCTGGCCACC CTGCTGATAC AGTATGAGCG GCTGCAGGGC GTACAGTCTT CGGGGGTCCT   480
CATTATCTTC TGGTTCCTGT GTGTGGTCTG CGCCATCGTC CCATTCCGCT CCAAGATCCT   540
TTTAGCCAAG GCAGAGGGTG AGATCTCAGA CCCCTTCCGC TTCACCACCT TCTACATCCA   600
CTTTGCCCTG GTACTCTCTG CCCTCATCTT GGCCTGCTTC AGGGAGAAAC CTCCATTTTT   660
CTCCGCAAAG AATGTCGACC CTAACCCCTA CCCTGAGACC AGCGCTGGCT TTCTCTCCCG   720
CCTGTTTTTC TGGTGGTTCA CAAAGATGGC CATCTATGGC TACCGGCATC CCCTGGAGGA   780
GAAGGACCTC TGGTCCCTAA AGGAAGAGGA CAGATCCCAG ATGGTGGTGC AGCAGCTGCT   840
GGAGGCATGG AGGAAGCAGG AAAAGCAGAC GGCACGACAC AAGGCTTCAG CAGCACCTGG   900
GAAAAATGCC TCCGGCGAGG ACGAGGTGCT GCTGGGTGCC CGGCCCAGGC CCCGGAAGCC   960
CTCCTTCCTG AAGGCCCTGC TGGCCACCTT CGGCTCCAGC TTCCTCATCA GTGCCTGCTT  1020
CAAGCTTATC CAGGACCTGC TCTCCTTCAT CAATCCACAG CTGCTCAGCA TCCTGATCAG  1080
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CCTGTGCTCC ATGATGCAGT CGCTGATCTT ACAACACTAT TACCACTACA TCTTTGTGAC  1200
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CATCCTGGCG ATCTACTTCC TCTGGCAGAA CCTAGGTCCC TCTGTCCTGG CTGGAGTCGC  1440
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CATCAAGGTG CTGAAGCTGT ACGCCTGGGA GCCCAGCTTC CTGAAGCAGG TGGAGGGCAT  1620
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CACCTGGATG TGCAGCCCCT TCCTGGTGAC CCTGATCACC CTCTGGGTGT ACGTGTACGT  1740
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GTCTCTGAAA CGGATCCAGC AATTCCTGAG CCAAGAGGAA CTTGACCCCC AGAGTGTGGA  1920
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GATGGAGAAG CTAGAAGGCA AAGTGCACAT GAAGGGCTCC GTGGCCTATG TGCCCCAGCA  2160
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CCTGCTGCAG CGCAACGGCT CCTTTGCCAA CTTTCTCTGC AACTATGCCC CCGATGAGGA  2640
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TGTGTTCTGG GATTATGCCA AGGCCGTGGG GCTCTGTACC ACGCTGGCCA TCTGTCTCCT  3000
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GCGGCTGGAA TCAGTCAGCC GCTCACCTAT CTACTCCCAC TTTTCGGAGA CAGTGACTGG  3540
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GAGGAGCAGC CTGAACCCGG GGCTGGTGGG CCTTTCTGTG TCCTACTCCT TGCAGGTGAC  3780
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CCGCCCTCCC GAAGGTTGGC CCCCACGTGG GGAGGTGGAG TTCCGGAATT ATTCTGTGCG  3960
CTACCGGCCG GGCCTAGACC TGGTGCTGAG AGACCTGAGT CTGCATGTGC ACGGTGGCGA  4020
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CCGCATCCTG GAGGCGGCAA AGGGTGAAAT CCGCATTGAT GGCCTCAATG TGGCAGACAT  4140
CGGCCTCCAT GACCTGCGCT CTCAGCTGAC CATCATCCCG CAGGACCCCA TCCTGTTCTC  4200
GGGGACCCTG CGCATGAACC TGGACCCCTT CGGCAGCTAC TCAGAGGAGG ACATTTGGTG  4260
GGCTTTGGAG CTGTCCCACC TGCACACGTT TGTGAGCTCC CAGCCGGCAG GCCTGGACTT  4320
CCAGTGCTCA GAGGGCGGGG AGAATCTCAG CGTGGGCCAG AGGCAGCTCG TGTGCCTGGC  4380
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CCTGGAGACT GACAACCTCA TCCAGGCTAC CATCCGCACC CAGTTTGATA CCTGCACTGT  4500
CCTGACCATC GCACACCGGC TTAACACTAT CATGGACTAC ACCAGGGTCC TGGTCCTGGA  4560
CAAAGGAGTA GTAGCTGAAT TTGATTCTCC AGCCAACCTC ATTGCAGCTA GAGGCATCTT  4620
CTACGGGATG GCCAGAGATG CTGGACTTGC CTAAAATATA TTCCTGAGAT TTCCTCCTGG  4680
CCTTTCCTGG TTTTCATCAG GAAGGAAATG ACACCAAATA TGTCCGCAGA ATGGACTTGA  4740
TAGCAAACAC TGGGGGCACC TTAAGATTTT GCACCTGTAA AGTGCCTTAC AGGGTAACTG  4800
TGCTGAATGC TTTAGATGAG GAAATGATCC CCAAGTGGTG AATGACACGC CTAAGGTCAC  4860
AGCTAGTTTG AGCCAGTTAG ACTAGTCCCC CGGTCTCCCG ATTCCCAACT GAGTGTTATT  4920
TGCACACTGC ACTGTTTTCA AATAACGATT TTATGAAATG ACCTCTGTCC TCCCTCTGAT  4980
TTTTCATATT TTCCTAAAGT TTCGTTTCTG TTTTTTAATA AAAAGCTTTT TCCTCCTGGA  5040
ACAGAAGACA GCTGCTGGGT CAGGCCACCC CTAGGAACTC AGTCCTGTAC TCTGGGGTGC  5100
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Seq ID NO: C180 DNA Sequence

Nucleic Acid Accession #: NM_004626
Coding sequence: 124..1188

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GGCGTGTGCT ATGGCATCAA GTGGCTGGCG CTGTCCAAGA CACCATCGGC CCTGGCACTG  240
AACCAGACGC AACACTGCAA GCAGCTGGAG GGTCTGGTGT CTGCACAGGT GCAGCTGTGC  300
CGCAGCAACC TGGAGCTCAT GCACACGGTG GTGCACGCCG CCCGCGAGGT CATGAAGGCC  360
TGTCGCCGGG CCTTTGCCGA CATGCGCTGG AACTGCTCCT CCATTGAGCT CGCCCCCAAC  420
TATTTGCTTG ACCTGGAGAG AGGGACCCGG GAGTCGGCCT TCGTGTATGC GCTGTCGGCC  480
GCCGCCATCA GCCACGCCAT CGCCCGGGCC TGCACCTCCG GCGACCTGCC CGGCTGCTCC  540
TGCGGCCCCG TCCCAGGTGA GCCACCCGGG CCCGGGAACC GCTGGGGAGG ATGTGCGGAC  600
AACCTCAGCT ACGGGCTCCT CATGGGGGCC AAGTTTTCCG ATGCTCCTAT GAAGGTGAAA  660
AAAACAGGAT CCCAAGCCAA TAAACTGATG CGTCTACACA ACAGTGAAGT GGGGAGACAG  720
GCTCTGCGCG CCTCTCTGGA AATGAAGTGT AAGTGCCATG GGGTGTCTGG CTCCTGCTCC  780
ATCCGCACCT GCTGGAAGGG GCTGCAGGAG CTGCAGGATG TGGCTGCTGA CCTCAAGACC  840
CGATACCTGT CGGCCACCAA GGTAGTGCAC CGACCCATGG GCACCCGCAA GCACCTGGTG  900
CCCAAGGACC TGGATATCCG GCCTGTGAAG GACTCGGAAC TCGTCTATCT GCAGAGCTCA  960
CCTGACTTCT GCATGAAGAA TGAGAAGGTG GGCTCCCACG GGACACAAGA CAGGCAGTGC 1020
AACAAGACAT CCAACGGAAG CGACAGCTGC GACCTTATGT GCTGCGGGCG TGGCTACAAC 1080
CCCTACACAG ACCGCGTGGT CGAGCGGTGC CACTGTAAGT ACCACTGGTG CTGCTACGTC 1140
ACCTGCCGCA GGTGTGAGCG TACCGTGGAG CGCTATGTCT GCAAGTGAGG CCCTGCCCTC 1200
CGCCCCACGC AGGAGCGAGG ACTCTGCTCA AGGACCCTCA GCAACTGGGG CCAGGGGCCT 1260
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TGCTTTGCCT TCACTTGGAA GCCACCAGGA ACAGAAGGTC TGGCCACCCT GGAAGGAGGG 1380
CAGGACATCA AAGGAAACCG ACAAGATTAA AAATAACTTG GCAGCCTGAG GCTCTGGAGT 1440
GCCCACAGGC TGGTGTAAGG AGCGGGGCTT GGGATCGGTG AGACTGATAC AGACTTGACC 1500
TTTCAGGGCC ACAGAGACCA GCCTCCGGGA AGGGGTCTGC CCGCCTTCTT CAGAATGTTC 1560
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TAGCTTGGGT TGTAAATGTT TTCTTTTGTT TTTTGCTTTT TCTTCCTTTG GGATGTGGAA 1680
GCTACAGAAA TATTTATAAA ACATAGCTTT TTCTTTGGGG TGGCACTTCT CAATTCCTCT 1740
TTATATATTT TATATATATA AATATATATG TATATATATA ATGATCTCTA TTTTAAAACT 1800
AGCTTTTTAA GCAGCTGTAT GAAATAAATG CTGAGTGAGC CCCAGCCCGC CCCTGCAGTT 1860
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Seq ID NO: C181 DNA Sequence
Nucleic Acid Accession #: NM_031866
Coding sequence: 6..2090

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ACGACACGCA AGACGAGGCG GGCCTGGAGG TGCACCAGTT CTGGCCGCTG GTGGAGATCC  240
AGTGCTCGCC CGATCTCAAG TTCTTCCTGT GCAGCATGTA CACGCCCATC TGCCTAGAGG  300
ACTACAAGAA GCCGCTGCCG CCCTGCCGCT CGGTGTGCGA GCGCGCCAAG GCCGGCTGCG  360
CGCCGCTCAT GCGCCAGTAC GGCTTCGCCT GGCCCGACCG CATGCGCTGC GACCGGCTGC  420
CCGAGCAAGG CAACCCTGAC ACGCTGTGCA TGGACTACAA CCGCACCGAC CTAACCACCG  480
CCGCGCCCAG CCCGCCGCGC CGCCTGCCGC CGCCGCCGCC CGGCGAGCAG CCGCCTTCGG  540
GCAGCGGCCA CGGCCGCCCG CCGGGGGCCA GGCCCCCGCA CCGCGGAGGC GGCAGGGGCG  600
GTGGCGGCGG GGACGCGGCG GCGCCCCCAG CTCGCGGCGG CGGCGGTGGC GGGAAGGCGC  660
GGCCCCCTGG CGGCGGCGCG GCTCCCTGCG AGCCCGGGTG CCAGTGCCGC GCGCCTATGG  720
TGAGCGTGTC CAGCGAGCGC CACCCGCTCT ACAACCGCGT CAAGACAGGC CAGATCGCTA  780
ACTGCGCGCT GCCCTGCCAC AACCCCTTTT TCAGCCAGGA CGAGCGCGCC TTCACCGTCT  840
TCTGGATCGG CCTGTGGTCG GTGCTCTGCT TCGTGTCCAC CTTCGCCACC GTCTCCACCT  900
TCCTTATCGA CATGGAGCGC TTCAAGTACC CGGAGCGGCC CATTATCTTC CTCTCGGCCT  960
GCTACCTCTT CGTGTCGGTG GGCTACCTAG TGCGCCTGGT GGCGGGCCAC GAGAAGGTGG 1020
CGTGCAGCGG TGGCGCGCCG GGCGCGGGGG GCGCTGGGGG CGCGGGCGGC GCGGCGGCGG 1080
GCGCGGGCGC GGCGGGCGCG GGCGCGGGCG GCCCGGGCGG GCGCGGCGAG TACGAGGAGC 1140
TGGGCGCGGT GGAGCAGCAC GTGCGCTACG AGACCACCGG CCCCGCGCTG TGCACCGTGG 1200
TCTTCTTGCT GGTCTACTTC TTCGGCATGG CCAGCTCCAT CTGGTGGGTG ATCTTGTCGC 1260
TCACATGGTT CCTGGCCGCC GGTATGAAGT GGGGCAACGA AGCCATCGCC GGCTACTCGC 1320
AGTACTTCCA CCTGGCCGCG TGGCTTGTGC CCAGCGTCAA GTCCATCGCG GTGCTGGCGC 1380
TCAGCTCGGT GGACGGCGAC CCGGTGGCGG GCATCTGCTA CGTGGGCAAC CAGAGCCTGG 1440
ACAACCTGCG CGGCTTCGTG CTGGCGCCGC TGGTCATCTA CCTCTTCATC GGCACCATGT 1500
TCCTGCTGGC CGGCTTCGTG TCCCTGTTCC GCATCCGCTC GGTCATCAAG CAACAGGACG 1560
GCCCCACCAA GACGCACAAG CTGGAGAAGC TGATGATCCG CCTGGGCCTG TTCACCGTGC 1620
TCTACACCGT GCCCGCCGCG GTGGTGGTCG CCTGCCTCTT CTACGAGCAG CACAACCGCC 1680
CGCGCTGGGA GGCCACGCAC AACTGCCCGT GCCTGCGGGA CCTGCAGCCC GACCAGGCAC 1740
GCAGGCCCGA CTACGCCGTC TTCATGCTCA AGTACTTCAT GTGCCTAGTG GTGGGCATCA 1800
CCTCGGGCGT GTGGGTCTGG TCCGGCAAGA CGCTGGAGTC CTGGCGCTCC CTGTGCACCC 1860
GCTGCTGCTG GGCCAGCAAG GGCGCCGCGG TGGGCGGGGG CGCGGGCGCC ACGGCCGCGG 1920
GGGGTGGCGG CGGGCCGGGG GGCGGCGGCG GCGGGGGACC CGGCGGCGGC GGGGGGCCGG 1980
GCGGCGGCGG GGGCTCCCTC TACAGCGACG TCAGCACTGG CCTGACGTGG CGGTCGGGCA 2040
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GGGGGCGCCC AGGAGGGGTG GGGAGGGGGG CGAGGAGACC CAAGTGCAGC GAAGGGACAC 2160
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TCTTAATGGT ATCCATTAGC TGGGACTTAA ATGACTCACT TAGAACAAAG TACCTGGCAT 2280
TGAAGCCTCC CAGACCCAGC CCCTTTTCCT CCATTGATGT GCGGGGAGCT CCTCCCGCCA 2340
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CGCGTTAATT TCTGTTGGCT GAGGAGGGTG GACTCTGCGG CGTTTCCAGA ACCCGAGATT   2400
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AAATGCCTTA AGTAAACAAA CAAGAAATGT CTTAATTATA CACCCCACGT AAATACGGGT   2640
TTCTTACATT AGAGGATGTA TTTATATAAT TATTTGTTAA ATTGTAAAAA AAAAAAGTGT   2700
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TACCCCTGTA AGAACAGATA TAAGTATTCT ATTTTGTCAA TAAAATGACT TTTGATAAAT   2820
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AGGACGCATG GGGAAAATGG ACATTTTCTG GCTTGTCATT CTGTACACTG ACCTTAGGCA   2940
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TGAACTGAAA TCAAAATTGA GTTTTTGCAC CTTCCCCAAA GACGGTGTTT TTCATGGGAG   3060
CTCTTTTCTG ATCCATGGAT AACAACTCTC ACTTTAGTGG ATGTAAATGG AACTTCTGCA   3120
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Seq ID NO: C182 DNA Sequence
Nucleic Acid Accession #: XM_050625
Coding sequence: 222..1109

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GCACCCAGCG AAGAGAGCGG GCCCGGGACA AGCTCGAACT CCGGCCGCCT CGCCCTTCCC   180
CGGCTCCGCT CCCTCTGCCC CCTCGGGGTC GCGCGCCCAC GATGCTGCAG GGCCCTGGCT   240
CGCTGCTGCT GCTCTTCCTC GCCTCGCACT GCTGCCTGGG CTCGGCGCGC GGGCTCTTCC   300
TCTTTGGCCA GCCCGACTTC TCCTACAAGC GCAGCAATTG CAAGCCCATC CCTGCCAACC   360
TGCAGCTGTG CCACGGCATC GAATACCAGA ACATGCGGCT GCCCAACCTG CTGGGCCACG   420
AGACCATGAA GGAGGTGCTG GAGCAGGCCG GCGCTTGGAT CCCGCTGGTC ATGAAGCAGT   480
GCCACCCGGA CACCAAGAAG TTCCTGTGCT CGCTCTTCGC CCCCGTCTGC CTCGATGACC   540
TAGACGAGAC CATCCAGCCA TGCCACTCGC TCTGCGTGCA GGTGAAGGAC CGCTGCGCCC   600
CGGTCATGTC CGCCTTCGGC TTCCCCTGGC CCGACATGCT TGAGTGCGAC CGTTTCCCCC   660
AGGACAACGA CCTTTGCATC CCCCTCGCTA GCAGCGACCA CCTCCTGCCA GCCACCGAGG   720
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AAACGCTTTG TAAAAATGAT TTTGCACTGA AAATAAAAGT GAAGGAGATA ACCTACATCA   840
ACCGAGATAC CAAAATCATC CTGGAGACCA AGAGCAAGAC CATTTACAAG CTGAACGGTG   900
TGTCCGAAAG GGACCTGAAG AAATCGGTGC TGTGGCTCAA AGACAGCTTG CAGTGCACCT   960
GTGAGGAGAT GAACGACATC AACGCCCCCT ATCTGGTCAT GGGACAGAAA CAGGGTGGGG   1020
AGCTGGTGAT CACCTCGGTG AAGCGGTGGC AGAAGGGGCA GAGAGAGTTC AAGCGCATCT   1080
CCCGCAGCAT CCGCAAGCTG CAGTGCTAGT CCCGGCATCC TGATGGCTCC GACAGGCCTG   1140
CTCCAGAGCA CGGCTGACCA TTTCTGCTCC GGGATCTCAG CTCCCGTTCC CCAAGCACAC   1200
TCCTAGCTGC TCCAGTCTCA GCCTGGGCAG CTTCCCCCTG CCTTTTGCAC GTTTGCATCC   1260
CCAGCATTTC CTGAGTTATA AGGCCACAGG AGTGGATAGC TGTTTTCACC TAAAGGAAAA   1320
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Seq ID NO: C183 DNA Sequence
Nucleic Acid Accession #: NM_001306.1
Coding sequence: 199..861

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CGCCAGGCCC AGCGGCCCCG GCCCCTCGTC TCCCCGCACC CGGAGCCACC CGGTGGAGCG   180
GGCCTTGCCG CGGCAGCCAT GTCCATGGGC CTGGAGATCA CGGGCACCGC GCTGGCCGTG   240
CTGGGCTGGC TGGGCACCAT CGTGTGCTGC GCGTTGCCCA TGTGGCGCGT GTCGGCCTTC   300
ATCGGCAGCA ACATCATCAC GTCGCAGAAC ATCTGGGAGG GCCTGTGGAT GAACTGCGTG   360
GTGCAGAGCA CCGGCCAGAT GCAGTGCAAG GTGTACGACT CGCTGCTGGC ACTGCCACAG   420
GACCTTCAGG CGGCCCGCGC CCTCATCGTG GTGGCCATCC TGCTGGCCGC CTTCGGGCTG   480
CTAGTGGCGC TGGTGGGCGC CCAGTGCACC AACTGCGTGC AGGACGACAC GGCCAAGGCC   540
AAGATCACCA TCGTGGCAGG CGTGCTGTTC CTTCTCGCCG CCCTGCTCAC CCTCGTGCCG   600
GTGTCCTGGT CGGCCAACAC CATTATCCGG GACTTCTACA ACCCCGTGGT GCCCGAGGCG   660
CAGAAGCGCG AGATGGGCGC GGGCCTGTAC GTGGGCTGGG CGGCCGCGGC GCTGCAGCTG   720
CTGGGGGGCG CGCTGCTCTG CTGCTCGTGT CCCCCACGCG AGAAGAAGTA CACGGCCACC   780
AAGGTCGTCT ACTCCGCGCC GCGCTCCACC GGCCCGGGAG CCAGCCTGGG CACAGGCTAC   840
GACCGCAAGG ACTACGTCTA AGGGACAGAC GCAGGGAGAC CCCACCACCA CCACCACCAC   900
CAACACCACC ACCACCACCG CGAGCTGGAG CGCGCACCAG GCCATCCAGC GTGCAGCCTT   960
GCCTCGGAGG CCAGCCCACC CCCAGAAGCC AGGAAGCCCC CGCGCTGGAC TGGGGCAGCT   1020
TCCCCAGCAG CCACGGCTTT GCGGGCCGGG CAGTCGACTT CGGGGCCCAG GGACCAACCT   1080
GCATGGACTG TGAAACCTCA CCCTTCTGGA GCACGGGGCC TGGGTGACCG CCAATACTTG   1140
ACCACCCCGT CGAGCCCCAT CGGGCCGCTG CCCCCATGTC GCGCTGGGCA GGGACCGGCA   1200
GCCCTGGAAG GGGCACTTGA TATTTTTCAA TAAAAGCCTC TCGTTTTAGC              1250
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Seq ID NO: C184 DNA Sequence
Nucleic Acid Accession #: NM_012449.1
Coding sequence: 66..1085

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AATTAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA   120
GGAGAAATTT AGAAGAAGAC GATTATTTGC ATAAGGACAC GGGAGAGACC AGCATGCTAA   180
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CAGAACTTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTTGCCAATT AAAATAGCTG   300
CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTTCTGAG GGAAGTAATT CACCCTTTAG   360
CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCATCAAC AAAGTCTTGC   420
CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG   480
TCCAACTTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT   540
TAACAAGAAA GCAGTTTGGG CTTCTCAGTT TCTTTTTTGC TGTACTGCAT GCAATTTATA   600
GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC   660
AGGTCCAACA AAATAAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT   720
ATGTGTCTCT GGGAATTGTG GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC   780
CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA   840
TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCCTGGAAT AAGTGGATAG   900
ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCCTTCCAA   960
TTGTTGTCCT GATATTTAAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA  1020
AGATTAGACA TGGTTGGGAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCCCAGT  1080
TGTAGAATTA CTGTTTACAC ACATTTTTGT TCAATATTGA TATATTTTAT CACCAACATT  1140
TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA       1195
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Seq ID NO: C185 DNA Sequence
Nucleic Acid Accession #: NM_001775.1
Coding sequence: 70..972

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TGGAGCCCTA TGGCCAACTG CGAGTTCAGC CCGGTGTCCG GGGACAAACC CTGCTGCCGG  120
CTCTCTAGGA GAGCCCAACT CTGTCTTGGC GTCAGTATCC TGGTCCTGAT CCTCGTCGTG  180
GTGCTCGCGG TGGTCGTCCC GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCACCAAG  240
CGCTTTCCCG AGACCGTCCT GGCGCGATGC GTCAAGTACA CTGAAATTCA TCCTGAGATG  300
AGACATGTAG ACTGCCAAAG TGTATGGGAT GCTTTCAAGG GTGCATTTAT TTCAAAACAT  360
CCTTGCAACA TTACTGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA  420
CCTTGCAACA AGATTCTTCT TTGGAGCAGA ATAAAAGATC TGGCCCATCA GTTCACACAG  480
GTCCAGCGGG ACATGTTCAC CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC  540
ACATGGTGTG GTGAATTCAA CACTTCCAAA ATAAACTATC AATCTTGCCC AGACTGGAGA  600
AAGGACTGCA GCAACAACCC TGTTTCAGTA TTCTGGAAAA CGGTTTCCCG CAGGTTTGCA  660
GAAGCTGCCT GTGATGTGGT CCATGTGATG CTCAATGGAT CCCGCAGTAA AATCTTTGAC  720
AAAAACAGCA CTTTTGGGAG TGTGGAAGTC CATAATTTGC AACCAGAGAA GGTTCAGACA  780
CTAGAGGCCT GGGTGATACA TGGTGGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC  840
ACCATAAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT  900
ATCTACAGAC CTGACAAGTT TCTTCAGTGT GTGAAAAATC CTGAGGATTC ATCTTGCACA  960
TCTGAGATCT GAGCCAGTCG CTGTGGTTGT TTTAGCTCCT TGACTCCTTG TGGTTTATGT 1020
CATCATACAT GACTCAGCAT ACCTGCTGGT GCAGAGCTGA AGATTTTGGA GGGTCCTCCA 1080
CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTCCCCCAA AGTCTTAAAA TAACTTATAT 1140
CATCAGCATA CCTTTATTGT GATCTATCAA TAGTCAAGAA AAATTATTGT ATAAGATTAG 1200
AATGAAAATT GTATGTTAAG TTACTTCCTT TAG                               1233
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Seq ID NO: C186 DNA Sequence
Nucleic Acid Accession #: XM_120513.2
Coding sequence: 1..2208

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AGGACCCCAA AGCCCCGTAA ACACCGCGCG ACCACCCGGG CCAAGATCTT CAAGAGGTTC  180
TTTTCAGAAG GATCGGAGAG CAATTCCCGA TTGGTAGAAG AACTTGCTGT AATACACACG  240
TACTCTGACG ACCCCGCCCC AACGACTAGC CCCTCCTCTG TGCAACCCCG AGAGTTTGGG  300
GTCATGCAGG GGGCGCCACG AGCTCGTTTC GGAAGCCGGA CCCCGCCCGC AGCCGCAGAA  360
GCCTCGAGTC CACATCTGGG CATTGGCGAG GCAGCCTGTC AATCAGGAGC TCGGGCGGCA  420
GCCCCCCGCG CGGGGGCTCG GCGATGCCAG CCTCAGCGAC AGGCGGCGGC GGCGGCGGCC  480
ACGGCACAGA CACACCCCT CCCACACGCG CGCACCAGGG CAGACCCGGC GGGCAGGCGG  540
CGGAGGCACC CTCGGAGCCC GGCGCCCGGC GGGGAGGGGA CGTGCTCCGA GGGACCGGCC  600
CCGAGGCGCC GGATGGAGGA AGAGATGCAG CCGGCAGAGG AGGGGCCCAG CGTCCCCAAA  660
ATCTACAAGC AGCGCAGCCC CTACAGCGTC CTCAAGACGT TCCCCAGCAA GAGACCGGCG  720
CTGGCCAAGC GCTACGAGCG ACCCACCCTG GTGGAGCTGC CGCACGGCCA CTTGAGGACT  780
CCGGCGCAGC CGCCGCCCGC GTCCCCCGCC GCCTCCTCGT CGTCTTCGTT CGCCGCTGTC  840
GTCAGACTCG GGGCTCCTCC GCGTCCGCCA CGCCGTGGAT TTCGGGCGCG GGGAACCATC  900
CCGCCCCTCC TTCCTGCCCC GGGAGTCGCA GGCACTCTGC TCCCACCGCC CACGTCGTCG  960
TCCCCGCCAT CCCCTCGTCC CCGTCCGTGG CACGCTGCCG CGCCGCGGGG AGGGACCTCA 1020
CATACACATA TGTGGAGGTC CCAGTCCACA CTTCCAGGAT CTGACACCAT GGTCTCTGTC 1080
TTTGGATTGA TGGCTCAGAG AAGATGGCAG CATAGATCTT TAAAGCAGTT TGAGTGGGGA 1140
ATTCTTGGAT CTTGGGGTAC TTGGCCATGT GGACAGGATT GGCTGGAGAA GGAGGGTCAG 1200
GTGGCGGTCC TGCTGCCAAG GTCTGAGGGT AATACTGCTC CTAAGAAGAG TCGAATGATC 1260
TTGGATGCCT TTGCCCAGCA GTGCAGTCGA GTTCTTAGCC TCTTAAATTG TGGAGGAAAA 1320
CTCCTGGACT CCAACCATTC TCAGTCCATG ATTTCTTGCG TAAAGCAGGA AGGCTCAAGT 1380
TACAACGAAA GACAGGAGCA CTGTCACATT GGGAAAGGGG TCCACAGTCA GACCTCAGAC 1440
AATGTAGACA TAGAGATGCA GTATATGCAA AGGAAACAAC AAACTTCTGC CTTTTGAGG  1500
GTTTTCACTG ACTCTCTACA AAATTACCTG CTCTCGGGAA GCTTTCCAAC TCCAAACCCC 1560
TCGTCAGCCA GTGAATATGG CCATCTGGCC GACGTGGATC CTCTGTCAAC CTCTCCTGTG 1620
CATACATTAG AAAATATTTC ACTTGATTCC ACAGCTTCCC TGTGTAAATC TAGGCATCTA 1680
TCCAGAGAGC CCCCAGTCAA GAGTGATTTT CCAAATCCTT TGCAGCAGGC CTTGGCTGGG 1740
GGTGCTTCAA GACCATTTTC AGGGGCACAG CAAAGCATCG CTTACAGGGT GAACTCTGAA 1800
CTTGAGGATG GCATCCGCAG CCCCGTCCCT TTGAGTTGTG AGGCCTTGGA AATGGATTTG 1860
ACCTCCTTGG GAAGCAAGCA GCTGTTGAAC AACTATCCTG TCTACATAAC GAGCAAACAG 1920
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TGGGATGAGG CTGTAAATTC TTCAAAGAAA GATGGGAGAC GGCTCCTTCG ATACCTCATC   1980
AGATTTGTTT TCACAACCGA TGAGCTTAAG TACTCATGCG GCCTTGGGAA AAGGAAAAGG   2040
TCAGTGCAGT CAGGAGAGAC AGGTCCCGAA AGACGCCCTC TGGATCCAGT TAAAGTAACA   2100
TGCCTCCGAG GTACTGCATC CTTCCGCTCA GTGTCACCAT CTGTGATCTC ATTTCACCGC   2160
ATTGGCTGTG GCTCTCCCCG TACAAGTGTT CAGCCTTCTG TATTTTGA                2208

Seq ID NO: C187 DNA Sequence
Nucleic Acid Accession #: AB037745.1
Coding sequence: 26..1744

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CTCAGACAAT GACTTCATGA TTCTCACTCT GGTTGTGCCA GGATTTAGAC CTCCGCAGTC  180
GGTGATGGCA GACACAGAGA ATAAAGAGGT GGCCAGAATC ACATTTGTCT TTGAGACCCT  240
CTGTTCTGTG AACTGTGAGC TCTACTTCAT GGTGGGTGTG AATTCTAGGA CCAACACTCC  300
TGTGGAGACG TGGAAAGGTT CCAAAGGCAA ACAGTCCTAT ACCTACATCA TTGAGGAGAA  360
CACTACCACG AGCTTCACCT GGGCCTTCCA GAGGACCACT TTTCATGAGG CAAGCAGGAA  420
GTACACCAAT GACGTTGCCA AGATCTACTC CATCAATGTC ACCAATGTTA TGAATGGCGT  480
GGCCTCCTAC TGCCGTCCCT GTGCCCTAGA AGCCTCTGAT GTGGGCTCCT CCTGCACCTC  540
TTGTCCTGCT GGTTACTATA TTGACCGAGA TTCAGGAACC TGCCACTCCT GCCCCCCTAA  600
CACAATTCTG AAAGCCCACC AGCCTTATGG TGTCCAGGCC TGTGTGCCCT GTGGTCCAGG  660
GACCAAGAAC AACAAGATCC ACTCTCTGTG CTACAATGAT TGCACCTTCT CACGCAACAC  720
TCCAACCAGG ACTTTCAACT ACAACTTCTC CGCTTTGGCA AACACCGTCA CTCTTGCTGG  780
AGGGCCAAGC TTCACTTCCA AAGGGTTGAA ATACTTCCAT CACTTTACCC TCAGTCTCTG  840
TGGAAACCAG GGTAGGAAAA TGTCTGTGTG CACCGACAAT GTCACTGACC TCCGGATTCC  900
TGAGGGTGAG TCAGGGTTCT CCAAATCTAT CACAGCCTAC GTCTGCCAGG CAGTCATCAT  960
CCCCCCAGAG GTGACAGGCT ACAAGGCCGG GGTTTCCTCA CAGCCTGTCA GCCTTGCTGA 1020
TCGACTTATT GGGGTGACAA CAGATATGAC TCTGGATGGA ATCACCTCCC CAGCTGAACT 1080
TTTCCACCTG GAGTCCTTGG GAATACCGGA CGTGATCTTC TTTTATAGGT CCAATGATGT 1140
GACCCAGTCC TGCAGTTCTG GGAGATCAAC CACCATCCGC GTCAGGTGCA GTCCACAGAA 1200
AACTGTCCCT GGAAGTTTGC TGCTGCCAGG AACGTGCTCA GATGGGACCT GTGATGGCTG 1260
CAACTTCCAC TTCCTGTGGG AGAGCGCGGC TGCTTGCCCG CTCTGCTCAG TGGCTGACTA 1320
CCATGCTATC GTCAGCAGCT GTGTGGCTGG GATCCAGAAG ACTACTTACG TGTGGCGAGA 1380
ACCCAAGCTA TGCTCTGGTG GCATTTCTCT GCCTGAGCAG AGAGTCACCA TCTGCAAAAC 1440
CATAGATTTC TGGCTGAAAG TGGGCATCTC TGCAGGCACC TGTACTGCCA TCCTGCTCAC 1500
CGTCTTGACC TGCTACTTTT GGAAAAAGAA TCAAAAACTA GAGTACAAGT ACTCCAAGCT 1560
GGTGATGAAT GCTACTCTCA AGGACTGTGA CCTGCCAGCA GCTGACAGCT GCGCCATCAT 1620
GGAAGGCGAG GATGTAGAGG ACGACCTCAT CTTTACCAGC AAGAAGTCAC TCTTTGGGAA 1680
GATCAAATCA TTTACCTCCA AGCAGCCAGC TCCTGTCACC ATCTCTCTTT CAGAGGACTC 1740
CTGATGGATT TGACTCAGTG CCGCTGAAGA CATCCTCAGG AGGCCCAGAC ATGGACCTGT 1800
GAGAGGCACT GCCTGCCTCA CCTGCCTCCT CACCTTGCAT AGCACCTTTG CAAGCCTGCG 1860
GCGATTTGGG TGCCAGCATC CTGCAACACC CACTGCTGGA AATCTCTTCA TTGTGGCCTT 1920
ATCAGATGTT TGAATTTCAG ATCTTTTTTT ATAGAGTACC CAAACCCTCC TTTCTGCTTG 1980
CCTCAAACCT GCCAAATATA CCCACACTTT GTTTGTAAAT TATGCCCTTG CTTGTATCTT 2040
GTTTCCCAAA ATGGCCCATC CGCCAGAGCC ATAGCTTCGT CTGCTCATAA TTCTTATAGC 2100
TTTGGAATGA AAATATTTCT ATCTTCTTAA GTATAGAAAC TATTTCCTCT GTCCTCTAAC 2160
TTAAGGGCAG AAACAGCTGG GAGTTTTCCT CGCATGCCCT CAGCTCATGA TCTCTTCAGG 2220
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GATCCATTTC CCCTGGATAA CCAGCTCAAA GGGAGTGAAA ATGGTAGTCT GAGGGCAAGG 2340
GGAGCAAGGC CTGGGTAAGA AAAGCCTTGA AAAGCATAAA AAGAGGCCGG GCGCGGTGGC 2400
TCACGCCTGT AATCCCAGCA CTTTGGGAGG CCGAGGCGGG CAGATCATGA GGTCGGGAGA 2460
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GCGTGGGCCT GGAAGGCGGA GCTTGCAGTG AGCCGAGATC GCGCCACTGC ACTCCATCCA 2640
GCCTGGGTGA CAGAGTGAGA CTCTGCCTCA AAAAAAAAAA AAAAAAAGAA AAGCACAAAG 2700
AGAGGCAACA AGGAATGTTT TTGTTTTTGA GACAGGCTCT CACTCTGTCA CCTAGGCTGG 2760
AGTGCAGTGG CGTAATCACT GTTCAGTGCA GCCTCAAGCT CTTGGGCTCA GGCTATCCTC 2820
CCATCTCAGC CTCTCAAGTA GCTGGGACTA CGAGTGTGCA CCACCAGGCT CACTAATTTT 2880
TGTGTTTTTT GTAGACACGG GGTTTCACCG TGTTGCCCAG GCTGGTCTCC AACTCCTGGG 2940
CTCAAGTGAT CTGTCCGCCT CGGCCTCCCA AACTGCTGGG ATTACAGGCA TAAGCCACTG 3000
CACTCAGCCT TTTATTTGTT TTTTAAACCA CGTAGCTCAT TGCCTTCTCT TAAGTAAATG 3060
ATAGATATTC TCACTGAAGC CAAAGGAATA AGTTCATCAA GAAAATGCCC AAAGCCCTGG 3120
TGGATACATC CTCCCTATCT TTTTTTTAAA CCTTCCACTA TCACTCTATG ACACTGAAAA 3180
GAACCAGGTA AGCCCCAAAC CCAGATGTTC CAGCCTTATC CTCTATTGGG TTTACCCACA 3240
GACATAGCAA ACCCTGTCAG TGAGGAAAAT TCCCCATCCT TGAGTGCCCC CGTCCTAGAA 3300
GTTTGGGCCA TATTATGGAA CAGGGGTCTC TTATTTGAAA AGAGCACAAG GAGGCCAAGA 3360
TTTTAATGGG GCACTTTAGG GGATACAGCC CACAATGGCA TGGGCCTGAG GTGGCCGTGA 3420
TGTCTGCTTC TAAGCTTAAC GCATCTGCTC AGGCACAGAA TAAACGTCTA GGCTGGCCAA 3480
AAAAGGAACT GAATCCCAGG CCCATACGCC AGCACCAGAA TCAAACCAGT CTTCAAGGAA 3540
GGAAGGCTAG GAGAGTTTAA CAAGATTTTC ACTGGGCCCA GCATGGTGGC TCACACCTGT 3600
AATCCCAAGG CAGAATGGTG GCTTGAGCTC AGGAGTTCAA GACCAGCCTG GGCAACACAG 3660
TGAGACCCTG TCTCTAAAAA ATTTAAAAAT AAACAAGGTG TTCACCAAGC TGGGATACTT 3720
CTCACTATTA AGCCCCTATC TTTCTCTTTT TTTCATTCTC AATTGCTTTG TGTGATAAAA 3780
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GGTGTCTTCT ATGCCCATTT TCCCCAATTT TACACAAACT ATTATCAATG AACTTTTAAG 3900
TACCTAGAAT GGGTAAAACC AGAGCAAGAC TTTAAATTAC CTTCTTCTTT CTTCTACTGG 3960
CAGTTCTGCC TCCATCACTA TCAGGCTAGG GTGACCTTCC CTTGGTCAAG CCCCAATTGC 4020
CCATGATTTG TGCCTGTGCC CTTTCTCCAG TGACCATTTG GTGACCAGAT GGTAGATATA 4080
GAAAGGGGAT GGCATTTGCA AGTGACTAGT CTGCCACAAA ATGCTCATCT GATTAGCCAC 4140
TGCTGCCCTG GCAATGGCTT TGTAAGAGTC AATGAGAACT AGAGCCAGGC TGTGGTCCCT 4200
GGCCATCAAC AGTGTTGGTG ACGGCAGGGA GTCCCTTTGG TTTAATAAAT CCAGTTTTTC 4260
TTTGGGTATC CAAATTCTCC CCTCCTTTTG TAGGAGTCAG GCTCTCAGAA CCTGTGTCCA 4320
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TGTTGGAACT TCCCCCAGTG TGGATGCAGA TACGCAGCTC CTGAGCTCCA GCCTAAAGTC   4380
TTCTGTAGCC TCAGCAATAC TTGGGCACCT GCTGTCTCAC TGAATAGCTT TCTTTTGTGA   4440
CAAAGGCCAC AGACAGCCCT TAGACTATTC CGGAAACAGT AGCAAAAATT ACATATGTCT   4500
TTGACTTCTT TATTCTGACT CCACTGATTT TAGCCATAAT ACTTTAAGGA GCTACTTTTT   4560
ACTACCCCTT ACCGTGCTGA CTTCTGCAGG TCTGCCCTGT GACCTGTCAG GAACTCCTGA   4620
GTTACGCTAC TGGGGTCACC TGTTGCTCCC CTAGCAAGTT AGGCATGTCA TATATTTTTA   4680
ACAGCTTTAT TGAGATATAA TTCACATATT ATACAATTCA CCTTTAAAAC ATACGATTCA   4740
ATGGTTTTCA GCAAACTCAC AGAGTTGTCC GCCCACTTGA GAGCAAACAC ATGTTCAATT   4800
TTCTTTTCCT TTTTTTTTTT GAGACAGAGT CAGCTTTGTC GCCCAGGCTG GAGTGCAGTG   4860
CCATGATCTT GGCTCACTGC AGCCTCCCCA TCCTGGGTTC AAGTGATCCT TCTGCTTCAG   4920
CCTCCCCAGT AGCTGGGATT ACAGGCATGC GCCACCACGC CTAGCTAATT TTTGTGTTTT   4980
TAGTAGAGAT GGGGTTTCAC CGTGTTGGCC AGGCTGGTCT CAAACTCCTG GACTCAAGTG   5040
ATCCACCCAC CTCGGCCTCC CAAAGTGCTG GGATTGCAGG TGTGAGCCAC CGTGCCTGGC   5100
CTACGTGTTC AATTTTCTAT GAACAAAGGC TTTAGTCCTT GACCCAGGGC TAAAGTGGTC   5160
TGTCCAAGCT GTTGTTGGTA GAGGGAGTAT GATAAAATGT TTAAATCTCA TTTGGTTACC   5220
TTGAGTCCTG GAACACGCAG TAACTGTCAT GCTATAGTCA TCATCTGTAT TTGGCTGGGA   5280
ATACAAATGA AGATTGTGGT GTATTCAAGC AGTAGGGTTT TTGCTTTTGT TTTTGTTTTA   5340
GTGCCAACAA AACTTTTTTT TGTCTGACTA CATTAAAGAT AAGACTGACT ATATTTATAC   5400
AACAGAAACT TTGTAATAGA TTTTTTCAGC TTTGTGAAAT CGAATTTTTT TTCATCAGGG   5460
CTGGTTGGAT TTCCTTTTTA CCCTGTAATC CAAGCGTTAA TAGTTTGTTA GAAGATGGGT   5520
TATTGCATGT CACTTTTTTT TTTTTGTAAA ATAAAAACAT ACCTTAC                 5567
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Seq ID NO: C188 DNA Sequence
Nucleic Acid Accession #: NM_014324.1
Coding sequence: 89..1237

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GTCCGGCCTG GCCCCGGGCC GTNTCTGTGC TATGGTCCTG GCTGACTTCG GGGCGCGTGT   180
GGTACGCGTG GACCGGCCCG GCTCCCGCTA CGACGTGAGC CGCTTGGGCC GGGGCAAGCG   240
CTCGCTAGTG CTGGACCTGA AGCAGCCGCG GGAGCCGCGT GCTGCGGCGT CTGTGCAAGC   300
GGTCGGATGT GCTGCTGGAG CCCTTCCGCC GCGGTGTCAT GGAGAAACTC CAGCTGGGCC   360
CAGAGATTCT GCAGCGGGAA AATCCAAGGC TTATTTATGC CAGGCTGAGT GGATTTGGCC   420
AGTTCAGGAA AGCTTCTGCC GGTTAGCTGG CCACGATATC AACTATTTGG CTTTGTCAGG   480
TGTTCTCTCA AAAATTGGCA GAAGTGGTGA GAATCCGTAT GCCCCGCTGA ATCTCGTGGC   540
TGACTTTGCT GGTGGTGGCC TTATGTGTGC ACTGGGCATT ATAATGGCTC TTTTTGACCG   600
CACACGCACT GACAAGGGTC AGGTCATTGA TGCAAATATG GTGGAAGGAA CAGCATATTT   660
AAGTTCTTTT CTGTGGAAAA CTCAGAAATC GAGTCTGTGG GAAGCACCTC GAGGACAGAA   720
CATGTTGGAT GGTGGAGCAC CTTTCTATAC GACTTACAGG ACAGCAGATG GGGAATTCAT   780
GGCTGTTGGA GCAATAGAAC CCCAGTTCTA CGAGCTGCTG ATCAAAGGAC TTGGACTAAA   840
GTCTGATGAA CTTCCCAATC AGATGAGCAC GGATGATTGG CCAGAAATGA AGAAGAAGTT   900
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TGCCTGTGTG ACTCCGGTTC TGACTTTTGA GGAGGTTGTT CATCATGATC ACAACAAGGA  1020
ACGGGGCTCG TTTATCACCA GTGAGGAGCA GGACGTGAGC CCCCGCCTTG CACCTCTGCT  1080
GTTAAACACC CCAGCCATCC CTTCTTCCAA AGGGGATCCT TTCATAGGAG AACACACTGA  1140
GGAGATACTT GAAGAATTTG GATTCAGCCG AGAAGAGATT TATCAGCTTA ACTCAGATAA  1200
AATCATTGAA AGTAATAAGG TAAAAGCTAG TCTCTAACTT CCAGGCCCAC GGCTCAAGTG  1260
AATTTGAATA CTGCATTTAC AGTGTAGAGT AACACATAAC ATTGTATGCA TGGAAACATG  1320
GAGGAACAGT ATTACAGTGT CCTACCACTC TAATCAAGAA AAGAATTACA GACTCTGATT  1380
CTACAGTGAT GATTGAATTC TAAAAATGGT TATCATTAGG GCTTTTGATT TATAAAACTT  1440
TGGGTACTTA TACTAAATTA TGGTAGTTAT TCTGCCTTCC AGTTTGCTTG ATATATTTGT  1500
TGATATTAAG ATTCTTGACT TATATTTTGA ATGGGTTCTA GTGAAAAAGG AATGATATAT  1560
TCTTGAAGAC ATCGATATAC ATTTATTTAC ACTCTTGATT CTACAATGTA GAAAATGAGG  1620
AAATGCCACA AATTGTATGG TGATAAAAGT CACGTGAAAC AGAGTGATTG GTTGCATCCA  1680
GGCCTTTTGT CTTGGTGTTC ATGATCTCCC TCTAAGCACA TTCCAAACTT TAGCAACAGT  1740
TATCACACTT TGTAATTTGC AAAGAAAAGT TTCACCTGTA TTGAATCAGA ATGCCTTCAA  1800
CTGAAAAAAA CATATCCAAA ATAATGAGGA AATGTGTTGG CTCACTACGT AGAGTCCAGA  1860
GGGACAGTCA GTTTTAGGGT TGCCTGTATC CAGTAACTCG GGGCCTGTTT CCCCGTGGGT  1920
CTCTGGGCTG TCAGCTTTCC TTTCTCCATG TGTTTGATTT CTCCTCAGGC TGGTAGCAAG  1980
TTCTGGATCT TATACCCAAC ACACAGCAAC ATCCAGAAAT AAAGATCTCA GGACCCCCCA  2040
AAAAAAAAAA AAAAAAAAAA AAAAAAAA                                     2068
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Seq ID NO: C189 DNA Sequence
Nucleic Acid Accession #: XM_091332.1
Coding sequence: 1..1401

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CCCCTGTTCT GGATGGAGTT CAAAGGCCAC TGCTATCGAT TCTTCCCTCT CAATAAGACC   180
TGGGCTGAGG CCGACCTCTA CTGTTCTGAG TTCTCTGTGG GCAGGAAGTC CGCCAAGCTG   240
GCCTCCATCC ACAGCTGGGA GGAGAATGTC TTTGTATATG ACCTCGTGAA CAGCTGTGTT   300
CCCGGCATCC CAGCTGACGT CTGGACAGGC CTTCATGATC ACAGACAGGA AGGGCAGTTT   360
GAATGGACTG ATGGCTCATC CTATGACTAC AGCTACTGGG ATGGCAGCCA GCCAGATGAT   420
GGCGTCCACG CGGACCCAGA AGAAGAGGAC TGCGTGCAGA TATGGTACAG GCCTACCAGT   480
GAGCAGCTAC AGGCCCCAGA GCCCCAGTTA CCCTTATCAA TCTCAGAGGC CACAGATGTC   540
TATCTCCCTG AGGATTTCCC AGCTGAGCCC AAGCTCATGG ACCAGTCCTG GGTGTCCAGG   600
AAGAGCCTGA AACCATCCAA GAGTCATCTT ATGGAGCCAC CCACTCCAGT GGCCAAGCAC   660
CAAAAGGCAA AGACCCGACA TAGGAGCCTG CGCGGCGTCT GGTGGCCATC AGGTAAGGCT   720
GGGTCATGGA AAGAAAGAAT GAATGCAGAC TACGGGCGAA GAAAGCGATC GGCCCCGAGG   780
CAGGAAGGCC GGCTCCGGTG CAGGGAGCGC CGCCTGCGGG CTGCTTCGGG CCAGGGTCGA   840
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CCCGAGGGCC AGCGCAAGCA GCGGCAACAG GAGCGCCAGG AGAGAGGCTG GGAAGAACTG   900
GGAGGGGTGT CCCCAATGCG GGGCGCCCAA GCGTGGCAGC ACGGGCTGGG AGCGGGGAGC   960
CAGCGGGGTG CGGCGCCGGA GTGCGGGGAG AACCACCAGG CGCCGGAATT GGGGAGCACG  1020
TGGAGGGGGC AGCGGCTCCA GCCCCAGACC GCCGCGCTCT GTCACTTTGC ATTAAGAAAG  1080
CTTCCGGGGA ATGCACACGG CCTGGCCGCC GCCTTCGTGC AGCCCGCCCT GCAGGTGCAG  1140
GAAGAAAAGA ATAATCGCAC CCGTTTCTCA GGTGCTTACT TCACCATGTC CGATCCGACG  1200
TGTGACCAAG ATAGCAAGGA GCAGTCTTTA AGGCGACACG GCAGAGAGGC AGAAAAAGAT  1260
GGGCCTTACC GGTTAGTTAA GAAAAAAAGA GGACCTGTTG CCTGTCCCTC TAGCTTTGAA  1320
CTACAAAGTG GAGGGGAAGT TTGTCTGGAT TTTCCTGTAG AACTGAGGGC AGGGACCTGG  1380
ATTGCTCGAG AACCTCCATA A                                             1401

Seq ID NO: C190 DNA Sequence
Nucleic Acid Accession #: XM_054869.2
Coding sequence: 26..2902

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GGACCTTCAC AGAAAAATGC ATAGCTGGAT GCTGCAGACT CTAGCGTTTG CTGTAACATC   120
TCTCGTCCTT TCGTGTGCAG AAACCATCGA TTATTATGGG GAAATCTGTG ACAATGCATG   180
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TCTTTTTGAC TTCCAACTGA TATTGGGAAG TTTGGTTGAG GTTCAAGTGT GACTCCTTCC   3960
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CCGGGAAACT CTGCTTCCCC ATTGTTTCCA TCTGATCAGC TGTGGTGTGA GGACTTCTCA   4140
GACAAAGGCA AGGCCTCGTG CCCCTGCCCA GCCCATTCAT GGAGCCCTGG GCCTTCTTGG   4200
CTTCCATAGA TCCTAAGCTC TTGACTGTAG TTTAGCCAGA CTTGTTTTGC TATCTTATAA   4260
GCAGTTCAGA ATTAGGGAAT GCTGGTTTTG AAGAGCAAAG GACAGGTAGT CTAGAGAGGG   4320
TCGTCTGGCC TGCTTGCTGG GTCTTTGTAA CCCAGCACTT CCTCTTGCCC TCCTGGCTTT   4380
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CACTTGTGGC CTCGAAGGAA GCACAAACCC TCCATCCACT TCCCATTTCC TCTGCCCTTT   5040
TCCACCTCCC CCTTCCATCC CACCAGCTGC CAGTGGCTCC CAGAAAGCCT TATTGAGCCC   5100
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AGGTCTTCCG TCCTCAGAGC CTTTCTGGAA CAAGGAGAAT GCCTGTGCAG GTGGACACAC   5220
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CTCTCCAGCT GGAGGCCGAG TTTCTGGGGA CTGCAGATTT TTCTACTCTG TGATCGATTC   5400
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GTGTATAAAG TTAAATACTG TGTATTTATC ACTAAAAAGT ACATGAACTT AAGAGACAAC   5520
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Seq ID NO: C193 DNA Sequence
Nucleic Acid Accession #: NM_018646
Coding sequence: 217..2394

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CGGCCTCAGG CCCCCAAGGA GCCGGCCCTA CACCCCATGG GTTTGTCACT GCCCAAGGAG   240
AAAGGGCTAA TTCTCTGCCT ATGGAGCAAG TTCTGCAGAT GGTTCCAGAG ACGGGAGTCC   300
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CTCCTTCTAG CTGCCAAAGA TAATGATGTC CAGGCCCTGA ACAAGTTGCT CAAGTATGAG   420
GATTGCAAGG TGCACCAGAG AGGAGCCATG GGGGAAACAG CGCTACACAT AGCAGCCCTC   480
TATGACAACC TGGAGGCCGC CATGGTGCTG ATGGAGGCTG CCCCGGAGCT GGTCTTTGAG   540
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AGAATGGGGG TCACTCGCTT CTTTGGACAG ACCATCCTTG GGGGCCCATT CCATGTCCTC   1500
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GACCTGATGC GATTCTGCTG GCTGATGGCT GTGGTCATCC TGGGCTTTGC TTCAGCCTTC   1740
TATATCATCT TCCAGACAGA GGACCCCGAG GAGCTAGGCC ACTTCTACGA CTACCCCATG   1800
GCCCTGTTCA GCACCTTCGA GCTGTTCCTT ACCATCATCG ATGGCCCAGC CAACTACAAC   1860
GTGGACCTGC CCTTCATGTA CAGCATCACC TATGCTGCCT TTGCCATCAT CGCCACACTG   1920
CTCATGCTCA ACCTCCTCAT TGCCATGATG GGCGACACTC ACTGGCGAGT GGCCCATGAG   1980
CGGGATGAGC TGTGGAGGGC CCAGATTGTG GCCACCACGG TGATGCTGGA GCGGAAGCTG   2040
CCTCGCTGCC TGTGGCCTCG CTCCGGGATC TGCGGACGGG AGTATGGCCT GGGAGACCGC   2100
TGGTTCCTGC GGGTGGAAGA CAGGCAAGAT CTCAACCGGC AGCGGATCCA ACGCTACGCA   2160
CAGGCCTTCC ACACCCGGGG CTCTGAGGAT TTGGACAAAG ACTCAGTGGA AAAACTAGAG   2220
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ACCCAGGCAG GTCCAGGGAA GTGCAGAGCT TGTGGAAAGC GTGTGAGTGA GGGAGACAGG   2820
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Seq ID NO: C194 DNA Sequence
Nucleic Acid Accession #: NM_021910.1
Coding sequence: 260..601

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CCCACTCCAC GGTGCAGCTG CGGCTTATCT CTCAGCCCAG CGAGATGCCA GCCTTCCTGT   240
CCCGGGCCAG CGCTCTGACA TGCAGAAGGT GACCCTGGGC CTGCTTGTGT TCCTGGCAGG   300
CTTTCCTGTC CTGGACGCCA ATGACCTAGA AGATAAAAAC AGTCCTTTCT ACTATGACTG   360
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CATCGTCATG AGTGAGTGGA GGAGCTCGGG GGAGCAGGCG GGCCGGGGCT GGGGCTCCCC   480
TCCCCTGACC ACTCAGCTCT CCCCAACAGG TGCAAAATGC AAATGCAAGT TTGGCCAGAA   540
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GGCAGGGCCT CATCTCACCT CTCGCAAGAG GGTCTCTTTG TTCAATTTTT TTTAATCTAA   780
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CTGCTTGTTG GGAAAAGCCC ACAGGCCTGT TCCCTTGTGG CTTGGGACAT GGCACAGGCC   960
CGCCCTCTGC CTCCTCAGCC ATGGGACCTC ATATGCAATT TGGGATTTAC TAGTAGCCAA  1020
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CATTCCAGGA AAACTGGGAC ATAGGATCGT CCCGCTATGA TGGAAGTGTT CAGACAGTTT  1140
ATAATAGTAA GCCCCTGTGA CCCTCTCACT TACCCCGAGA CCTCACTTTA TTACAAGATC  1200
TTTCCAAATA CCCAAATATC CCTGCAAGCC CGTTAAATAA TTCCCTATGC TACCCTTAAT  1260
AACATACAAT GACCACATAG TGTGAGAACT TCCAACAAGC CTCAAAGTCC CTTGAGACTC  1320
CCCAATACCT AATAAGGCAT GCGAAATGTT CTCATGAACT ACCCCACAAC ACGCCTAAAA  1380
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ACAATAAACT CGTGACTTGT CCCCTC                                       1466
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Seq ID NO: C195 DNA Sequence
Nucleic Acid Accession #: NM_005971.2
Coding sequence: 176..439

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GAAGGTGACC CTGGGCCTGC TTGTGTTCCT GGCAGGCTTT CCTGTCCTGG ACGCCAATGA   240
CCTAGAAGAT AAAAACAGTC CTTTCTACTA TGACTGGCAC AGCCTCCAGG TTGGCGGGCT   300
CATCTGCGCT GGGGTTCTGT GCGCCATGGG CATCATCATC GTCATGAGTG CAAAATGCAA   360
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CCCTATGCTA CCCTTAATAA CATACAATGA CCACATAGTG TGAGAACTTC CAACAAGCCT  1140
CAAAGTCCCT TGAGACTCCC CAATACCTAA TAAGGCATGC GAAATGTTCT CATGAACTAC  1200
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Seq ID NO: C196 DNA Sequence
Nucleic Acid Accession #: NM_004961.2
Coding sequence: 55..1575

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CAGCCTCTGG AAAATCAGCT CCTCTCTGAG GAAACAAAGT CAACTGAGAC TGAGACTGGG  240
AGCAGAGTTG GCAAACTGCC AGAAGCCTCT CGCATCCTGA ACACTATCCT GAGTAATTAT  300
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TCCCAGACCT GGTACGACGA ACGCCTCTGT TACAACGACA CCTTTGAGTC TCTTGTTCTG  480
AATGGCAATG TGGTGAGCCA GCTATGGATC CCGGACACCT TTTTTAGGAA TTCTAAGAGG  540
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CCAATGGATT CTCACTCTTG CCCTCTATCT TTCTCTAGCT TTTCCTATCC TGAGAATGAG  720
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ACTTAGTGAT CAGCTCCCTA AAACCATGCC TAAGTACAGG CGGATTAGCT ATCTTCCAAC 1920
AATGCTGACC ACCAGACAAT TACTGCATTT TTCCAGAAGC CCACTATTGC CTTTGTAGTG 1980
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GGCACCTCAT TAAGATGCTG GGCAGCAGTA TAACAGGAGG AAGAGATCCC TCTCCTTTGG 2100
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ACTTTCCCAG TGACTTCCCC TAGCCCTGAC CCAGGCACTA GGCCTTGGTG ACTTCCTGGG 2460
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CACTGTTATA CCCGGGGCAC TCTAACCATC ACAATCAATC AATCAAATTC CCTTAAATTT 2640
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GAGTCACAGA TTTCTGTGGG ACTGTGGATC TCACTGGAAG CTATCCAAGA GCCCACTGTC 2820
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CTCTGCTGGC ACACCAGTGG CAAGGCCCAG AATGGCGACC TCTCTTTAGC TCAATTTCTG 2940
GGCCTGAGGT GCTCAGACTG CCCCCAAGAT CAAATCTCTC CTGGCTGTAG TAACCCAGTG 3000
GAATGAATTT GGACATGCCC CAATGCTTCT ATATGCTAAG TGAAATCTGT GTCTGTAATT 3060
TGTTGGGGGG TGGATAGGGT GGGGTCTCCA TCTACTTTTT GTCACCATCA TCTGAAATGG 3120
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Seq ID NO: C197 DNA Sequence
Nucleic Acid Accession #: NM_021984.1
Coding sequence: 572..1753

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AATGGATTCT CACTCTTGCC CTCTATCTTT CTCTAGCTTT TCCTATCCTG AGAATGAGAT  900
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CCTGATCTAC AACCAGACAA AAGCCCATGC TTCTCCTAAA CTCCGCCATC CTCGTATCAA   1380
TAGCCGTGCC CATGCCCGTA CCCGTGCACG TTCCCGAGCC TGTGCCCGCC AACATCAGGA   1440
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GCTGGCCTGC TGTGAGTGGT GCAAGCGTTT TAAGAAGTAC TTCTGCATGG TCCCCGATTG   1620
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AAATATGTAA ATAAATATAT CAGCAAAGC                                     3329
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Seq ID NO: C198 DNA Sequence
Nucleic Acid Accession #: NM_021987.1
Coding sequence: 572..1657

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CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG   180
GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCCTTTGT   240
CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC   300
TCAGACTGAA TCAAAGAATG AAGCCTCTTC CCGTGATGTT GTCTATGGCC CCCAGCCCCA   360
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG   420
CAGAGTTGGC AAACTGCCAG AAGCCTCTCG CATCCTGAAC ACTATCCTGA GTAATTATGA   480
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CAACAGCCTT GGTCCTCTCT CTATCCTAGA CATGGAATAC ACCATTGACA TCATCTTCTC   600
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GTACTTCTGC ATGGTCCCCG ATTGTGAGGG CAGTACCTGG CAGCAGGGCC GCCTCTGCAT   1560
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CAATGTGCTC TACTGGCTTG TTTGCCTTAA CTTGTAGGTA CCAGCTGGTA CCCTGTGGGG   1680
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GACTAGTTGC TTGCCTATAC CTGGCACCTC ATTAAGATGC TGGGCAGCAG TATAACAGGA   2160
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CCTTTCTCTG CAGATAGATA GACACTGGCA TTATCCCTTT AGGAAGAGGG GGGGGCAGCA 2280
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GTGAAATCTG TGTCTGTAAT TTGTTGGGGG GTGGATAGGG TGGGGTCTCC ATCTACTTTT 3180
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Seq ID NO: C199 DNA Sequence
Nucleic Acid Accession #: NM_021990.1
Coding sequence: 1309..2490

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CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGT GAGTTTCATA 300
CCTTGGCAGA TGGCCTTTAA CATTTTTGTT TAATTCAATT ATTCTTACTA ATCTTCTTCT 360
TTTTCTTGGC TGTGGTGCAT GGCTGTGGAG CTCAGGGTGG ACTCCTGTTG GGCAGCCAGT 420
TCCTGGATGG CTGTCTGTGG GTGGAGGACT CCTGCCTTTC CTGTTTAGAC ACCCACAAAG 480
GCTGCTCTTT AGCCTCCTTC CCTTCATCCC CTTCCCCTGC CCCCAGTGCA ACGAGTATTA 540
CACAACCAAC AAAACCGCAA AATATTCCCA CAATTTTCTG GTCCTCTCTG GGAGAGGCCG 600
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TCAGGCTGAC TAGAGGCCAA GGCGACCAAC ACTAGGCAAA CGCGGCCAGC GCTCAGACAT 720
AAATGCCCTC TTCATTTCAC GTGTAACATT CTTTTAAAAT CTAGGTCTTG GTTTTGTTGA 780
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CAGCAAGGTT TTAAAGAAAT TCACAAGCCT AATCTGTCAC TGTCTTATAA TTTGCTATTA 900
CCAGTCACAA TTTAACTAGG TTTTGTGTTG AAAACTTGTT TTGGTTTGCT TCTGTCCCAA 960
GAGGCACTAG CTGGGGCCCC TACAGAGTGC AGGGCAGAGC TTCATTTTTC GTTTGAATGT 1020
TCTAGGGTCG AGGGACCTCA GACTGAATCA AAGAATGAAG CCTCTTCCCG TGATGTTGTC 1080
TATGGCCCCC AGCCCCAGCC TCTGGAAAAT CAGCTCCTCT CTGAGGAAAC AAAGTCAACT 1140
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ATCCTGAGTA ATTATGACCA CAAACTGCGC CCTGGCATTG GAGAGAAGCC CACTGTGGTC 1260
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ATTGACATCA TCTTCTCCCA GACCTGGTAC GACGAACGCC TCTGTTACAA CGACACCTTT 1380
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AGGAATTCTA AGAGGACCCA CGAGCATGAG ATCACCATGC CCAACCAGAT GGTCCGCATC 1500
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ACAACCCCAG TTGGTGACTT CATGGTCATG ACGATTTTCT TCAATGTGAG CAGGCGGTTT 1800
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TAGCTATCTT CCAACAATGC TGACCACCAG ACAATTACTG CATTTTTCCA GAAGCCCACT 2880
ATTGCCTTTG CAGTGCTTTC GGCCCAGTTC TGGCCTCAGC CTCAAAGTGC ACCGACTAGT 2940
TGCTTGCCTA TACCTGGCAC CTCATTAAGA TGCTGGGCAG CAGTATAACA GGAGGAAGAG 3000
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CTATTTGGGA CAGCATTCCT CTCTCTCTGC TGCTGTGACA TCTCCCTCTC CTTGCTGGCT 3180
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CCCATAAACC AGTCCACTGT TATACCCGGG GCACTCTAAC CATCACAATC AATCAATCAA 3540
ATTCCCTTAA ATTTGTATGG CACTGGAACT TTGGCAAAGC ACTTTTGACA AGTTGTGTCT 3600

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Seq ID NO: C200 DNA Sequence
Nucleic Acid Accession #: NM_021819.1
Coding sequence: 39..1619

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GGGCTGGAAT ACCCTTCTGG AGCCATCATG GAGACGCCAT CCTGGGCCTG GAGGAAGTGC  240
GGCTGACGCC ATCCATGAGG AACCGGAGTG GCGCCGTGTG GAGCAGGGCC TCTGTCCCCT  300
TCTCTGCCTG GGAAGTAGAG GTGCAAATGA GGGTGACGGG ACTGGGGCGC CGGGGAGCCC  360
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GTCCTGCCAT CCGTGTGCTG GCCAGCGACG GGCACATCCC CTCTGAGCAG CCTGGGGATG  540
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GAGCACGGAT CACCTACTGG GGGCAGAGGC TGCGCATGTC CTTGAACAGT GGCCTCACTC  660
CCAGTGATCC AGGTGAGTTC TGTGTGGATG TGGGGCCCCT GCTTTTGGTC CCTGGAGGTT  720
TCTTTGGGGT CTCAGCAGCC ACCGGCACCC TGGCAGATGA TCATGATGTC CTGTCCTTCC  780
TGACCTTCAG CCTGAGTGAG CCCAGCCCAG AGGTTCCCCC TCAGCCCTTC CTGGAGATGC  840
AGCAGCTCCG CCTGGCGAGG CAGCTGGAAG GGCTGTGGGC AAGGCTGGGC TTGGGCACCA  900
GGGAGGATGT AACTCCAAAA TCAGACTCTG AAGCTCAAGG AGAAGGGGAA AGGCTCTTTG  960
ACCTGGAGGA GACGCTGGGC AGACACCGCC GGATCCTGCA GGCTCTGCGG GGTCTCTCCA 1020
AGCAGCTGGC CCAGGCTGAG AGACAATGGA AGAAGCAGCT GGGGCCCCCA GGCCAAGCCA 1080
GGCCTGACGG AGGCTGGGCC CTGGATGCTT CCTGCCAGAT TCCATCCACC CCAGGGAGGG 1140
GTGGCCACCT CTCCATGTCA CTCAATAAGG ACTCTGCCAA GGTCGGTGCC CTGCTCCATG 1200
GACAGTGGAC TCTGCTCCAG GCCCTGCAAG AGATGAGGGA TGCAGCTGTC CGCATGGCTG 1260
CAGAAGCCCA GGTCTCCTAC CTGCCTGTGG GCATTGAGCA TCATTTCTTA GAGCTGGACC 1320
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CCCGCCCACC TGGCCAGCCC CCAAGGGCCT CCTCGTGCCT GCAGCCTGGC ATCTTCCTGT 1440
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TCAGTATCCT CTCCGTCTGG GTGCCCAGCT CCCACGCACA CCTGAGCTTT CGGCATGCTC 1740
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Seq ID NO: C201 DNA Sequence
Nucleic Acid Accession #: XM_117036.1
Coding sequence: 25..495

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GGCCCGTGGG GGCTGTTCCG ACCACACAGG TGCCCGAGGG AGGCAGGGCA GGCCCCGGTG  240
GGACCCAGCC CCGAAACGCA GGGTGTCGCC CACGTTTGCA GCCGCGCTCG CGTGTCGGTG  300
GATGAGCGGG AACCGGGGGG CGGCGCCTAC GCAATGCACG TTACGCCGCG GTGGAAGGGG  360
TGTCACCGCC ACAGCGGCCG CACCGTGCGT GGCTCTGTTT CCTGGAAACG TCCAGAACAG  420
GCAGCCCCCG AGACAGGGAG GGGCCCAGCG GTCGCCAGGG GAAGTGGGGA TGGGAATGAG  480
TGCGGATGGG GCTGAGGTTC TTCCTGAAGG ATGAATGCTC TGAAACTGTG AATAGACACA  540
CGGAACTGTG CACGTTCACN GGTGAACCGT GTGGGGAGTG AATCCATCTC AACAGAGCTG  600
TTACACAGTG AACAAGAGCA CGANGGGTGG AGGCCNCTTG TCTGCTCCTG CAGATCGAGC  660
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Seq ID NO: C202 DNA Sequence
Nucleic Acid Accession #: XM_167803.2
Coding sequence: 1162..1488

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GAGGGCAGCG ACCCCGAGGC CTCGTGGACG TGGGAGAGAG TGTGGTGGGA AGTCTTGAGC  240
GGAGGAGGGG ATCTGCCCTT CTCCACTCCT CTCTTGGATC CGCCTCGGTT TCCTGTCCCC  300
CCACCACCCG CCTGCCCCGC GGAAGACCGC CCAGTGAGCC AGCCCCCACC TTCCAGGCGC  360
CTTCGCCCTG GGGATCCAAC CAACTTGTAT CGAGTGGGCG GGGCAACGGC TCCCCATTTT  420
TCCCGAGCCC CGCCCACAGA GCTCTTAGCC AATCCTATGC AGAGAGCATC TCCTGGCAGG  480
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CGCCCCACCA CCACCACGTG CAGGTGGAGC TCTGGGATGC TATGTTGGGG CGGCAAGCGG  600
TGGGCCGAGG GCCGGGTAGG CTAGCACGGG AGGTAAGGGT GGTATGGGAT GGGGCGGGGG  660
CGGTCTAGGG CAATAGGAGA GCAGAGAATG GGGGAACTTG AGGGTGGGGG GAGGGCACCG  720
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GAGCCTTGCC ACCATCCCAG GACTTTGGGC AAGTCACCCG CACTCCCTGG GCCTCGGTTT   780
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CACCATCACC TGACCTGGGG GTCAAGGCAG GAGGACTCCG AAGGTGCTAC CCGTGAGCAA   900
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GGCTTCGTCT GCCATCTTTG TGGGTGCCCT AGACTTAGTC CTTATCTTGT CCTGGTTTCC  1080
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ACAAAATTTT TCCACCACAC ATACCCTCTA AGCCAGCAAG ATTTCCTCTT TGCAAAATCA  1440
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Seq ID NO: C203 DNA Sequence
Nucleic Acid Accession #: NM_024780.1
Coding sequence: 31..1023

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ACCCTCATTG GCCAGGACAT CTACCGGCTC CTTCTGATGG ATTTTGTGTT CTCTTTAGTC  240
AATTCCTTCC TGGGGGAGTT TCTGAGGAGA ATCATTGGGA TGCAACTGAT CACAAGTCTT  300
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AAAATGTTCC TGATAGAAAA ATTGATCAAG CTGCAGGATA TGGAGAAGAA AGCAAACCCC  900
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CATGATGGCA GTCTTGACTT GCGATCTAGA AGATCAGTTC AAGAAGGTAA TCCAAGGGCC 1020
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ATTTCTTCCA TGCCACCTGT GCCTTTAGGA ACTGCCCAGA AGAAAATCCA AGGCTTTAGC 1140
CAGGAGCGGA AACTGACTAC CATGTAATTA TCAAAGTAAA ATTGGGCATT CCATGCTATT 1200
TTTAATACCT GGATTGCTGA TTTTTCAAGA CAAAATACTT GGGGTTTTCC AATAAAGATT 1260
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ACTTTGAACT AAAGACATCC CCCATGTCCC AAAGGTGGAA TACAACCAGA GGTCTCATCT 1560
CTGAACTTTC TTGCGTACTG ATTACATGAG TCTTTGGAGT CGGGGATGGA GGAGGTTCTG 1620
CCCCTGTGAG GTGTTATACA TGACCATCAA AGTCCTACGT CAAGCTAGCT TTGCAGTGGC 1680
AGTACCGTAG CCAATGAGAT TTATCCGAGA CGCGATTATT GCTAATTGGA AATTTTCCCA 1740
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GAGACTGAAT AAG                                                     1813
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Seq ID NO: C204 Protein Sequence
Protein Accession #: Eos sequence

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CCCTGCGAGT CCCAATCAAT GCGGGTGTGA CTGCTGTATG AAGTCTCAGG AAGCCCACCC  180
CAGTGGAGAA GAAGGCTTGC AGGAGGCAGG AGATGCTGTC CGATGACCAC GTGAATGAAA  240
TCATCATACA GGTTGAGAAT GTTTCCTCTG GGGTCCAAAG CCACCCATCC TCAAATCAGA  300
TTTTTCAAGA AAAGGTGCTG CTAGACTCAA GCATCAACAT GGTTTTGTCA ATATCTGACA  360
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CCCTTATACC CATGACATCC AGAGACAGAA TTAAAGCCAT CAGGAACCAG CCAAGGACCA  600
TGGAAGAGAA AAGGAACCTT AGGAAAATAG TTGACAAAGA AAAAAGCAAA CAGACCCATC  660
GTATCCTTCA GCTCAATTGC TGTATTCAGT GTCTGAACTC CATTTCCCGG GCTTATCGGA  720
GATCCAAGAA CAGCCTGTCG GAAATTCTGA ATTCCATCAG CCTGTGGCAG AAGACGCTGA  780
AGATCATTGG AGGCAAGTTT GGAACCAGCG TCCTCTCCTA TTTCAACTTT CTGAGATGGC  840
TTTTGAAGTT CAACATTTTC TCATTCATCC TGAACTTCAG CTTCATCATA ATCCCTCAGT  900
TTACCGTGGC CAAAAAGAAC ACCCTCCAGT TCACTGGGCT GGAGTTTTTC ACTGGGGTGG  960
GTTATTTTAG GGACACAGTG ATGTACTATG GCTTTTACAC CAATTCCACC ATCCAGCACG 1020
GGAACAGCGG GGCATCCTAC AACATGCAGC TGGCCTACAT CTTCACAATC GGAGCATGCT 1080
TGACCACCTG CTTCTTCAGT TTGCTGTTCA GCATGGCCAA GTATTTCCGG AACAACTTCA 1140
TTAATCCCCA CATTTACTCC GGAGGGATCA CCAAGCTGAT CTTTTGCTGG GACTTCACTG 1200
TCACTCATGA AAAAGCTGTG AAGCTAAAAC AGAAGAATCT TAGCACTGAG ATAAGGGAGA 1260
ACCTGTCAGA GCTCCGTCAG GAGAATTCCA AGTTGACGTT CAATCAGCTG CTGACCCGCT 1320
TCTCTGCCTA CATGGTAGCC TGGGTTGTCT CTACAGGAGT GGCCATAGCC TGCTGTGCAG 1380
CCGTTTATTA CCTGGCTGAG TACAACTTAG AGTTCCTGAA GACACACAGT AACCCTGGGG 1440
CGGTGCTGTT ACTGCCTTTC GTTGTGTCCT GCATTAATCT GGCCGTGCCA TGCATCTACT 1500
CCATGTTCAG GCTTGTGGAG AGGTACGAGA TGCCACGGCA CGAAGTCTAC GTTCTCCTGA 1560
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TCCGAAACAT CTTTTTGAAA ATATCAATCA TTGGCATTCT TTGTTACTAT TGGCTCAACA   1620
CCGTGGCCCT GTCTGGTGAA GAGTGTTGGG AAACCCTCAT TGGCCAGGAC ATCTACCGGC   1680
TCCTTCTGAT GGATTTTGTG TTCTCTTTAG TCAATTCCTT CCTGGGGGAG TTTCTGAGGA   1740
GAATCATTGG GATGCAACTG ATCACAAGTC TTGGCCTTCA GGAGTTTGAC ATTGCCAGGA   1800
ACGTTCTAGA ACTGATCTAT GCACAAACTC TGGTGTGGAT TGGCATCTTC TTCTGCCCCC   1860
TGCTGCCCTT TATCCAAATG ATTATGCTTT TCATCATGTT CTACTCCAAA AATATCAGCC   1920
TGATGATGAA TTTCCAGCCT CCGAGCAAAG CCTGGCGGGC CTCACAGATG ATGACTTTCT   1980
TCATCTTCTT GCTCTTTTTC CCATCCTTCA CCGGGGTCTT GTGCACCCTG GCCATCACCA   2040
TCTGGAGATT GAAGCCTTCA GCTGACTGTG GCCCTTTTCG AGGTCTGCCT CTCTTCATTC   2100
ACTCCATCTA CAGCTGGATC GACACCCTAA GTACACGGCC TGGCTACCTG TGGGTTGTTT   2160
GGATCTATCG GAACCTCATT GGAAGTGTGC ACTTCTTTTT CATCCTCACC CTCATTGTGC   2220
TAATCATCAC CTATCTTTAC TGGCAGATCA CAGAGGGAAG GAAGATTATG ATAAGGCTGC   2280
TCCATGAGCA GATCATTAAT GAGGGCAAAG ATAAAATGTT CCTGATAGAA AAATTGATCA   2340
AGCTGCAGGA TATGGAGAAG AAAGCAAACC CCAGCTCACT TGTTCTGGAA AGGAGAGAGG   2400
TGGAGCAACA AGGCTTTTTG CATTTGGGGG AACATGATGG CAGTCTTGAC TTGCGATCTA   2460
GAAGATCAGT TCAAGAAGGT AATCCAAGGG CCTGATGACT CTTTTGGTAA CCAGACACCA   2520
ATCAAATAAG GGGAGGAGAY GAAAATGGAA TGATTTCTTC CATGCCACCT GTGCCTTTAG   2580
GAACTGCCCA GAAGAAAATC CAAGGCTTTA GCCAGGAGCG GAAACTGACT ACCATGTAAT   2640
TATCAAAGTA AAATTGGGCA TTCCATGCTA TTTTTAATAC CTGGATTGCT GATTTTTCAA   2700
GACAAAATAC TTGGGGTTTT CCAATAAAGA TTGTTGTAAT ATTGAAAWRA RMMWAMAAAA   2760
ACCTAGGAAG AGATAACTAG GGAATAATGT ATATTATCTT CAAGAAGTGT GTGCAGGAAT   2820
GATTGGTTCT TAGAAATCTC TCCTGCCAGA CTTCCCAGAC CTGGCAAAGG TTTAGAAACT   2880
GTTGCTAAGA AAAGTGGTCC ATCCTGAATA AACATGTAAT ACTCCAGCAG GGATATGAAG   2940
CCTCTGAATT GTAGAACCTG CATTTATTTG TGACTTTGAA CTAAAGACAT CCCCCATGTC   3000
CCAAAGGTGG AATACAACCA GAGGTCTCAT CTCTGAACTT TCTTGCGTAC TGATTACATG   3060
AGTCTTTGGA GTCGGGGATG GAGGAGGTTC TGCCCCTGTG AGGTGTTATA CATGACCATC   3120
AAAGTCCTAC GTCAAGCTAG CTTTGCAGTG GCAGTACCGT AGCCAATGAG ATTTATCCGA   3180
GACGCGATTA TTGCTAATTG GAAATTTTCC CAATACCCCA CCGTGATGAC TTGAAATATA   3240
ATCAGCGCTG GCAATTTTTG ACAGTCTCTA CGGAGACTGA ATAAG                   3285
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Seq ID NO: C205 DNA Sequence
Nucleic Acid Accession #: NM_002250.1
Coding sequence: 397..1680

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1          11         21         31         41         51
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GTCCTTCGGT GTCTGGGTGT GGTGAGTAGA GGTGTGTGTC ACAAAGTACA GACCATTGTG   60
TGTGACAAAG CCCATCGTGT GTCTGTGTGT GTCTTTATCC ACGTGGATGG ACGTCTCTTT  120
CTTGCTCTGC CCCAAGACAC ACCCTAGCCC CTCCTTATTC TCAAAAGGGG GAGCTGGGGA  180
GCCTCCCCCT ACCCTGGGGC CTCCCCTGCC CCTCCCCGCC CTGCCTGGCC GTCACCACTC  240
CCCAGAGGGC ACAGGGCTCT GCTGTGCCTC AGAGCAAAAG TCCCAGAGCC AGCAGAGCAG  300
GCTGACGACC TGCAAGCCAC AGTGGCTGCC CTGTGCGTGC TGCGAGGTGG GGGACCCTGG  360
GCAGGAAGCT GGCTGAGCCC CAAGACCCCG GGGGCCATGG GCGGGGATCT GGTGCTTGGC  420
CTGGGGGCCT TGAGACGCCG AAAGCGCTTG CTGGAGCAGG AGAAGTCTCT GGCCGGCTGG  480
GCACTGGTGC TGGCAGGAAC TGGCATTGGA CTCATGGTGC TGCATGCAGA GATGCTGTGG  540
TTCGGGGGGT GCTCGTGGGC GCTCTACCTG TTCCTGGTTA AATGCACGAT CAGCATTTCC  600
ACCTTCTTAC TCCTCTGCCT CATCGTGGCC TTTCATGCCA AAGAGGTCCA GCTGTTCATG  660
ACCGACAACG GGCTGCGGGA CTGGCGCGTG GCGCTGACCG GGCGGCAGGC GGCGCAGATC  720
GTGCTGGAGC TGGTGGTGTG TGGGCTGCAC CCGGCGCCCG TGCGGGGCCC GCCGTGCGTG  780
CAGGATTTAG GGGCGCCGCT GACCTCCCCG CAGCCCTGGC CGGGATTCCT GGGCCAAGGG  840
GAAGCGCTGC TGTCCCTGGC CATGCTGCTG CGTCTCTACC TGGTGCCCCG CGCCGTGCTC  900
CTGCGCAGCG GCGTCCTGCT CAACGCTTCC TACCGCAGCA TCGGCGCTCT CAATCAAGTC  960
CGCTTCCGCC ACTGGTTCGT GGCCAAGCTT TACATGAACA CGCACCCTGG CCGCCTGCTG 1020
CTCGGCCTCA CGCTTGGCCT CTGGCTGACC ACCGCCTGGG TGCTGTCCGT GGCCGAGAGG 1080
CAGGCTGTTA ATGCCACTGG GCACCTTTCA GACACACTTT GGCTGATCCC CATCACATTC 1140
CTGACCATCG GCTATGGTGA CGTGGTGCCG GGCACCATGT GGGGCAAGAT CGTCTGCCTG 1200
TGCACTGGAG TCATGGGTGT CTGCTGCACA GCCCTGCTGG TGGCCGTGGT GGCCCGGAAG 1260
CTGGAGTTTA ACAAGGCAGA GAAGCACGTG CACAACTTCA TGATGGATAT CCAGTATACC 1320
AAAGAGATGA AGGAGTCCGC TGCCCGAGTG CTACAAGAAG CCTGGATGTT CTACAAACAT 1380
ACTCGCAGGA AGGAGTCTCA TGCTGCCCGC AGGCATCAGC GCAAGCTGCT GGCCGCCATC 1440
AACGCGTTCC GCCAGGTGCG GCTGAAACAC CGGAAGCTCC GGGAACAAGT GAACTCCATG 1500
GTGGACATCT CCAAGATGCA CATGATCCTG TATGACCTGC AGCAGAATCT GAGCAGCTCA 1560
CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CCTGACTGAG 1620
CTGCTTAGCA CTGCCCTGGG GCCGAGGCAG CTTCCAGAAC CCAGCCAGCA GTCCAAGTAG 1680
CTGGACCCAC GAGGAGGAAC CAGGCTACTT TCCCCAGTAC TGAGGTGGTG GACATCGTCT 1740
CTGCCACTCC TGACCCAGCC CTGAACAAAG CACCTCAAGT GCAAGGACCA AAGGGGGCCC 1800
TGGCTTGGAG TGGGTTGGCT TGCTGATGGC TGCTGGAGGG GACGCTGGCT AAAGTGGGTA 1860
GGCCTTGGCC CACCTGAGGC CCCAGGTGGG AACATGGTCA CCCCCACTCT GCATACCCTC 1920
ATCAAAAACA CTCTCACTAT GCTGCTATGG ACGACCTCCA GCTCTCAGTT ACAAGTGCAG 1980
GCGACTGGAG GCAGGACTCC TGGGTCCCTG GGAAAGAGGG TACTAGGGGC CCGGATCCAG 2040
GATTCTGGGA GGCTTCAGTT ACCGCTGGCC GAGCTGAAGA ACTGGGTATG AGGCTGGGGC 2100
GGGGCTGGAG GTGGCGCCCC CTGGTGGGAC AACAAAGAGG ACACCATTTT TCCAGAGCTG 2160
CAGAGAGCAC CTGGTGGGGA GGAAGAAGTG TAACTCACCA GCCTCTGCTC TTATCTTTGT 2220
AATAAATGTT AAAGCCAG                                               2238
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Seq ID NO: C206 DNA Sequence
Nucleic Acid Accession #: NM_025257.1
Coding sequence: 1..2139

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ATGGGGGGAA AGCAGCGGGA CGAGGATGAC GAGGCCTACG GGAAGCCAGT CAAATACGAC   60
CCCTCCTTTC GAGGCCCCAT CAAGAACAGA AGCTGCACAG ATGTCATCTG CTGCGTCCTC  120
TTCCTGCTCT TCATTCTAGG TTACATCGTG GTGGGGATTG TGGCCTGGTT GTATGGAGAC  180
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CCCCGGCAAG TCCTCTACCC CAGGAACTCT ACTGGGGCCT ACTGTGGCAT GGGGGAGAAC   240
AAAGATAAGC CGTATCTCCT GTACTTCAAC ATCTTCAGCT GCATCCTGTC CAGCAACATC   300
ATCTCAGTTG CTGAGAACGG CCTACAGTGC CCCACACCCC AGGTGTGTGT GTCCTCCTGC   360
CCGGAGGACC CATGGACTGT GGGAAAAAAC GAGTTCTCAC AGACTGTTGG GGAAGTCTTC   420
TATACAAAAA ACAGGAACTT TTGTCTGCCA GGGGTACCCT GGAATATGAC GGTGATCACA   480
AGCCTGCAAC AGGAACTCTG CCCCAGTTTC CTCCTCCCCT CTGCTCCAGC TCTGGGACGC   540
TGCTTTCCAT GGACCAACAT TACTCCACCG GCGCTCCCAG GGATCACCAA TGACACCACC   600
ATACAGCAGG GGATCAGCGG TCTTATTGAC AGCCTCAATG CCCGAGACAT CAGTGTTAAG   660
ATCTTTGAAG ATTTTGCCCA GTCCTGGTAT TGGATTCTTG TTGCCCTGGG GGTGGCTCTG   720
GTCTTGAGCC TACTGTTTAT CTTGCTTCTG CGCCTGGTGG CTGGGCCCCT GGTGCTGGTG   780
CTGATCCTGG GAGTGCTGGG CGTGCTGGCA TATGGCATCT ACTACTGCTG GGAGGAGTAC   840
CGAGTGCTGC GGGACAAGGG CGCCTCCATC TCCCAGCTGG GTTTCACCAC CAACCTCAGT   900
GCCTACCAGA GCGTGCAGGA CACCTGGCTG GCCGCCCTGA TCGTGTTGGC GGTGCTTGAA   960
GCCATCCTGC TGCTGGTGCT CATCTTCCTG CGGCAGCGGA TTCGTATTGC CATCGCCCTC  1020
CTGAAGGAGG CCAGCAAGGC TGTGGGACAG ATGATGTCTA CCATGTTCTA CCCACTGGTC  1080
ACCTTTGTCC TCCTCCTCAT CTGCATTGCC TACTGGGCCA TGACTGCTCT GTATCCTCTG  1140
CCCACGCAGC CAGCCACTCT TGGATATGTG CTCTGGGCAT CCAACATCAG CTCCCCCGGC  1200
TGTGAGAAAG TGCCAATAAA TACATCATGC AACCCCACGG CCCACCTTGT GAACTCCTCG  1260
TGCCCAGGGC TGATGTGCGT CTTCCAGGGC TACTCATCCA AAGGCCTAAT CCAACGTTCT  1320
GTCTTCAATC TGCAAATCTA TGGGGTCCTG GGGCTCTTCT GGACCCTTAA CTGGGTACTG  1380
GCCCTGGGCC AATGCGTCCT CGCTGGAGCC TTTGCCTCCT TCTACTGGGC CTTCCACAAG  1440
CCCCAGGACA TCCCTACCTT CCCCTTAATC TCTGCCTTCA TCCGCACACT CCGTTACCAC  1500
ACTGGGTCAT TGGCATTTGG AGCCCTCATC CTGACCCTTG TGCAGATAGC CCGGGTCATC  1560
TTGGAGTATA TTGACCACAA GCTCAGAGGA GTGCAGAACC CTGTAGCCCG CTGCATCATG  1620
TGCTGTTTCA AGTGCTGCCT CTGGTGTCTG GAAAAATTTA TCAAGTTCCT AAACCGCAAT  1680
GCATACATCA TGATCGCCAT CTACGGGAAG AATTTCTGTG TCTCAGCCAA AAATGCGTTC  1740
ATGCTACTCA TGCGAAACAT TGTCAGGGTG GTCGTCCTGG ACAAAGTCAC AGACCTGCTG  1800
CTGTTCTTTG GGAAGCTGCT GGTGGTCGGA GGCGTGGGGG TCCTGTCCTT CTTTTTTTTC  1860
TCCGGTCGCA TCCCGGGGCT GGGTAAAGAC TTTAAGAGCC CCCACCTCAA CTATTACTGG  1920
CTGCCCATCA TGACCTCCAT CCTGGGGGCC TATGTCATCG CCAGCGGCTT CTTCAGCGTT  1980
TTCGGCATGT GTGTGGACAC GCTCTTCCTC TGCTTCCTGG AAGACCTGGA GCGGAACAAC  2040
GGCTCCCTGG ACCGGCCCTA CTACATGTCC AAGAGCCTTC TAAAGATTCT GGGCAAGAAG  2100
AACGAGGCGC CCCCGGACAA CAAGAAGAGG AAGAAGTGAC AGCTCCGGCC CTGATCCAGG  2160
ACTGCACCCC ACCCCCACCG TCCAGCCATC CAACCTCACT TCGCCTTACA GGTCTCCATT  2220
TTGTGGTAAA AAAAGGTTTT AGGCCAGGCG CCGTGGCTCA CGCCTGTAAT CCAACACTTT  2280
GAGAGGCTGA GGCGGGCGGA TCACCTGAGT CAGGAGTTCG AGACCAGCCT GGCCAACATG  2340
GTGAAAC                                                            2347
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Seq ID NO: C207 DNA Sequence
Nucleic Acid Accession #: NM_016180.1
Coding sequence: 26..1618

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CAGGAAGGTT CCTCTCCCAG TGGCCATGGG TAGCAACAGT GGGCAGGCTG GCCGCCACAT   60
CTATAAATCC CTAGCTGATG ATGGCCCCTT TGACTCTGTG GAGCCGCCTA AAAGACCCAC  120
CAGCAGACTC ATCATGCACA GCATGGCCAT GTTCGGAAGA GAGTTCTGCT ACGCGGTGGA  180
GGCAGCGTAT GTGACCCCAG TCCTGCTCAG CGTAGGTCTG CCCAGCAGCC TGTACAGCAT  240
TGTGTGGTTC CTCAGCCCCA TCCTGGGATT CCTGCTGCAG CCCGTGGTCG GATCGGCCAG  300
CGACCACTGC CGGTCCAGGT GGGGCCGCCG GAGACCCTAC ATCCTCACCC TGGGAGTCAT  360
GATGCTCGTG GGCATGGCTC TGTACCTCAA TGGGGCTACT GTTGTAGCAG CTTTGATTGC  420
TAACCCAAGG AGGAAGCTGG TTTGGGCCAT AAGTGTCACC ATGATAGGTG TCGTTCTCTT  480
TGATTTTGCT GCCGACTTCA TTGATGGGCC CATCAAAGCC TACTTATTTG ATGTCTGCTC  540
CCATCAGGAC AAGGAGAAGG GCCTCCACTA CCATGCCCTC TTCACAGGTT TTGGAGGTGC  600
CCTGGGTTAC CTTTTGGGTG CTATAGACTG GGCCCATCTG GAGCTGGGAA GACTGTTGGG  660
TACAGAATTC CAGGTCATGT TCTTCTTCTC TGCATTGGTG CTCACTTTGT GTTTTACTGT  720
TCATCTGTGC AGTATCTCTG AAGCCCCACT TACAGAGGTT GCAAAGGGCA TTCCCCCACA  780
GCAAACCCCT CAGGACCCTC CATTGTCATC AGATGGAATG TACGAGTATG GTTCTATCGA  840
GAAAGTTAAA AATGGTTACG TAAATCCAGA GCTGGCAATG CAGGGAGCAA AAAACAAAAA  900
TCATGCTGAA CAGACTCGCA GGGCAATGAC ATTAAAGTCA CTGCTGAGAG CACTGGTGAA  960
CATGCCTCCT CACTACCGCT ACCTTTGCAT CAGCCACCTC ATTGGATGGA CGGCCTTCCT 1020
GTCCAACATG CTGTTCTTCA CAGATTTCAT GGGCCAGATT GTGTACCGCG GGGATCCCTA 1080
TAGTGCACAC AACTCCACAG AGTTTCTCAT CTACGAAAGA GGAGTCGAGG TTGGATGTTG 1140
GGGCTTCTGC ATCAACTCCG TGTTTTCCTC ACTTTATTCT TACTTTCAGA AAGTTTTGGT 1200
ATCCTACATT GGATTAAAGG GTCTTTACTT CACGGGATAT TTGCTGTTTG GCCTGGGGAC 1260
GGGATTTATT GGGCTCTTCC CGAATGTCTA CTCCACCCTG GTCCTGTGCA GCCTGTTTGG 1320
TGTAATGTCC AGCACCCTGT ACACTGTGCC CTTTAACCTC ATTACTGAGT ACCACCGCGA 1380
GGAAGAAAAG GAGAGGCAGC AGGCCCCAGG AGGGGACCCA GACAACAGCG TGAGAGGGAA 1440
GGGCATGGAC TGCGCCACCC TCACATGCAT GGTGCAGCTG GCTCAGATCC TGGTCGGAGG 1500
TGGCCTGGGC TTTCTGGTCA ACACAGCCGG GACCGTTGTC GTCGTGGTGA TCACAGCGTC 1560
TGCGGTGGCA CTGATAGGCT GTTGCTTTGT CGCTCTCTTT GTTAGATATG TGGATTAGGT 1620
CAATAAAGAG ACAATGACCC TAAAAAAAAA                                   1650
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Seq ID NO: C208 DNA Sequence
Nucleic Acid Accession #: NM_003273.1
Coding sequence: 255..2024

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TGTTTCCTTG ACTGACTATT GTGAGCGCCC TCTCTCTCCG GCGGAGCGGA GACCATGGCC  120
CCCACTCAGG CCCCCGGGCC CCGCTGGAAT TCGGAGGGCC CCTGGGTAAT GGGGCAGAGA  180
GATGGGACCT GGGGCAAAGG CTAAGCGAAG GAGAGCTGGA GCGGGTGAAC TAAGAGCGGG  240
GGCGAGATCT GAGGATGGAA GGCTTTGGGG GTGTCGGAGG CAGAGGGACC CGGGGGTTTG  300
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CAGCGAAGGG TGTCTGGAGA GGGAGAGCTG AGGAGGGGCC GGTTCTGGGG GCTGCAGAAC   360
GGGGATTTAT GGTGTCGACT GGGAGCAGGA GGAGGGTCTT CGAGGGGCCT GGGGGCGGGG   420
GACTAAGATG GACGCCTGGG AAGGGAACTG GGAGGCAGCG GGGTGCCTGG GGGCCGAGGG   480
CTGAGGACGG GGTGCCGAGG CGCACTCTGG GAATGCCGAG AGGGTCCCGC AGAGACGTCA   540
GGGCGCCGTG CGGGCCGGCG GGGAGCTGGG GGGCTAGGGG CGGACGCCGA CGTGATGGCC   600
CTTCCCGCAG GCGCCGCGGC TCTGCTACTG CTGCTGCCCG CCACCATGTT CCACCTGCTC   660
CTGGCGGCCC GTTCGGGCCC CGCGCGCCTG CTGGGTCCAC CCGCGTCCCT GCCCGGGCTG   720
GAGGTGCTGT GGAGCCCACG GGCGCTGCTG CTGTGGCTCG CCTGGCTCGG CCTGCAGGCG   780
GCGCTCTACC TACTGCCGGC GCGCAAGGTG CGGGCCCCGC TCGCGGACGC TCGGGGGAGG   840
GAAGCGAATG GGCTCGGCGA GGGAAAGGAC GCCCCGGGCC TTATCAGAGC CCCCTTGGAC   900
CCGCAGTGGC CGAGGGGCAG GAATTGAAGG ACAAGAGTCG CCTGCGCTAT CCTATTAACG   960
GCTTCCAGGC CCTGGTGCTG ACAGCCCTGT TGGTGGGGCT GGGGATGTCA GCGGGGCTGC  1020
CTCTGGGGGC GCTCCCGGAA ATGCTCCTGC CCTTGGCGTT TGTCGCCACC CTCACCGCTT  1080
TCATCTTCAG CCTCTTTCTC TACATGAAGG CGCAGGTAGC CCCAGTTTCG GCCCTGGCAC  1140
CTGGGGGGAA CTCAGGCAAT CCGATTTACG ACTTTTTTCT GGGACGAGAG CTCAACCCTC  1200
GTATCTGTTT CTTCGACTTC AAATATTTCT GTGAACTGCG ACCCGGCCTC ATCGGCTGGG  1260
TCCTCATCAA CCTGGCCCTG TTGATGAAGG AGGCAGAGCT TCGAGGCAGT CCCTCACTGG  1320
CCATGTGGCT GGTCAATGGC TTCCAGTTGC TCTACGTGGG TGATGCCCTC TGGCACGAGG  1380
AGGCCGTCCT CACCACCATG GATATCACAC ATGACGGGTT TGGCTTCATG CTGGCGTTTG  1440
GGGACATGGC CTGGGTGCCC TTCACCTACA GCCTGCAGGC CCAGTTCCTG CTGCACCACC  1500
CGCAGCCCCT GGGGTTGCCC ATGGCCTCTG TCATCTGCCT CATCAATGCT ACTGGTTACT  1560
ACATCTTCCG TGGGGCGAAT TCCCAGAAAA ACACTTTCCG AAAGAATCCT TCTGACCCCA  1620
GAGTGGCTGG GCTTGAGACC ATCTCTACAG CCACAGGGCG GAAACTGCTG GTGTCTGGGT  1680
GGTGGGGTAT GGTCCGCCAT CCCAACTATC TTGGAGACCT CATCATGGCT CTGGCTTGGT  1740
CCTTGCCCTG CGGGGTGTCA CACCTGCTGC CCTACTTCTA CCTCCTCTAC TTCACCGCGC  1800
TGCTGGTGCA CCGTGAGGCC CGGGATGAGC GGAGTGCCTG CAGAAGTACG GCCTGGCCTG  1860
GCAGGAGTAC TGCCGGCGTG TGCCTTACCG CATCATGCCC TACATCTACT GAAGCGGCTC  1920
CACCACCCCA GGTGGGGCAT GTGCCCACTC ATCCACCAGC ACACCCAGGA CCAGGAGCCT  1980
CGACACACTT GGGACTCAAG GGCTTGCACC CCACCCAGCC CTGAGGATGA ACAACCTCAG  2040
AGAAGAGGTG GTTTAGAGCA AGGAAAAAAA TGAAACCAGT GACCAAAAAA AAAAAAAAAA  2100
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Seq ID NO: C209 DNA Sequence
Nucleic Acid Accession #: NM_015720.1
Coding sequence: 21..1838

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CTGATGAGCC TGGCCCAGAG GGCCTCACCT CCACCTCCCT GCTAGACCTC CTGCTGCCCA  180
CTGGCTTGGA GCCACTGGAC TCAGAGGAGC CTAGTGAGAC CATGGGCCTG GGAGCTGGGC  240
TGGGAGCCCC TGGCTCAGGC TTCCCCAGCG AAGAGAATGA AGAGTCTCGG ATTCTGCAGC  300
CACCACAGTA CTTCTGGGAA GAGGAGGAAG AGCTGAATGA CTCAAGTCTG GACCTGGGAC  360
CCACTGCAGA TTATGTTTTT CCTGACTTAA CTGAGAAGGC AGGTTCCATT GAAGACACTA  420
GCCAGGCTCA AGAGCTGCCA AACCTCCCCT CTCCCTTGCC CAAGATGAAT CTGGTTGAGC  480
CTCCCTGGCA TATGCCTCCC AGAGAGGAGG AAGAAGAGGA AGAGGAAGAG GAGGAGAGGG  540
AGAAGGAAGA GGTAGAGAAA CAAGAGGAGG AGGAAGAGGA GGAGCTGCTC CCTGTGAATG  600
GATCCCAAGA AGAAGCCAAG CCTCAGGTCC GTGACTTTTC TCTCACCAGC AGCAGCCAGA  660
CCCCAGGGGC CACCAAAAGC AGGCATGAAG ACTCCGGGGA CCAGGCCTCA TCAGGTGTGG  720
AGGTGGAGAG CAGCATGGGG CCCAGCTTGC TGCTGCCTTC AGTCACCCCA ACTACAGTGA  780
CTCCGGGGGA CCAGGACTCC ACCAGCCAAG AGGCAGAGGC CACAGTGCTG CCAGCTGCAG  840
GGCTTGGGGT AGAGTTCGAG GCTCCTCAGG AAGCAAGCGA GGAAGCCACT GCAGGAGCAG  900
CTGGTTTGTC TGGCCAGCAC GAGGAGGTGC CGGCCTTGCC TTCATTCCCT CAAACCACAG  960
CTCCCAGTGG GGCCGAGCAC CCAGATGAAG ATCCCCTTGG CTCTAGAACC TCAGCCTCTT 1020
CCCCACTGGC CCCTGGAGAC ATGGAACTGA CACCTTCCTC TGCTACCTTG GGACAAGAAG 1080
ATCTCAACCA GCAGCTCCTA GAAGGGCAGG CAGCTGAAGC TCAATCCAGG ATACCCTGGG 1140
ATTCTACGCA GGTGATCTGC AAGGACTGGA GCAATCTGGC TGGGAAAAAC TACATCATTC 1200
TGAACATGAC AGAGAACATA GACTGTGAGG TGTTCCGGCA GCACCGGGGG CCACAGCTCC 1260
TGGCCCTGGT GGAAGAGGTG CTGCCCCGCC ATGGCAGTGG CCACCATGGG GCCTGGCACA 1320
TCTCTCTGAG CAAGCCCAGC GAGAAGGAGC AGCACCTTCT CATGACACTG GTGGGCGAGC 1380
AGGGGGTGGT GCCCACTCAA GATGTCCTTT CCATGCTGGG TGACATCCGC AGGAGCCTGG 1440
AGGAGATTGG CATCCAGAAC TATTCCACAA CCAGCAGCTG CCAGGCGCGG GCCAGCCAGG 1500
TGCGCAGCGA CTACGGCACG CTCTTCGTGG TGCTGGTGGT CATTGGGGCC ATCTGCATCA 1560
TCATCATTGC GCTTGGCCTG CTCTACAACT GCTGGCAGCG CCGGCTGCCC AAGCTCAAGC 1620
ACGTGTCGCA CGGCGAGGAG CTGCGCTTCG TGGAGAACGG CTGCCACGAC AACCCCACGC 1680
TGGACGTGGC CAGCGACAGC CAGTCGGAGA TGCAGGAGAA GCACCCCAGC CTGAACGGCG 1740
GCGGGGCCCT CAACGGCCCG GGGAGCTGGG GGGCGCTCAT GGGGGGCAAG CGGGACCCCG 1800
AGGACTCGGA CGTGTTCGAG GAGGACACGC ACCTGTGAGC GCAGCGAGGC GCAGGCCGAG 1860
TGGGCCGCCA GGACCAAGCG AGGTGGACCC CGAAACGGAC GGCCCGGAGC CCGCACCAGC 1920
CCCGCGCCTA CCCGGCCGCC CCCGCGCCTG GCCCTCGGCG CGGGCTCCTT CCCGCTTCCC 1980
CCGACTTCAC ACGGCGGCTT CGGACCAACT CCCTCACTCC CGCCCGAGGG GCAGGCCTCA 2040
AAGCCCGCCT TGGCCCCGCT TTCCCGCCCC TGAACCCCGG CCCCGCGGGC GGCGGGCGCG 2100
CTTCCTGCGC CCCGGGACTC AATTAAACCC GCCCGGAGAC CACGCGGGCC CAGCGAAAAA 2160
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2220
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAA            2269
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Seq ID NO: C210 DNA Sequence
Nucleic Acid Accession #: NM_001197.3
Coding sequence: 61..543

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GACACGAAGC CTCCCGGGTG GCTTACAGAC GCTGCCAGCA TCGCCGCCGC CAGAGGAGAA   60
ATGTCTGAAG TAAGACCCCT CTCCAGAGAC ATCTTGATGG AGACCCTCCT GTATGAGCAG  120
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CTCCTGGAAC CCCCGACCAT GGAGGTTCTT GGCATGACTG ACTCTGAAGA GGACCTGGAC   180
CCTATGGAGG ACTTCGATTC TTTGGAATGC ATGGAGGGCA GTGACGCATT GGCCCTGCGG   240
CTGGCCTGCA TCGGGGACGA GATGGACGTG AGCCTCAGGG CCCCGCGCCT GGCCCAGCTC   300
TCCGAGGTGG CCATGCACAG CCTGGGTCTG GCTTTCATCT ACGACCAGAC TGAGGACATC   360
AGGGATGTTC TTAGAAGTTT CATGGACGGT TTCACCACAC TTAAGGAGAA CATAATGAGG   420
TTCTGGAGAT CCCCGAACCC CGGGTCCTGG GTGTCCTGCG AACAGGTGCT GCTGGCGCTG   480
CTGCTGCTGC TGGCGCTGCT GCTGCCGCTG CTCAGCGGGG GCCTGCACCT GCTGCTCAAG   540
TGAGGCCCCG GCGGCTCAGG GCGGGGCTGG CCCCACCCCC ATGACCACTG CCCTGGAGGT   600
GGCGGCCTGC TGCTGTTATC TTTTTAACTG TTTTCTCATG ATGCCTTTTT ATATTTAAAC   660
CCCGAGATAG TGCTGGAACA CTGCTGAGGT TTTATACTCA GGTTTTTTGT TTTTTTTTTA   720
TTCCAGTTTT CGTTTTTTCT AAAAGATGAA TTCCTATGGC TCTGCAATTG TCACCGGTTA   780
ACTGTGGCCT GTGCCCAGGA AGAGCCATTC ACTCCTGCCC CTGCCCACAC GGCAGGTAGC   840
AGGGGGAGTG CTGGTCACAC CCCTGTGTGA TATGTGATGC CCTCGGCAAA GAATCTACTG   900
GAATAGATTC CGAGGAGCAG GAGTGCTCAA TAAAATGTTG GTTTCCAGCA AAAAAAAAAA   960
AAA                                                                963
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Seq ID NO: C211 DNA Sequence
Nucleic Acid Accession #: AF272357
Coding sequence: 83..1060

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GCCCCGGCGG CGGCGCTGAA GGATGGCGAC GCCGCTGCCT CCGCCCTCCC CGCGGCACCT   120
GCGGCTGCTG CGGCTGCTGC TCTCCGGCCT CGTCCTCGGC GCCGCCCTGC GTGGAGCCGC   180
CGCCGGCCAC CCGGATGTAG CCGCCTGTCC CGGGAGCCTG GACTGTGCCC TGAAGAGGCG   240
GGCAAGGTGT CCTCCTGGTG CACATGCCTG TGGGCCCTGC CTTCAGCCCT TCCAGGAGGA   300
CCAGCAAGGG CTCTGTGTGC CCAGGATGCG CCGGCCTCCA GGCGGGGGCC GGCCCCAGCC   360
CAGACTGGAA GATGAGATTG ACTTCCTGGC CCAGGAGCTT GCCCGGAAGG AGTCTGGACA   420
ATCAACTCCG CCCCTACCCA AGGACCGACA GCGGCTCCCG GAGCCTGCCA CCCTGGGCTT   480
CTCGGCACGG GGGCAGGGGC TGGAGCTGGG CCTCCCCTCC ACTCCAGGAA CCCCCACGCC   540
CACGCCCCAC ACCTCCCTGG GCTCCCCTGT GTCATCCGAC CCGGTGCACA TGTCGCCCCT   600
GGAGCCCCGG GGAGGGCAAG GCGACGGCCT CGCCCTTGTG CTGATCCTGG CGTTCTGTGT   660
GGCCGGTGCA GCCGCCCTCT CCGTAGCCTC CCTCTGCTGG TGCAGGCTGC AGCGTGAGAT   720
CCGCCTGACT CAGAAGGCCG ACTACGCCAC TGCGAAGGCC CCTGGCTCAC CTGCAGCTCC   780
CCGGATCTCG CCTGGGGACC AGCGGCTGGC ACAGAGCGCG GAGATGTACC ACTACCAGCA   840
CCAACGGCAA CAGATGCTGT GCCTGGAGCG GCATAAAGAG CCACCCAAGG AGCTGGACAC   900
GGCCTCCTCG GATGAGGAGA ATGAGGACGG AGACTTCACG GTGTACGAGT GCCCGGGCCT   960
GGCCCCGACC GGGGAAATGG AGGTGCGCAA CCCTCTGTTC GACCACGCCG CACTGTCCGC  1020
GCCCCTGCCG GCCCCCAGCT CACCGCCTGC ACTGCCATGA CCTGGAGGCA GACAGACGCC  1080
CACCTGCTCC CCGACCTCGA GGCCCCCGGG GAGGGGCAGG GCCTGGAGCT TCCCACTAAA  1140
AACATGTTTT GATGCTGTGT GCTTTTGGCT GGGCCTCGGG CTCCAGGCCC TGGGACCCCT  1200
TGCCAGGGAG ACCCCCGAAC CTTTGTGCCA GGACACCTCC TGGTCCCCTG CACCTCTCCT  1260
GTTCGGTTTA GACCCCCAAA CTGGAGGGGG CATGGAGAAC CGTAGAGCGC AGGAACGGGT  1320
GGGTAATTCT AGAGACAAAA GCCAATTAAA GTCCATTTCA GAAAAAAAAA A            1371
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Seq ID NO: C212 DNA Sequence
Nucleic Acid Accession #: NM_004445.1
Coding sequence: 799..3819

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GACCCGGGAC CCAGCTTGGC GACGGCGATT CTCGACGCGG GCCCCCAGGA TTCTCCCGGC   120
GCCCCACCTC TGGAGCAGCC CCTGCCGCCA GCGTCAGGTC CACCCCGGAA TCCCAGGGAC   180
TCTCGGCGCC GAACGGACCC GGGCCGGTGC AACGGGGTCC CCGGACTGGA GAAGACGCGG   240
GTGGCACCGT GCGAGCTCCA GGAGCCCCGG GTCCACTGCG AGGCCTCGGG GGGCGCAGAC   300
CTGCAGAGAC TGCGGCCAAC GGGAAGAAAT AAAGGGATTA TAGTCCACCC AATTCACAGA   360
CTTCTGAGAC TCAGACACGA GGAGAGATAG AGAACCGCCA ATCTCTAGAT CAACAAGCAA   420
AGGAGGTGCC AAGCCTGTTT GTCTTCATTG TGACACTGGA GTCTAGATGC TGGGAAGTCC   480
AAGATCAGGG TGCCGGCATG GTCAGTTCCT GGCGAAGCCT CTCTTCTAGG TTTCAGACTG   540
CCCTCTTCTT TGTTGTGTCC TCGAATGGCA GAAAAAGGGG TGGCTGTTGG AGGAAGGGAG   600
GAGAGTAAAT GAAGAGAAAG AACTGGAATA ACCCCTTGCA GAAAAAAAAA AAAAGGGAAG   660
CTTAGCTGTA CACCCTGAGT CTTGCAAAAG CTGCAGCCCC ACCCAGGAGC AGGGTGGTGG   720
CTGGGGCGAT GGTGGACGCC CTGAAGATGT CCCATGGCTA CTGAAGGGGC TGCCCAGTTA   780
GGGAACAGAG TGGCGGGCAT GGTGTGTAGC CTATGGGTGC TGCTCCTGGT GTCTTCAGTT   840
CTGGCTCTGG AAGAGGTATT GCTGGACACC ACCGGAGAGA CATCTGAGAT TGGCTGGCTC   900
ACCTACCCAC CAGGGGGGTG GGACGAGGTG AGTGTTCTGG ACGACCAGCG ACGCCTGACT   960
CGGACCTTTG AGGCATGTCA TGTGGCAGGG GCCCCTCCAG GCACCGGGCA GGACAATTGG  1020
TTGCAGACAC ACTTTGTGGA GCGGCGCGGG GCCCAGAGGG CGCACATTCG ACTCCACTTC  1080
TCTGTGCGGG CATGCTCCAG CCTGGGTGTG AGCGGCGGCA CCTGCCGGGA GACCTTCACC  1140
CTTTACTACC GTCAGGCTGA GGAGCCCGAC AGCCCTGACA GCGTTTCCTC CTGGCACCTC  1200
AAACGCTGGA CCAAGGTGGA CACAATTGCA GCAGACGAGA GCTTTCCCTC CTCCTCCTCC  1260
TCCTCCTCCT CTTCTTCCTC TGCAGCGTGG GCTGTGGGAC CCCACGGGGC TGGGCAGCGG  1320
GCTGGACTGC AACTGAACGT CAAAGAGCGG AGCTTTGGGC CTCTCACCCA ACGCGGCTTC  1380
TACGTGGCCT TCCAGGACAC GGGGGCCTGC CTGGCCCTGG TCGCTGTCAG GCTCTTCTCC  1440
TACACCTGCC CTGCCGTGCT CCGATCCTTT GCTTCCTTTC CAGAGACGCA GGCCAGTGGG  1500
GCTGGGGGGG CCTCCCTGGT GGCAGCTGTG GGCACCTGTG TGGCTCATGC AGAGCCAGAG  1560
GAGGATGGAG TAGGGGGCCA GGCAGGAGGC AGCCCCCCCA GGCTGCACTG CAACGGGGAG  1620
GGCAAGTGGA TGGTAGCTGT CGGGGGCTGC CGCTGCCAGC CTGGATACCA ACCAGCACGA  1680
GGAGACAAGG CCTGCCAAGC CTGCCCACGG GGGCTCTATA AGTCTTCTGC TGGGAATGCT  1740
CCCTGCTCAC CATGCCCTGC CCGCAGTCAC GCTCCCAACC CAGCAGCCCC CGTTTGCCCC  1800
TGCCTGGAGG GCTTCTACCG GGCCAGTTCC GACCCACCAG AGGCCCCCTG CACTGGTCCT  1860
CCATCGGCTC CCCAGGAGCT TTGGTTTGAG GTGCAAGGCT CAGCACTCAT GCTACACTGG  1920
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CGCCTGCCTC GGGAGCTGGG GGGTCGAGGG GACCTGCTCT TCAATGTCGT GTGCAAGGAG   1980
TGTGAAGGCC GCCAGGAACC TGCCAGCGGT GGTGGGGGCA CTTGTCACCG CTGCAGGGAT   2040
GAGGTCCACT TCGACCCTCG CCAGAGAGGC CTGACTGAGA GCCGAGTGTT AGTGGGGGGA   2100
CTCCGGGCAC ACGTACCCTA CATCTTAGAG GTGCAGGCTG TTAATGGGGT GTCTGAGCTC   2160
AGCCCTGACC CTCCTCAGGC TGCAGCCATC AATGTCAGCA CCAGCCATGA AGTGCCCTCT   2220
GCTGTCCCTG TGGTGCACCA GGTGAGCCGG GCATCCAACA GCATCACGGT GTCCTGGCCG   2280
CAGCCCGACC AGACCAATGG GAACATCCTG GACTATCAGC TCCGCTACTA TGACCAGGCA   2340
GAAGACGAAT CCCACTCCTT CACCCTGACC AGCGAGACCA ACACTGCCAC CGTGACACAG   2400
CTGAGCCCTG GCCACATCTA TGGTTTCCAG GTGCGGGCCC GGACTGCTGC CGGCCACGGC   2460
CCCTACGGGG GCAAAGTCTA TTTCCAGACA CTTCCTCAAG GGGAGCTGTC TTCCCAGCTT   2520
CCGGAAAGAC TCTCCTTGGT GATCGGCTCC ATCCTGGGGG CTTTGGCCTT CCTCCTGCTG   2580
GCAGCCATCA CCGTGCTGGC GGTCGTCTTC CAGCGGAAGC GGCGTGGGAC TGGCTACACG   2640
GAGCAGCTGC AGCAATACAG CAGCCCAGGA CTCGGGGTGA AGTATTACAT CGACCCCTCC   2700
ACCTACGAGG ACCCCTGTCA GGCCATCCGA GAACTTGCCC GGGAAGTCGA TCCTGCTTAT   2760
ATCAAGATTG AGGAGGTCAT TGGGACAGGC TCTTTTGGAG AAGTGCGCCA GGGCCGCCTG   2820
CAGCCACGGG GACGGAGGGA GCAGACTGTG GCCATCCAGG CCCTGTGGGC CGGGGGCGCC   2880
GAAAGCCTGC AGATGACCTT CCTGGGCCGG GCCGCAGTGC TGGGTCAGTT CCAGCACCCC   2940
AACATCCTGC GGCTGGAGGG CGTGGTCACC AAGAGCCGAC CCCTCATGGT GCTGACGGAG   3000
TTCATGGAGC TTGGCCCCCT GGACAGCTTC CTCAGGCAGC GGGAGGGCCA GTTCAGCAGC   3060
CTGCAGCTGG TGGCCATGCA GCGGGGAGTG GCTGCTGCCA TGCAGTACCT GTCCAGCTTT   3120
GCCTTCGTCC ATCGCTCGCT GTCTGCCCAC AGCGTGCTGG TGAATAGCCA CTTGGTGTGC   3180
AAGGTGGCCC GTCTTGGCCA CAGTCCTCAG GGCCCAAGTT GTTTGCTTCG CTGGGCAGCC   3240
CCAGAGGTCA TTGCACATGG AAAGCATACA ACATCCAGTG ATGTCTGGAG CTTTGGGATA   3300
CTCATGTGGG AAGTGATGAG TTATGGAGAA CGGCCTTACT GGGACATGAG TGAGCAGGAG   3360
GTACTAAATG CAATAGAGCA GGAGTTCCGG CTGCCCCCGC CTCCAGGCTG TCCTCCTGGA   3420
TTACATCTAC TTATGTTGGA CACTTGGCAG AAGGACCGTG CCCGGCGGCC TCATTTTGAC   3480
CAGCTGGTGG CTGCATTTGA CAAGATGATC CGCAAGCCAG ATACCCTGCA GGCTGGCGGG   3540
GACCCAGGGG AAAGGCCTTC CCAGGCCCTT CTGACCCCTG TGGCCCTGGA CTTTCCTTGT   3600
CTGGACTCAC CCCAGGCCTG GCTTTCAGCC ATTGGACTGG AGTGCTACCA GGACAACTTC   3660
TCCAAGTTTG GCCTCTGTAC CTTCAGTGAT GTGGCTCAGC TCAGCCTAGA AGACCTGCCT   3720
GCCCTGGGCA TCACCCTGGC TGGCCACCAG AAGAAGCTGC TGCACCACAT CCAGCTCCTT   3780
CAGCAACACC TGAGGCAGCA GGGCTCAGTG GAGGTCTGAG AATGACGATA CCCGTGACTC   3840
AGCCCTGGAC ACTGGTCCGA GAAGGGACAT GTGGGACGTG AGCCGGGCTC CAACAGCCTC   3900
TGTGAGAGAT GCCCCACACC AAACCCAACC CTCCCGATGG CTGCATTCCC TGGTCCTCCG   3960
CCTCTCCACC AGCCCCCTCC TCATTAAAGG GAAAGAAGGG AATTTGCAAA              4010
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Seq ID NO: C213 DNA Sequence
Nucleic Acid Accession #: XM_043340.4
Coding sequence: 195..1067

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GTGGCGAGTG GCGAGTGTCA GGGGGGCGGC CGGCGGGGGC GGGGCGGCCG GAGGAGGCGT  120
TGGCAGCGGG CTCGGACCCA CGCGGCGCCG CGGCCCGCCT GGCCTGCAGC GCTCCCACCC  180
CCGGCGGCGG CACGATGCCC TTTGACTTCA GGAGGTTTGA CATCTACAGG AAGGTGCCCA  240
AGGACCTTAC GCAGCCAACG TACACCGGGG CCATTATCTC CATCTGCTGC TGCCTCTTCA  300
TCCTCTTCCT CTTCCTCTCG GAGCTCACCG GATTTATAAC GACAGAAGTT GTGAACGAGC  360
TCTATGTCGA TGACCCAGAC AAGGACAGCG GTGGCAAGAT CGACGTCAGT CTGAACATCA  420
GTTTACCCAA TCTGCACTGC GAGTTGGTTG GGCTTGACAT TCAGGATGAG ATGGGCAGGC  480
ACGAAGTGGG CCACATCGAC AACTCCATGA AGATCCCGCT GAACAATGGG GCAGGCTGCC  540
GCTTCGAGGG GCAGTTCAGC ATCAACAAGG TCCCCGGCAA CTTCCACGTG TCCACACACA  600
GTGCCACAGC CCAGCCACAG AACCCAGACA TGACGCATGT CATCCACAAG CTCTCCTTTG  660
GGGACACGCT ACAGGTCCAG AACATCCACG GAGCTTTCAA TGCTCTCGGG GGAGCAGACA  720
GACTCACCTC CAACCCCCTG GCCTCCCACG ACTACATCCT GAAGATTGTG CCCACGGTTT  780
ATGAGGACAA GAGTGGCAAG CAGCGGTACT CCTACCAGTA CACGGTGGCC AACAAGGAAT  840
ACGTCGCCTA CAGCCACACG GGCCGCATCA TCCCTGCAAT CTGGTTCCGC TACGACCTCA  900
GCCCCATCAC GGTCAAGTAC ACAGAGAGAC GGCAGCCGCT GTACAGATTC ATCACCACGA  960
TCTGTGCCAT CATTGGCGGG ACCTTCACCG TCGCCGGCAT CCTGGACTCA TGCATCTTCA 1020
CAGCCTCTGA GGCCTGGAAG AAGATCCAGC TGGGCAAGAT GCATTGACGC CACACCCAGC 1080
CTAATGGCCG AGGACCCTGG GCATCGCCAG CCTTGCCTCC AGTGCCCTGT CTCCTTTGGC 1140
CCTCAATCTG GTCCCAAATC TGGCTGTGTC CCAAAGGGTG TGTGGGAAGT GGGGGGAAAG 1200
TAGAGGATGG CTCGATGTTT TGCAGCTACC TCTTTTCCCC GTGTTTCTTT TTAGACAAAT 1260
TACACTGCCT GAAGTTGCAG TTCCCCTTTC CCTGGGGAGC CCCAAGAACA GAGTCAGGCA 1320
AGGGGTGGGG AGTCCAGGGG AACATCCCAG AATGCATATC GATCAGCTCT CAGCCAGGCT 1380
TCGACAATCT CGCAGCCCCC ACTAGGTGGA CACATTAATG ATTTGGTTTC TCCCCTGGGC 1440
AGCCAACCTG CCCCAGAGGC ACCAGACCTG GGCTTTCAGC TTTGGGACCA GGCTGCCCAA 1500
AGGTACTCCT TTATACACCC GGCACCTTCC ACGAAAGATG GTACTTCCCA AGCAAGCCCC 1560
TATGATTTGT CACTATAGAT GGAAATGTGT GGCATGCACA TGAGTTGAAA TTCTTTTATG 1620
CATTTTTTTG AAGAAAAAAA AAAAAACAAC TCTGAGGACA TAGGGGATGT CAGTTTCCTA 1680
TGGAAGAGAC ACCTCTGACC CGTTATTCTT ATAATCAAAA TCTGAAGGGA AAAAAATGTT 1740
TTAGTTCTTT CCCCACTCGT TGGGTTCAAC TAGATTAAAA GGCTGATTTT CAG          1793
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Seq ID NO: C214 DNA Sequence
Nucleic Acid Accession #: NM_002151.1
Coding sequence: 246..1499

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AGGCCCCACG CCACCGCCTC TGCCTCCAGG CCGCCCGCTG CTGCGGGGCC ACCATGCTCC  120
TGCCCAGGCC TGGAGACTGA CCCGACCCCG GCACTACCTC GAGGCTCCGC CCCCACCTGC  180
TGGACCCCAG GGTCCCACCC TGGCCCAGGA GGTCAGCCAG GGAATCATTA ACAAGAGGCA  240
GTGACATGGC GCAGAAGGAG GGTGGCCGGA CTGTGCCATG CTGCTCCAGA CCCAAGGTGG  300
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CAGCTCTCAC TGCGGGGACC CTGCTACTTC TGACAGCCAT CGGGGCGGCA TCCTGGGCCA   360
TTGTGGCTGT TCTCCTCAGG AGTGACCAGG AGCCGCTGTA CCCAGTGCAG GTCAGCTCTG   420
CGGACGCTCG GCTCATGGTC TTTGACAAGA CGGAAGGGAC GTGGCGGCTG CTGTGCTCCT   480
CGCGCTCCAA CGCCAGGGTA GCCGGACTCA GCTGCGAGGA GATGGGCTTC CTCAGGGCAC   540
TGACCCACTC CGAGCTGGAC GTGCGAACGG CGGGCGCCAA TGGCACGTCG GGCTTCTTCT   600
GTGTGGACGA GGGGAGGCTG CCCCACACCC AGAGGCTGCT GGAGGTCATC TCCGTGTGTG   660
ATTGCCCCAG AGGCCGTTTC TTGGCCGCCA TCTGCCAAGA CTGTGGCCGC AGGAAGCTGC   720
CCGTGGACCG CATCGTGGGA GGCCGGGACA CCAGCTTGGG CCGGTGGCCG TGGCAAGTCA   780
GCCTTCGCTA TGATGGAGCA CACCTCTGTG GGGGATCCCT GCTCTCCGGG GACTGGGTGC   840
TGACAGCCGC CCACTGCTTC CCGGAGCGGA ACCGGGTCCT GTCCCGATGG CGAGTGTTTG   900
CCGGTGCCGT GGCCCAGGCC TCTCCCCACG GTCTGCAGCT GGGGGTGCAG GCTGTGGTCT   960
ACCACGGGGG CTATCTTCCC TTTCGGGACC CCAACAGCGA GGAGAACAGC AACGATATTG  1020
CCCTGGTCCA CCTCTCCAGT CCCCTGCCCC TCACAGAATA CATCCAGCCT GTGTGCCTCC  1080
CAGCTGCCGG CCAGGCCCTG GTGGATGGCA AGATCTGTAC CGTGACGGGC TGGGGCAACA  1140
CGCAGTACTA TGGCCAACAG GCCGGGGTAC TCCAGGAGGC TCGAGTCCCC ATAATCAGCA  1200
ATGATGTCTG CAATGGCGCT GACTTCTATG GAAACCAGAT CAAGCCCAAG ATGTTCTGTG  1260
CTGGCTACCC CGAGGGTGGC ATTGATGCCT GCCAGGGCGA CAGCGGTGGT CCCTTTGTGT  1320
GTGAGGACAG CATCTCTCGG ACGCCACGTT GGCGGCTGTG TGGCATTGTG AGTTGGGGCA  1380
CTGGCTGTGC CCTGGCCCAG AAGCCAGGCG TCTACACCAA AGTCAGTGAC TTCCGGGAGT  1440
GGATCTTCCA GGCCATAAAG ACTCACTCCG AAGCCAGCGG CATGGTGACC CAGCTCTGAC  1500
CGGTGGCTTC TCGCTGCGCA GCCTCCAGGG CCCGAGGTGA TCCCGGTGGT GGGATCCACG  1560
CTGGGCCGAG GATGGGACGT TTTTCTTCTT GGGCCCGGTC CACAGGTCCA AGGACACCCT  1620
CCCTCCAGGG TCCTCTCTTC CACAGTGGCG GGCCCACTCA GCCCCGAGAC CACCCAACCT  1680
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Seq ID NO: C215 DNA Sequence
Nucleic Acid Accession #: AB037745.1
Coding sequence: 26..1744

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CTCAGACAAT GACTTCATGA TTCTCACTCT GGTTGTGCCA GGATTTAGAC CTCCGCAGTC  180
GGTGATGGCA GACACAGAGA ATAAAGAGGT GGCCAGAATC ACATTTGTCT TTGAGACCCT  240
CTGTTCTGTG AACTGTGAGC TCTACTTCAT GGTGGGTGTG AATTCTAGGA CCAACACTCC  300
TGTGGAGACG TGGAAAGGTT CCAAAGGCAA ACAGTCCTAT ACCTACATCA TTGAGGAGAA  360
CACTACCACG AGCTTCACCT GGGCCTTCCA GAGGACCACT TTTCATGAGG CAAGCAGGAA  420
GTACACCAAT GACGTTGCCA AGATCTACTC CATCAATGTC ACCAATGTTA TGAATGGCGT  480
GGCCTCCTAC TGCCGTCCCT GTGCCCTAGA AGCCTCTGAT GTGGGCTCCT CCTGCACCTC  540
TTGTCCTGCT GGTTACTATA TTGACCGAGA TTCAGGAACC TGCCACTCCT GCCCCCCTAA  600
CACAATTCTG AAAGCCCACC AGCCTTATGG TGTCCAGGCC TGTGTGCCCT GTGGTCCAGG  660
GACCAAGAAC AACAAGATCC ACTCTCTGTG CTACAATGAT TGCACCTTCT CACGCAACAC  720
TCCAACCAGG ACTTTCAACT ACAACTTCTC CGCTTTGGCA AACACCGTCA CTCTTGCTGG  780
AGGGCCAAGC TTCACTTCCA AAGGGTTGAA ATACTTCCAT CACTTTACCC TCAGTCTCTG  840
TGGAAACCAG GGTAGGAAAA TGTCTGTGTG CACCGACAAT GTCACTGACC TCCGGATTCC  900
TGAGGGTGAG TCAGGGTTCT CCAAATCTAT CACAGCCTAC GTCTGCCAGG CAGTCATCAT  960
CCCCCCAGAG GTGACAGGCT ACAAGGCCGG GGTTTCCTCA CAGCCTGTCA GCCTTGCTGA 1020
TCGACTTATT GGGGTGACAA CAGATATGAC TCTGGATGGA ATCACCTCCC CAGCTGAACT 1080
TTTCCACCTG GAGTCCTTGG GAATACCGGA CGTGATCTTC TTTTATAGGT CCAATGATGT 1140
GACCCAGTCC TGCAGTTCTG GGAGATCAAC CACCATCCGC GTCAGGTGCA GTCCACAGAA 1200
AACTGTCCCT GGAAGTTTGC TGCTGCCAGG AACGTGCTCA GATGGGACCT GTGATGGCTG 1260
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CATAGATTTC TGGCTGAAAG TGGGCATCTC TGCAGGCACC TGTACTGCCA TCCTGCTCAC 1500
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GGTGATGAAT GCTACTCTCA AGGACTGTGA CCTGCCAGCA GCTGACAGCT GCGCCATCAT 1620
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GCGATTTGGG TGCCAGCATC CTGCAACACC CACTGCTGGA AATCTCTTCA TTGTGGCCTT 1920
ATCAGATGTT TGAATTTCAG ATCTTTTTTT ATAGAGTACC CAAACCCTCC TTTCTGCTTG 1980
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TTAAGGGCAG AAACAGCTGG GAGTTTTCCT CGCATGCCCT CAGCTCATGA TCTCTTCAGG 2220
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ATAGATATTC TCACTGAAGC CAAAGGAATA AGTTCATCAA GAAAATGCCC AAAGCCCTGG 3120
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TTTTAATGGG GCACTTTAGG GGATACAGCC CACAATGGCA TGGGCCTGAG GTGGCCGTGA   3420
TGTCTGCTTC TAAGCTTAAC GCATCTGCTC AGGCACAGAA TAAACGTCTA GGCTGGCCAA   3480
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TGAGACCCTG TCTCTAAAAA ATTTAAAAAT AAACAAGGTG TTCACCAAGC TGGGATACTT   3720
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AACTAAAGAG ACTTCTGGTC CAATTTCTGG CAACATCCCT TCTGAAAGGT GAGTAGAGTG   3840
GGTGTCTTCT ATGCCCATTT TCCCCAATTT TACACAAACT ATTATCAATG AACTTTTAAG   3900
TACCTAGAAT GGGTAAAACC AGAGCAAGAC TTTAAATTAC CTTCTTCTTT CTTCTACTGG   3960
CAGTTCTGCC TCCATCACTA TCAGGCTAGG GTGACCTTCC CTTGGTCAAG CCCCAATTGC   4020
CCATGATTTG TGCCTGTGCC CTTTCTCCAG TGACCATTTG GTGACCAGAT GGTAGATATA   4080
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GGCCATCAAC AGTGTTGGTG ACGGCAGGGA GTCCCTTTGG TTTAATAAAT CCAGTTTTTC   4260
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TGTTGGAACT TCCCCCAGTG TGGATGCAGA TACGCAGCTC CTGAGCTCCA GCCTAAAGTC   4380
TTCTGTAGCC TCAGCAATAC TTGGGCACCT GCTGTCTCAC TGAATAGCTT TCTTTTGTGA   4440
CAAAGGCCAC AGACAGCCCT TAGACTATTC CGGAAACAGT AGGAAAAATT ACATATGTCT   4500
TTGACTTCTT TATTCTGACT CCACTGATTT TAGCCATAAT ACTTTAAGGA GCTACTTTTT   4560
ACTACCCCTT ACCGTGCTGA CTTCTGCAGG TCTGCCCTGT GACCTGTCAG GAACTCCTGA   4620
GTTACGCTAC TGGGGTCACC TGTTGCTCCC CTAGCAAGTT AGGCATGTCA TATATTTTTA   4680
ACAGCTTTAT TGAGATATAA TTCACATATT ATACAATTCA CCTTTAAAAC ATACGATTCA   4740
ATGGTTTTCA GCAAACTCAC AGAGTTGTCC GCCCACTTGA GAGCAAACAC ATGTTCAATT   4800
TTCTTTTCCT TTTTTTTTTT GAGACAGAGT CAGCTTTGTC GCCCAGGCTG GAGTGCAGTG   4860
CCATGATCTT GGCTCACTGC AGCCTCCCCA TCCTGGGTTC AAGTGATCCT TCTGCTTCAG   4920
CCTCCCCAGT AGCTGGGATT ACAGGCATGC GCCACCACGC CTAGCTAATT TTTGTGTTTT   4980
TAGTAGAGAT GGGGTTTCAC CGTGTTGGCC AGGCTGGTCT CAAACTCCTG GACTCAAGTG   5040
ATCCACCCAC CTCGGCCTCC CAAAGTGCTG GGATTGCAGG TGTGAGCCAC CGTGCCTGGC   5100
CTACGTGTTC AATTTTCTAT GAACAAAGGC TTTAGTCCTT GACCCAGGGC TAAAGTGGTC   5160
TGTCCAAGCT GTTGTTGGTA GAGGGAGTAT GATAAAATGT TTAAATCTCA TTTGGTTACC   5220
TTGAGTCCTG GAACACGCAG TAACTGTCAT GCTATAGTCA TCATCTGTAT TTGGCTGGGA   5280
ATACAAATGA AGATTGTGGT GTATTCAAGC AGTAGGGTTT TTGCTTTTGT TTTTGTTTTA   5340
GTGCCAACAA AACTTTTTTT TGTCTGACTA CATTAAAGAT AAGACTGACT ATATTTATAC   5400
AACAGAAACT TTGTAATAGA TTTTTTCAGC TTTGTGAAAT CGAATTTTTT TTCATCAGGG   5460
CTGGTTGGAT TTCCTTTTTA CCCTGTAATC CAAGCGTTAA TAGTTTGTTA GAAGATGGGT   5520
TATTGCATGT CACTTTTTTT TTTTTGTAAA ATAAAAACAT ACCTTAC                 5567
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Seq ID NO: C216 DNA Sequence
Nucleic Acid Accession #: NM_004864.1
Coding sequence: 26-952

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1          11         21         31         41         51
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TCAGATGCTC CTGGTGTTGC TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT  120
GGCCGAGGCG AGCCGCGCAA GTTTCCCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG  180
ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCAACCAGAG  240
CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCCTGCA GTCCGGATAC TCACGCCAGA  300
AGTGCGGCTG GGATCCGGCG GCCACCTGCA CCTGCGTATC TCTCGGGCCG CCCTTCCCGA  360
GGGGCTCCCC GAGGCCTCCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGGCGTC  420
AAGGTCGTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC  480
GCCCGCGCTG CACCTGCGAC TGTCGCCGCC GCCGTCGCAG TCGGACCAAC TGCTGGCAGA  540
ATCTTCGTCC GCACGGCCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGGCG  600
CCGCAGAGCG CGTGCGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG  660
TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTCGCC  720
ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA  780
CATGCACGCG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACGG AGCCAGCGCC  840
CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT  900
GTCGCTCCAG ACCTATGATG ACTTGTTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT  960
GGTCCTTCCA CTGTGCACCT GCGCGGGGGA GGCGACCTCA GTTGTCCTGC CCTGTGGAAT 1020
GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG 1080
TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1140
ACTGTGTATT TATTTAAAAC TCTGGTGATA AAAATAAAGC TGTCTGAACT GTTAAAAAAA 1200
AAAA                                                              1204
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Seq ID NO: C432 DNA Sequence
Nucleic Acid Accession #: NM_052858.1
Coding sequence: 54..1259

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1          11         21         31         41         51
|          |          |          |          |          |
GGCACGAGGT GTTGCCCTCA GGTCGCTCCC GGGCGCGGAC ACGGAACCCG GCCATGGAAG   60
ATCCGTCGGG GGCTCGCGAG CCCCGGGCCC GGCCGAGAGA GCGGGACCCG GGACGGCGCC  120
CCCACCCAGA CCAAGGCCGC ACCCACGATC GACCGCGGGA CCGACCCGGG GACCCGCGCA  180
GGAAGCGAAG CAGCGACGGG AACCGGCGAA GGGACGGGGA CCGGGACCCG AAGAGAGACC  240
AGGAGAGGGA CGGGAACCGC GACCGGAACC GGGACCGGGA GAGGGAGAGA GAGAGGGAAA  300
GAGACCCGGA CCGAGGCCCC CGCCGGGACA CACACAGGGA CGCGGGCCCT CGCGCAGGTG  360
AACACGGAGT TTGGGAAAAA CCGCGCCAAA GCCGGACGCG GGACGGAGCC CGGGGACTGA  420
CCTGGGACGC AGCCGCGCCT CCTGGGCCCG CGCCCTGGGA AGCCCCGGAG CCGCCGCAGC  480
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CGCAGAGGAA GGGAGACCCC GGGCGCCGCA GACCCGAAAG TGAACCCCCT TCGGAGAGAT   540
ATCTGCCCTC GACCCCCAGG CCTGGACGAG AGGAGGTGGA ATATTACCAG TCAGAGGCGG   600
AAGGACTCCT GGAATGCCAC AAATGCAAAT ACTTGTGCAC TGGGAGAGCC TGCTGCCAAA   660
TGCTGGAGGT TCTCCTGAAC TTGCTGATCC TGGCCTGCAG CTCTGTGTCT TACAGTTCCA   720
CAGGGGGCTA CACGGGCATC ACCAGCTTGG GGGGCATTTA CTACTATCAG TTCGGAGGGG   780
CTTACAGTGG CTTTGATGGT GCTGACGGGG AGAAGGCCCA GCAACTGGAT GTCCAGTTCT   840
ACCAGCTAAA GCTGCCCATG GTCACTGTGG CAATGGCCTG TAGTGGAGCC CTCACAGCCC   900
TCTGCTGCCT CTTCGTTGCC ATGGGTGTCC TGCGGGTCCC GTGGCATTGT CCACTGTTGC   960
TGGTGACCGA AGGCTTGTTG GACATGCTCA TCGCGGGGGG GTACATCCCG GCCTTGTACT  1020
TCTACTTCCA CTACCTCTCT GCTGCCTATG GCTCTCCTGT GTGTAAAGAG AGGCAGGCGC  1080
TGTACCAAAG CAAAGGCTAC AGCGGTTTCG GCTGCAGTTT CCACGGAGCA GATATAGGAG  1140
CTGGAATCTT TGCTGCCCTG GGCATTGTGG TCTTTGCCCT GGGGGCGGTC CTGGCCATAA  1200
AGGGCTACCG AAAAGTTAGG AAGCTAAAAG AGAAGCCAGC AGAAATGTTT GAATTTTAAG  1260
GGTTTCTAAA ACGCTCTGAC AGATGCAAGT GGTGGTGGAA GGTAGTCTGA GCCACTGCCT  1320
TTCCCAAGAA TCCCTTGTTG TGGAAGTTTC CAATGCTGGA AAAGCAGCGA GCCAGCGTTG  1380
GTGTGGTGGG CGGAGCTCCC AGTCGCATGG AGCGGTGTTC ATGGATGCAA CAGACCCTGG  1440
CTTCTGGAGT CCTCTGTGAG TGAGGGACCA ATCAAAATTA TTTTTCAAAA AGCAAAAAAA  1500
TGGCCGGCCT CGGCGGCTCA CACCTGTAAC CCCAGCACTT TGGGAGGCTG AGGTGGGTGG  1560
ATCACTTGAG GTCAGGAGCT CGAGACCAGC TTGGCCAACA TGGTGAGCCC CCGTCTCTAC  1620
TAAAATACAA AAAAATTAGC CAGGCGTGGT GGCGGGCGCC TGTAATCCCA GCTACTTGGG  1680
AGGCTGAGGC AGGAGAATCG CTTGAATCTG GGAGGCGGAG ATTGCAGTGA GCCGAGATCC  1740
CGCCACTGCA CTCCAGCCCA GGTGACAGAG CGAGACTCCA TCTCAAAAAA AAAAAAAAAA  1800
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Seq ID NO: C434 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 261..2861

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1          11         21         31         41         51
|          |          |          |          |          |
GAGCTAGCGC TCAAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG    60
CGGCGCGGGG AGCCAGCGGG GCTGAGCGCG GCCAGGGTCT GAACCCAGAT TTCCCAGACT   120
AGCTACCACT CCGCTTGCCC ACGCCCCGGG AGCTCGCGGC GCCTGGCGGT CAGCGACCAG   180
ACGTCCGGGG CCGCTGCGCT CCTGGCCCGC GAGGCGTGAC ACTGTCTCGG CTACAGACCC   240
AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGGCCA   300
TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCCTGG GGCCACATCC ACAGTGGCTG   360
CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCCTGGAA CCCTGGCCAT GACCAAGACC   420
ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT   480
CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT   540
TGCGAACCCG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCCTCT   600
GCCCTTTCCA GGGCAATTTC ACCATCATTT TGTATGGAAG GGCTGATGAA GGTATTCAGC   660
CGGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTTGAGTTGC   720
ATGGACAGAA AAAGCTCTCC TGGACATTTC TGAACAAGAC CCTTCACCCA GGTGGCATGG   780
CAGAAGGAGG CTATTTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA   840
TCGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA   900
AAGAGAGTGA ACGTCTGGTC CAGTATTTGA ACGCGGTGCC CGATGGCAGG ATCCTTTCTG   960
TTGCAGTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA  1020
AATTGGGAAG CAAACACTTC CTGCACCTTG GATTTAGACA CCCTTGGAGT TTTCTAACTG  1080
TGAAAGGAAA TCCATCATCT TCAGTGGAAG ACCATATTGA ATATCATGGA CATCGAGGCT  1140
CTGCTGCTGC CCGGGTATTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT  1200
CTTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCGAT CATGATAAAG  1260
TATCTCAGAC TAAAGGTGGG GAGAAAATTT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA  1320
TATGCAATCG TCCCATTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGCACCG  1380
AGGTTGTCTA CAAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT  1440
GCCGGAGCTA CCGTGTACGG TTCCTCTGTG GGAAGCCTGT GAGGCCCAAA CTCACAGTCA  1500
CCATTGACAC CAATGTGAAC AGCACCATTC TGAACTTGGA GGATAATGTA CAGTCATGGA  1560
AACCTGGAGA TACCCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT  1620
TCCAGGTGCT TCCCTGCAGA TCCTGCGCCC CCAACCAGGT CAAAGTGGCA GGGAAACCAA  1680
TGTACCTGCA CATCGGGGAG GAGATAGACG GCGTGGACAT GCGGGCGGAG GTTGGGCTTC  1740
TGAGCCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC  1800
ACATCTGCAA TTTCTTTGAC TTCGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT  1860
TTAAGGCAGC ACACTTGGAG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGGTGGGTC  1920
AGTACCCGAT TCACTTCCAC CTGGCCGGTG ATGTAGACGA AAGGGGAGGT TATGACCCAC  1980
CCACATACAT CAGGGACCTC TCCATCCATC ATACATTCTC TCGCTGCGTC ACAGTCCATG  2040
GCTCCAATGG CTTGTTGATC AAGGACGTTG TGGGCTATAA CTCTTTGGGC CACTGCTTCT  2100
TCACGGAAGA TGGGCCGGAG GAACGCAACA CTTTTGACCA CTGTCTTGGC CTCCTTGTCA  2160
AGTCTGGAAC CCTCCTCCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCACAGAGG  2220
ACTCCTACCC AGGGTACATC CCCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT  2280
GGATGGCCAA TCCCAACAAC AACCTCATCA ACTGTGCCGC TGCAGGATCT GAGGAAACTG  2340
GATTTTGGTT TATTTTTCAC CACGTACCAA CGGGCCCCTC CGTGGGAATG TACTCCCCAG  2400
GTTATTCAGA GCACATTCCA CTGGGAAAAT TCTATAACAA CCGAGCACAT TCCAACTACC  2460
GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCACCGA GGCCTCTGCC AAGGACAAGC  2520
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AGCCCCGGGA GCCGGCCATC ATCAGACACT TCATTGCCTA CAAGAACCAG GACCACGGGG  2640
CCTGGCTGCG CGGCGGGGAT GTGTGGCTGG ACAGCTGCCA TTTCAGAGGG GAGGCTCAGG  2700
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CTCTGACTCC AAGAGGGTGA AGTCCACAGA AGTGAGCTCC TGCCTTAGGG CCTCATTTGC  3000
TCTTCATCCA GGGAACTGAG CACAGGGGGC CTCCAGGAGA CCCTAGATGT GCTCGTACTC  3060
CCTCGGCCTG GGATTTCAGA GCTGGAAATA TAGAAAATAT CTAGCCCAAA GCCTTCATTT  3120
TAACAGATGG GGAAAGTGAG CCCCCAAGAT GGGAAAGAAC CACACAGCTA AGGGAGGGCC  3180
TGGGGAGCCC CACCCTAGCC CTTGCTGCCA CACCACATTG CCTCAACAAC CGGCCCCAGA  3240
GTGCCCAGGC ACTCCTGAGG TAGCTTCTGG AAATGGGGAC AAGTCCCCTC GAAGGAAAGG  3300
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AAATGACTAG AGTAGAATGA CAGCTAGCAG ATCTCTTCCC TCCTGCTCCC AGCGCACACA   3360
AACCCGCCCT CCCCTTGGTG TTGGCGGTCC CTGTGGCCTT CACTTTGTTC ACTACCTGTC   3420
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TCTGCAGCTC TACAGGTGAG GCCCAGCAGA GGGAGTAGGG CTCGCCATGT TTCTGGTGAG   3540
CCAATTTGGC TGATCTTGGG TGTCTGAACA GCTATTGGGT CCACCCCAGT CCCTTTCAGC   3600
TGCTGCTTAA TGCCCTGCTC TCTCCCTGGC CCACCTTATA GAGAGCCCAA AGAGCTCCTG   3660
TAAGAGGGAG AACTCTATCT GTGGTTTATA ATCTTGCACG AGGCACCAGA GTCTCCCTGG   3720
GTCTTGTGAT GAACTACATT TATCCCCTTT CCTGCCCCAA CCACAAACTC TTTCCTTCAA   3780
AGAGGGCCTG CCTGGCTCCC TCCACCCAAC TGCACCCATG AGACTCGGTC CAAGAGTCCA   3840
TTCCCCAGGT GGGAGCCAAC TGTCAGGGAG GTCTTTCCCA CCAAACATCT TTCAGCTGCT   3900
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GGAAGGACTT CTTCCAGGGA GATTAGTGGT GATGGAGAGG AGAGTTAAAA TGACCTCATG   4020
TCCTTCTTGT CCACGGTTTT GTTGAGTTTT CACTCTTCTA ATGCAAGGGT CTCACACTGT   4080
GAACCACTTA GGATGTGATC ACTTTCAGGT GGCCAGGAAT GTTGAATGTC TTTGGCTCAG   4140
TTCATTTAAA AAAGATATCT ATTTGAAAGT TCTCAGAGTT GTACATATGT TTCACAGTAC   4200
AGGATCTGTA CATAAAAGTT TCTTTCCTAA ACCATTCACC AAGAGCCAAT ATCTAGGCAT   4260
TTTCTTGGTA GCACAAATTT TCTTATTGCT TAGAAAATTG TCCTCCTTGT TATTTCTGTT   4320
TGTAAGACTT AAGTGAGTTA GGTCTTTAAG GAAAGCAACG CTCCTCTGAA ATGCTTGTCT   4380
TTTTTCTGTT GCCGAAATAG CTGGTCCTTT TTCGGGAGTT AGATGTATAG AGTGTTTGTA   4440
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ATGTGCACTT CAAGAAGTCA CTGTCAGAGA AATAAAGAAT TGTCTTAAAT GTCATGATTG   4560
GAGATGTCCT TTGCATTGCT TGGAAGGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT   4620
TTGGAAAAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAAAAA   4680
AAAAAAAAAA AAAAAAAAAA AA                                             4702
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Seq ID NO: C217 Protein Sequence
Protein Accession #: NP_005805.1

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MVGKMWPVLW TLCAVRVTVD AISVETPQDV LRASQGKSVT LPCTYHTSTS SREGLIQWDK   60
LLLTHTERVV IWPFSNKNYI HGELYKNRVS ISNNAEQSDA SITIDQLTMA DNGTYECSVS   120
LMSDLEGNTK SRVRLLVLVP PSKPECGIEG ETIIGNNIQL TCQSKEGSPT PQYSWKRYNI   180
LNQEQPLAQP ASGQPVSLKN ISTDTSGYYI CTSSNEEGTQ FCNITVAVRS PSMNVALYVG   240
IAVGVVAALI IIGIIIYCCC CRGKDDNTED KEDARPNREA YEEPPEQLRE LSRERFEEDD   300
YRQEEQRSTG RESPDHLDQ                                                319
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Seq ID NO: C218 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MGSRTPESPL HAVQLRWGPR RRPPLLPLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF   60
GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL   120
LESSLSSSEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCYLST   180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ   240
IAESYYPEYL INLVQGQLQT RQASSIYDDS YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY   300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ   360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET   420
QQGVVFVFPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRDLDGNG YPDLIVGSFG   480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI   540
GFTVELQLDW QKQKGGVRRA LFLASRQATL TQTLLIQNGA REDCREMKIY LRNESEFRDK   600
LSPIHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF   660
GEQNHVYLGD KNALNLTFHA QNVGEGGAYE AELRVTAPPE AEYSGLVRHP GNFSSLSCDY   720
FAVNQSRLLV CDLGNPMKAG ASLWGGLRFT VPHLRDTKKT IQFDFQILSK NLNNSQSDVV   780
SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPQKEE DLGPAVHHVY ELINQGPSSI   840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLHH QQKREAPSRS   900
SASSGPQILK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV   960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IIILAILFGL LLLGLLIYIL   1020
YKLGFFKRSL PYGTAMEKAQ LKPPATSDA                                     1049
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Seq ID NO: C219 Protein Sequence
Protein Accession #: NP_002412.1

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1          11         21         31         41         51
|          |          |          |          |          |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV   60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN   120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGQADIM ISFVRGDHRD NSPFDGPGGN   180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSLGLSHST DIGALMYPSY   240
TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR   300
FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFADRDEV RFFKGNKYWA VQGQNVLHGY   360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDPG YPKMIAHDFP   420
GIGHKVDAVF MKDGPFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN               469
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Seq ID NO: C220 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV   60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN   120
YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGQADIM ISFVRGDHRD NSPFDGPGGN   180
LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSLGLSHST DIGALMYPSY   240
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TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR   300
FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFADRDEV RFFKGNKYWA VQGQNVLHGY   360
PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDPG YPKMIAHDFP   420
GIGHKVDAVF MKDGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN               469

Seq ID NO: C221 Protein Sequence
Protein Accession #: NP_055146.1

1          11         21         31         41         51
|          |          |          |          |          |
MVRKPVVSTI SKGGYLQGNV NGRLPSLGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA   60
GIFISPKGVL QNTGSVGMSL TIWTVCGVLS LFGALSYAEL GTTIKKSGGH YTYILEVFGP   120
LPAFVRVWVE LLIIRPAATA VISLAFGRYI LEPFFIQCEI PELAIKLITA VGITVVMVLN   180
SMSVSWSARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY   240
YGMYAYAGWF YLNFVTEEVE NPEKTIPLAI CISMAITIGV YVLTNVAYFT TINAEELLLS   300
NAVAVTFSER LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV   360
RKHTPLPAVI VLHPLTMIML FSGDLDSLLN FLSFARWLFI GLAVAGLIYL RYKCPDMHRP   420
FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM   480
SEKITRTLQI ILEVVPEEDK L                                             501

Seq ID NO: C222 Protein Sequence
Protein Accession #: NP_003237.1

1          11         21         31         41         51
|          |          |          |          |          |
MGLAWGLGVL FLMHVCGTNR IPESGGDNSV FDIFELTGAA RKGSGRRLVK GPDPSSPAFR   60
IEDANLIPPV PDDKFQDLVD AVRAEKGFLL LASLRQMKKT RGTLLALERK DHSGQVFSVV   120
SNGKAGTLDL SLTVQGKQHV VSVEEALLAT GQWKSITLFV QEDRAQLYID CEKMENAELD   180
VPIQSVFTRD LASIARLRIA KGGVNDNFQG VLQNVRFVFG TTPEDILRNK GCSSSTSVLL   240
TLDNNVVNGS SPAIRTNYIG HKTKDLQAIC GISCDELSSM VLELRGLRTI VTTLQDSIRK   300
VTEENKELAN ELRRPPLCYH NGVQYRNNEE WTVDSCTECH CQNSVTICKK VSCPIMPCSN   360
ATVPDGECCP RCWPSDSADD GWSPWSEWTS CSTSCGNGIQ QRGRSCDSLN NRCEGSSVQT   420
RTCHIQECDK RFKQDGGWSH WSPWSSCSVT CGDGVITRIR LCNSPSPQMN GKPCEGEARE   480
TKACKKDACP INGGWGPWSP WDICSVTCGG GVQKRSRLCN NPAPQFGGKD CVGDVTENQI   540
CNKQDCPIDG CLSNPCFAGV KCTSYPDGSW KCGACPPGYS GNGIQCTDVD ECKEVPDACF   600
NHNGEHRCEN TDPGYNCLPC PPRFTGSQPF GQGVEHATAN KQVCKPRNPC TDGTHDCNKN   660
AKCNYLGHYS DPMYRCECKP GYAGNGIICG EDTDLDGWPN ENLVCVANAT YHCKKDNCPN   720
LPNSGQEDYD KDGIGDACDD DDDNDKIPDD RDNCPFHYNP AQYDYDRDDV GDRCDNCPYN   780
HNPDQADTDN NGEGDACAAD IDGDGILNER DNCQYVYNVD QRDTDMDGVG DQCDNCPLEH   840
NPDQLDSDSD RIGDTCDNNQ DIDEDGHQNN LDNCPYVPNA NQADHDKDGK GDACDHDDDN   900
DGIPDDKDNC RLVPNPDQKD SDGDGRGDAC KDDFDHDSVP DIDDICPENV DISETDFRRF   960
QMIPLDPKGT SQNDPNWVVR HQGKELVQTV NCDPGLAVGY DEFNAVDFSG TFFINTERDD   1020
DYAGFVFGYQ SSSRFYVVMW KQVTQSYWDT NPTRAQGYSG LSVKVVNSTT GPGEHLRNAL   1080
WHTGNTPGQV RTLWHDPRHI GWKDFTAYRW RLSHRPKTGF IRVVMYEGKK IMADSGPIYD   1140
KTYAGGRLGL FVFSQEMVFF SDLKYECRDP                                    1170

Seq ID NO: C223 Protein Sequence
Protein Accession #: NP_002183.1

1          11         21         31         41         51
|          |          |          |          |          |
MPLLWLRGFL LASCWIIVRS SPTPGSEGHS AAPDCPSCAL AALPKDVPNS QPEMVEAVKK   60
HILNMLHLKK RPDVTQPVPK AALLNAIRKL HVGKVGENGY VEIEDDIGRR AEMNELMEQT   120
SEIITFAESG TARKTLHFEI SKEGSDLSVV ERAEVWLFLK VPKANRTRTK VTIRLFQQQK   180
HPQGSLDTGE EAEEVGLKGE RSELLLSEKV VDARKSTWHV FPVSSSIQRL LDQGKSSLDV   240
RIACEQCQES GASLVLLGKK KKKEEEGEGK KKGGGEGGAG ADEEKEQSHR PFLMLQARQS   300
EDHPHRRRRR GLECDGKVNI CCKKQFFVSF KDIGWNDWII APSGYHANYC EGECPSHIAG   360
TSGSSLSFHS TVINHYRMRG HSPFANLKSC CVPTKLRPMS MLYYDDGQNI IKKDIQNMIV   420
EECGCS                                                              426

Seq ID NO: C224 Protein Sequence
Protein Accession #: NP_000086.1

1          11         21         31         41         51
|          |          |          |          |          |
MVPDTACVLL LTLAALGASG QGQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT   60
FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG   120
NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD   180
INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH   240
ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ   300
EDVDRDGIGD ACDPDADGDG VPNEKDNCPL VRNPDQRNTD EDKWGDACDN CRSQKNDDQK   360
DTDQDGRGDA CDDDIDGDRI RNQADNCPRV PNSDQKDSDG DGIGDACDNC PQKSNPDQAD   420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPDS   480
RDNCRLVPNP GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD   540
PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI   600
FGYQDSSSFY VVMWKQMEQT YWQANPFRAV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT   660
ESQVRLLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG   720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA                            757

Seq ID NO: C225 Protein Sequence
Protein Accession #: NP_612464

1          11         21         31         41         51
|          |          |          |          |          |
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MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA   60
GVPGRDGSPG ANGIPGTPGI PGRDGFKGEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL  120
GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIIYLDQ  180
GSPEMNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIIEE  240
LPK                                                                243

Seq ID NO: C226 Protein Sequence
Protein Accession #: NP_003216.1

1          11         21         31         41         51
|          |          |          |          |          |
MATMENKVIC ALVLVSMLAL GTLAEAQTET CTVAPRERQN CGFPGVTPSQ CANKGCCFDD   60
TVRGVPWCFY PNTIDVPPEE ECEF                                         84

Seq ID NO: C227 Protein Sequence
Protein Accession #: NP_056234.1

1          11         21         31         41         51
|          |          |          |          |          |
MPKRAHWGAL SVVLILLWGH PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI   60
NLGFNSIQAL SETSFAGLTK LELLMIHGNE IPSIPDGALR DLSSLQVFKF SYNKLRVITG  120
QTLQGLSNLM RLHIDHNKIE FIHPQAFNGL TSLRLLHLEG NLLHQLHPST FSTFTFLDYF  180
RLSTIRHLYL AENMVRTLPA SMLRNMPLLE NLYLQGNPWT CDCEMRWFLE WDAKSRGILK  240
CKKDKAYEGG QLCAMCFSPK KLYKHEIHKL KDMTCLKPSI ESPLRQNRSR SIEEEQEQEE  300
DGGSQLILEK FQLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHLNQT DPPDIDINAT  360
VALDFECPMT RENYEKLWKL IAYYSEVPVK LHRELMLSKD PRVSYQYRQD ADEEALYYTG  420
VRAQILAEPE WVMQPSIDIQ LNRRQSTAKK VLLSYYTQYS QTISTKDTRQ ARGRSWVMIE  480
PSGAVQRDQT VLEGGPCQLS CNVKASESPS IFWVLPDGSI LKAPMDDPDS KFSILSSGWL  540
RIKSMEPSDS GLYQCIAQVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN  600
ALAIPEAHLS WILPNRRIIN DLANTSHVYM LPNGTLSIPK VQVSDSGYYR CVAVNQQGAD  660
HFTVGITVTK KGSGLPSKRG RRPGAKALSR VREDIVEDEG GSGMGDEENT SRRLLHPKDQ  720
EVFLKTKDDA INGDKKAKKG RRKLKLWKHS EKEPETNVAE GRRVFESRRR INMANKQINP  780
ERWADILAKV RGKNLPKGTE VPPLIKTTSP PSLSLEVTPP FPAVSPPSAS PVQTVTSAEE  840
SSADVPLLGE EEHVLGTISS ASMGLEHNHN GVILVEPEVT STPLEEVVDD LSEKTEEITS  900
TEGDLKGTAA PTLISEPYEP SPTLHTLDTV YEKPTHEETA TEGWSAADVG SSPEPTSSEY  960
EPPLDAVSLA ESEPMQYFDP DLETKSQPDE DKMKEDTFAH LTPTPTIWVN DSSTSQLFED 1020
STIGEPGVPG QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLQGG NMLEGDPTHS 1080
RSSESEGQES KSITLPDSTL GIMSSMSPVK KPAETTVGTL LDKDTTTVTT TPRQKVAPSS 1140
TMSTHPSRRR PNGRRRLRPN KFRHRHKQTP PTTFAPSETF STQPTQAPDI KISSQVESSL 1200
VPTAWVDNTV NTPKQLEMEK NAEPTSKGTP RRKHGKRPNK HRYTPSTVSS RASGSKPSPS 1260
PENKHRNIVT PSSETILLPR TVSLKTEGPY DSLDYMTTTR KIYSSYPKVQ ETLPVTYKPT 1320
SDGKEIKDDV ATNVDKHKSD ILVTGESITN AIPTSRSLVS TMGEFKEESS PVGFPGTPTW 1380
NPSRTAQPGR LQTDIPVTTS GENLTDPPLL KELEDVDFTS EFLSSLTVST PFHQEEAGSS 1440
TTLSSIKVEV ASSQAETTTL DQDHLETTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500
MSLGQTTTTK PALPSPRISQ ASRDSKENVF LNYVGNPETE ATPVNNEGTQ HMSGPNELST 1560
PSSDRDAFNL STKLELEKQV FGSRSLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620
LPEMSTQSAS RYFVTSQSPR HWTNKPEITT YPSGALPENK QFTTPRLSST TIPLPLHMSK 1680
PSIPSKFTDR RTDQFNGYSK VFGNNNIPEA RNPVGKPPSP RIPHYSNGRL PFFTNKTLSF 1740
PQLGVTRRPQ IPTSPAPVMR ERKVIPGSYN RIHSHSTFHL DFGPPAPPLL HTPQTTGSPS 1800
TNLQNIPMVS STQSSISFIT SSVQSSGSFH QSSSKFFAGG PPASKFWSLG EKPQILTKSP 1860
QTVSVTAETD TVFPCEATGK PKPFVTWTKV STGALMTPNT RIQRFEVLKN GTLVIRKVQV 1920
QDRGQYMCTA SNLHGLDRMV VLLSVTVQQP QILASHYQDV TVYLGDTIAM ECLAKGTPAP 1980
QISWIFPDRR VWQTVSPVES RITLHENRTL SIKEASFSDR GVYKCVASNA AGADSLAIRL 2040
HVAALPPVIH QEKLENISLP PGLSIHIHCT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100
VFPNGTLYIR NLAPKDSGRY ECVAANLVGS ARRTVQLNVQ RAAANARITG TSPRRTDVRY 2160
GGTLKLDCSA SGDPWPRILW RLPSKRMIDA LFSFDSRIKV FANGTLVVKS VTDKDAGDYL 2220
CVARNKVGDD YVVLKVDVVM KPAKIEHKEE NDHKVFYCGD LKVDCVATGL PNPEISWSLP 2280
DGSLVNSFMQ SDDSGGRTKR YVVFNNGTLY FNEVGMREEG DYTCFAENQV GKDEMRVRVK 2340
VVTAPATIRN KTYLAVQVPY GDVVTVACEA KGEPMPKVTW LSPTNKVIPT SSEKYQIYQD 2400
GTLLIQKAQR SDSGNYTCLV RNSAGEDRKT VWIHVNVQPP KINGNPNPIT TVREIAAGGS 2460
RKLIDCKAEG IPTPRVLWAF PEGVVLPAPY YGNRITVHGN GSLDIRSLRK SDSVQLVCMA 2520
RNEGGEARLI VQLTVLEPME KPIFHDPISE KITAMAGHTI SLNCSAAGTP TPSLVWVLPN 2580
GTDLQSGQQL QRFYHKADGM LHISGLSSVD AGAYRCVARN AAGHTERLVS LKVGLKPEAN 2640
KQYHNLVSII NGETLKLPCT PPGAGQGRFS WTLPNGMHLE GPQTLGRVSL LDNGTLTVRE 2700
ASVFDRGTYV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVIYTRPGNT VKLNCMAMGI 2760
PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820
KTTYIHVF                                                           2828

Seq ID NO: C228 Protein Sequence
Protein Accession #: Eos sequence

1          11         21         31         41         51
|          |          |          |          |          |
MPGTKLTRTG APADYRVILK TSQEDELDVP DDISVRVMSS QSVLVSWVDP VLEKQKKVVA   60
SRQYTVRYRE KGELARWDYK QIANRRVLIE NLIPDTVYEF AVRISQGERD GKWSTSVFQR  120
TPESAPTTAP ENLNVWPVNG KPTVVAASWD ALPETEGKVK VCLLDTGLFS VSSFQPSAKS  180
FQNTFFHTPR LSNHLEQSPS PILETLLLPW WMVCSLGNAI FSKSGPQTGE AWDLTPKPSL  240
SLCQQECSCT QKDFSCLAYL IDIQTKQVNK DPQLEGSVFG PCFLFYFLTF MLDIGGFSFI  300
MCYEDP?VSS LTGNSLKSVA ASKADVQQNT EDNGKPEKPE PSSPSPRAPA SSQHPSVPAS  360
PQGRNAKDLL LDLKNKILAN GGAPRKPQLR AKKAEELDLQ STEITGEEEL GSREDSPMSP  420
SDTQDQKRTL RPPSRHGHSV VAPGRTAVRA RMPALPRREG VDKPGFSLAT QPRPGAPPSA  480
SASPAHHAST QGTSHRPSLP ASLNDNDLVD SDEDERAVGS LHPKGAFAQP RPALSPSRQS  540
PSSVLRDRSS VHPGAKPASP ARRTPHSGAA EEDSSASAPP SRLSPPHGGS SRLLPTQPHL  600
SSPLSKGGKD GEDAPATNSN APSRSTMSSS VSSHLSSRTQ VSEGAEASDG ESHGDGDRED  660
```

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GGRQAEATAQ TLRARPASGH FHLLRHKPFA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR   720
AHPRVPSHSD SHPKLSSGIH GDEEDEKPLP ATVVNDHVPS SSRQPISRGW EDLRRSPQRG   780
ASLHRKEPIP ENPKSTGADT HPQGKYSSLA SKAQDVQQST DADTEGHSPK AQPGSTDRHA   840
SPARPPAARS QQHPSVPRRM TPGRAPEQQP PPPVATSQHH PGPQSRDAGR SPSQPRLSLT   900
QAGRPRPTSQ GRSHSSSDPY TASSRGMLPT ALQNQDEDAQ GSYDDDSTEV EAQDVRAPAH   960
AARAKEAAAS LPKHQQVESP TGAGAGGDHR SQRGHAASPA RPSRPGGPQS RARVPSRAAP  1020
GKSEPPSKRP LSSKSQQSVS AEDEEEEDAG FFKGGKEDLL SSSVPKWPSS STPRGGKDAD  1080
GSLAKEEREP AIALAPRGGS LAPVKRPLPP PPGSSPRASH VPSRPPPRSA ATVSPVAGTH  1140
PWPRYTTRAP PGHFSTTPML SLRQRMMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVLP  1200
GSNGKPNGQR IINGPQGTKW VVDLDRGLVL NAEGRYLQDS HGNPLRIKLG GDGRTIVDLE  1260
GTPVVSPDGL PLFGQGRHGT PLANAQDKPI LSLGGKPLVG LEVIKKTTHP PTTTMQPTTT  1320
TTPLPTTTTP RPTTATTMQP TTTTTPLPTT TPRPTTATTR RTTTRRPTTT VRTTTRTTTT  1380
TTPKPTTPIP TCPPGTLERH DDDGNLIMSS NGIPECYAEE DEFSGLETDT AVPTEEAYVI  1440
YDEDYEFETS RPPTTTEPST TATTPRVIPE EGAISSFPEE EFDLAGRKRF VAPYVTYLNK  1500
DPSAPCSLTD ALDHFQVDSL DEIIPNDLKK SDLPPQHAPR NITVVAVEGC HSFVIVDWDK  1560
ATPGDLVTGY LVYSASYEDF IRNKFSTQAS SVTHLPIENL KPNTRYYFKV QAQNPHGYGP  1620
ISPSVSFVTE SDNPLLVVRP PGGELSGSHS LSNMIPATRT AMDGNM                  1666
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Seq ID NO: C229 Protein Sequence
Protein Accession #: NP_003005.1

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1          11         21         31         41         51
|          |          |          |          |          |
MFLSILVALC LWLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ    60
YEELVDVNCS AVLRFFFCAM YAPICTLEFL HDPIKPCKSV CQRARDDCEP LMKMYNHSWP   120
ESLACDELPV YDRGVCISPE AIVTDLPEDV KWIDITPDMM VQERPLDVDC KRLSPDRCKC   180
KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIPKSSSPI PRTQVPLITN   240
SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD   300
KKKTAGRTSR SNPPKPKGKP PAPKPASPKK NIKTRSAQKR TNPKRV                  346
```

Seq ID NO: C230 Protein Sequence
Protein Accession #: NP_005931.1

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1          11         21         31         41         51
|          |          |          |          |          |
MAPAAWLRSA AARALLPPML LLLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA    60
PAPATQEAPR PASSLRPPRC GVPDPSDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ   120
LVQEQVRQTM AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DGPGGILAHA   180
FFPKTHREGD VHFDYDETWT IGDDQGTDLL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR   240
YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA   300
VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA QGHIWFFQGA   360
QYWVYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS   420
PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC   480
AEPANTFL                                                            488
```

Seq ID NO: C231 Protein Sequence
Protein Accession #: NP_076927

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1          11         21         31         41         51
|          |          |          |          |          |
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI    60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF   120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK   180
VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH   240
LCGGSVITPL WIITAAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR   300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLNHAA   360
VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF   420
GIGCAEVNKP GVYTRVTSFL DWIHEQMERD LKT                                453
```

Seq ID NO: C232 Protein Sequence
Protein Accession #: NP_003211

```
1          11         21         31         41         51
|          |          |          |          |          |
MLWKLTDNIK YEDCEDRHDG TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP    60
PYQPIYPQSQ DPYSHVNDPY SLNPLHAQPQ PQHPGWPGQR QSQESGLLHT HRGLPHQLSG   120
LDPRRDYRRH EDLLHGPHAL SSGLGDLSIH SLPHAIEEVP HVEDPGINIP DQTVIKKGPV   180
SLSKSNSNAV SAIPINKDNL FGGVVNPNEV FCSVPGRLSL LSSTSKYKVT VAEVQRRLSP   240
PECLNASLLG GVLRRAKSKN GGRSLREKLD KIGLNLPAGR RKAANVTLLT SLVEGEAVHL   300
ARDFGYVCET EFPAKAVAEF LNRQHSDPNE QVTRKNMLLA TKQICKEFTD LLAQDRSPLG   360
NSRPNPILEP GIQSCLTHFN LISHGFGSPA VCAAVTALQN YLTEALKAMD KMYLSNNPNS   420
HTDNNAKSSD KEEKHRK                                                  437
```

Seq ID NO: C233 Protein Sequence
Protein Accession #: NP_002979.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCPKPGVI    60
LLTKRGRQIC ADPNKKWVQK YISDLKLNA                                      89
```

Seq ID NO: C234 Protein Sequence
Protein Accession #: NP_004054.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MILQAHLHSL CLLMLYLATG YGQEGKFSGP LKPMTFSIYE GQEPSQIIFQ FKANPPAVTF   60
ELTGETDNIF VIEREGLLYY NRALDRETRS THNLQVAALD ANGIIVEGPV PITIEVKDIN   120
DNRPTFLQSK YEGSVRQNSR PGKPFLYVNA TDLDDPATPN GQLYYQIVIQ LPMINNVMYF   180
QINNKTGAIS LTREGSQELN PAKNPSYNLV ISVKDMGGQS ENSFSDTTSV DIIVTENIWK   240
APKPVEMVEN STDPHPIKIT QVRWNDPGAQ YSLVDKEKLP RFPFSIDQEG DIYVTQPLDR   300
EEKDAYVFYA VAKDEYGKPL SYPLEIHVKV KDINDNPPTC PSPVTVFEVQ ENERLGNSIG   360
TLTAHDRDEE NTANSFLNYR IVEQTPKLPM DGLFLIQTYA GMLQLAKQSL KKQDTPQYNL   420
TIEVSDKDFK TLCFVQINVI DINDQIPIFE KSDYGNLTLA EDTNIGSTIL TIQATDADEP   480
FTGSSKILYH IIKGDSEGRL GVDTDPHTNT GYVIIKKPLD FETAAVSNIV FKAENPEPLV   540
FGVKYNASSF AKFTLIVTDV NEAPQFSQHV FQAKVSEDVA IGTKVGNVTA KDPEGLDISY   600
SLRGDTRGWL KIDHVTGEIF SVAPLDREAG SPYRVQVVAT EVGGSSLSSV SEFHLILMDV   660
NDNPPRLAKD YTGLFFCHPL SAPGSLIFEA TDDDQHLFRG PHFTFSLGSG SLQNDWEVSK   720
INGTHARLST RHTEFEEREY VVLIRINDGG RPPLEGIVSL PVTFCSCVEG SCFRPAGHQT   780
GIPTVGMAVG ILLTTLLVIG IILAVVFIRI KKDKGKDNVE SAQASEVKPL RS           832
```

Seq ID NO: C235 Protein Sequence
Protein Accession #: NP_004434.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MARARPPPPP SPPPGLLPLL PPLLLLPLLL LPAGCRALEE TLMDTKWVTS ELAWTSHPES   60
GWEEVSGYDE AMNPIRTYQV CNVRESSQNN WLRTGFIWRR DVQRVYVELK FTVRDCNSIP   120
NIPGSCKETF NLFYYEADSD VASASSPFWM ENPYVKVDTI APDESFSRLD AGRVNTKVRS   180
FGPLSKAGFY LAFQDQGACM SLISVRAFYK KCASTTAGFA LFPETLTGAE PTSLVIAPGT   240
CIPNAVEVSV PLKLYCNGDG EWMVPVGACT CATGHEPAAK ESQCRPCPPG SYKAKQGEGP   300
CLPCPPNSRT TSPAASICTC HNNFYRADSD SADSACTTVP SPPRGVISNV NETSLILEWS   360
EPRDLGGRDD LLYNVICKKC HGAGGASACS RCDDNVEFVP RQLGLTERRV HISHLLAHTR   420
YTFEVQAVNG VSGKSPLPPR YAAVNITTNQ AAPSEVPTLR LHSSSGSSLT LSWAPPERPN   480
GVILDYEMKY FEKSEGIAST VTSQMNSVQL DGLRPDARYV VQVRARTVAG YGQYSRPAEF   540
ETTSERGSGA QQLQEQLPLI VGSATAGLVF VVAVVVIAIV CLRKQRHGSD SEYTEKLQQY   600
IAPGMKVYID PFTYEDPNEA VREFAKEIDV SCVKIEEVIG AGEFGEVCRG RLKQPGRREV   660
FVAIKTLKVG YTERQRRDFL SEASIMGQFD HPNIIRLEGV VTKSRPVMIL TEFMENCALD   720
SFLRLNDGQF TVIQLVGMLR GIAAGMKYLS EMNYVHRDLA ARNILVNSNL VCKVSDFGLS   780
RFLEDDPSDP TYTSSLGGKI PIRWTAPEAI AYRKFTSASD VWSYGIVMWE VMSYGERPYW   840
DMSNQDVINA VEQDYRLPPP MDCPTALHQL MLDCWVRDRN LRPKFSQIVN TLDKLIRNAA   900
SLKVIASAQS GMSQPLLDRT VPDYTTFTTV GDWLDAIKMG RYKESFVSAG FASFDLVAQM   960
TAEDLLRIGV TLAGHQKKIL SSIQDMRLQM NQTLPVQV                          998
```

Seq ID NO: C236 Protein Sequence
Protein Accession #: NP_001795.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MYVGYVLDKD SPVYPGPARP ASLGLGPANY GPPAPPPAPP QYPDFSSYSH VEPAPAPPTA   60
WGAPFPAPKD DWAAAYGPGP AAPAASPASL AFGPPPDFSP VPAPPGPGPG LLAQPLGGPG   120
TPSSPGAQRP TPYEWMRRSV AAGGGGGSGK TRTKDKYRVV YTDHQRLELE KEFHYSRYIT   180
IRRKSELAAN LGLTERQVKI WFQNRRAKER KVNKKKQQQQ QPPQPPMAHD ITATPAGPSL   240
GGLCPSNTSL LATSSPMPVK EEFLP                                        265
```

Seq ID NO: C237 Protein Sequence
Protein Accession #: NP_068813.1

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1          11         21         31         41         51
|          |          |          |          |          |
MCSDRARKGG GGPKDFGAGL KYNSRHEKVN GLEEGVEFLP VNNVKKVEKH GPGRWVVLAA   60
VLIGLLLVLL GIGFLVWHLQ YRDVRVQKVF NGYMRITNEN FVDAYENSNS TEFVSLASKV   120
KDALKLLYSG VPFLGPYHKE SAVTAFSEGS VIAYYWSEFS IPQHLVEEAE RVMAEERVVM   180
LPPRARSLKS FVVTSVVAFP TDSKTVQRTQ DNSCSFGLHA RGVELMRFTT PGFPDSPYPA   240
HARCQWALRG DADSVLSLTF RSFDLASCDE RGSDLVTVYN TLSPMEPHAL VQLCGTYPPS   300
YNLTFHSSQN VLLITLITNT ERRHPGFEAT FFQLPRMSSC GGRLRKAQGT FNSPYYPGHY   360
PPNIDCTWNI EVPNNQHVKV RFKFFYLLEP GVPAGTCPKD YVEINGEKYC GERSQFVVTS   420
NSNKITVRFH SDQSYTDTGF LAEYLSYDSS DPCPGQFTCR TGRCIRKELR CDGWADCTDH   480
SDELNCSCDA GHQFTCKNKF CKPLFWVCDS VNDCGDNSDE QGCSCPAQTF RCSNGKCLSK   540
SQQCNGKDDC GDGSDEASCP KVNVVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDGSDEK   600
DCDCGLRSFT RQARVVGGTD ADEGEWPWQV SLHALGQGHI CGASLISPNW LVSAAHCYID   660
DRGFRYSDPT QWTAFLGLHD QSQRSAPGVQ ERRLKRIISH PFFNDFTFDY DIALLELEKP   720
AEYSSMVRPI CLPDASHVFP AGKAIWVTGW GHTQYGGTGA LILQKGEIRV INQTTCENLL   780
PQQITPRMMC VGFLSGGVDS CQGDSGGPLS SVEADGRIFQ AGVVSWGDGC AQRNKPGVYT   840
RLPLFRDWIK ENTGV                                                   855
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Seq ID NO: C238 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN   60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
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RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK RPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP                              755

Seq ID NO: C239 Protein Sequence
Protein Accession #: Eos sequence

1          11         21         31         41         51
|          |          |          |          |          |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN   60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR   120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV   180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH   240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD   300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL   360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT   420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS   480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA   540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ   600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI   660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP   720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS   780
RTPPSNYREG LGTEMVPTFW NVCAPGP                                       807

Seq ID NO: C240 Protein Sequence
Protein Accession #: XP_097386.1

1          11         21         31         41         51
|          |          |          |          |          |
MPKSEPLGCL SPASRAPGSA AATGAWLPAA SGGPGPLGPP CTCPPRSLGR GRAGSRAGSS   60
PSGCVCVSGI LRVVSVGDPA SRRWVDLDSN SEDLSLLLTP MIVGTGGVGG GWARGWVPAQ   120
EKEVAEGSGH AGRGNGRRLQ RVYGARSWIL GRKPCLQRLL PASGGPVQPQ PCPSPATACR   180
WGFKFGVAFW GAAQHPPLCR LGGGRAVPSA TRTLDGF                            217

Seq ID NO: C241 Protein Sequence
Protein Accession #: CAC03433

1          11         21         31         41         51
|          |          |          |          |          |
MLSSTDFTFA SWELVVRVDH PNEEQQKDVT LRVSGDLHVG GVMLKLVEQI NISQDWSDFA   60
LWWEQKHCWL LKTHWTLDKY GVQADAKLLF TPQHKMLRLR LPNLKMVRLR VSFSAVVFKA   120
VSDICKILNI RRSEELSLLK PSGDYFKKKK KKDKNNKEPI IEDILNLESS PTASGSSVSP   180
GLYSKTMTPI YDPINGTPAS STMTWFSDSP LTEQNCSILA FSQPPQSPEA LADMYQPRSL   240
VDKAKLNAGW LDSSRSLMEQ GIQEDEQLLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI   300
LLEEIDCTEE EMLIFAALQY HISKLSLSAE TQDFAGESEV DEIEAALSNL EVTLEGGKAD   360
SLLEDITDIP KLADNLKLFR PKKLLPKAFK QYWFIFKDTS IAYFKNKELE QGEPLEKLNL   420
RGCEVVPDVN VAGRKFGIKL LIPVADGMNE MYLRCDHENQ YAQWMAACML ASKGKTMADS   480
SYQPEVLNIL SFLRMKNRNS ASQVASSLEN MDMNPECFVS PRCAKKHKSK QLAARILEAH   540
QNVAQMPLVE AKLRFIQAWQ SLPEFGLTYY LVRFKGSKKD DILGVSYNRL IKIDAATGIP   600
VTTWRFTNIK QWNVNWETRQ VVIEFDQNVF TAFTCLSADC KIVHEYIGGY IFLSTRSKDQ   660
NETLDEDLFH KLTGGQD                                                  677

Seq ID NO: C242 DNA Sequence
Nucleic Acid Accession #: NM_005170
Coding sequence: 337..918

1          11         21         31         41         51
|          |          |          |          |          |
GGGCGTGAGA AAGGCGACGG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TTAAAAACCA   60
GCCGCCTGCG CCGCGCCTGC GGAGACCTGG GAGAGTCCGG CCGCACGCGC GGGACACGAG   120
CGTCCCACGC TCCCTGGCGC GTACGGCCTG CCACCACTAG GCCTCCTATC CCCGGGCTCC   180
AGACGACCTA GGACGCGTGC CCTGGGGAGT TGCCTGGCGG CGCCGTGCCA GAAGCCCCCT   240
TGGGGCGCCA CAGTTTTCCC CGTCGCCTCC GGTTCCTCTG CCTGCACCTT CCTGCGGCGC   300
GCCGGGACCT GGAGCGGGCG GGTGGATGCA GGCGCGATGG ACGGCGGCAC ACTGCCCAGG   360
TCCGCGCCCC CTGCGCCCCC CGTCCCTGTC GGCTGCGCTG CCCGGCGGAG ACCCGCGTCC   420
CCGGAACTGT TGCGCTGCAG CCGGCCGCGG CGACCGGCCA CCGCAGAGAC CGGAGGCCGC   480
GCAGCGGCCG TAGCGCGGCG CAATGAGCGC GAGCGCAACC GCGTGAAGCT GGTGAACTTG   540
GGCTTCCAGG CGCTGCGGCA GCACGTGCCG CACGGCGGCG CCAGCAAGAA GCTGAGCAAG   600
GTGGAGACGC TGCGCTCAGC CGTGGAGTAC ATCCGCGCGC TGCAGCGCCT GCTGGCCGAG   660
CACGACGCCG TGCGCAACGC GCTGGCGGGA GGGCTGAGGC CGCAGGCCGT GCGGCCGTCT   720
GCGCCCCGCG GGCCGCCAGG GACCACCCCG GTCGCCGCCT CGCCCTCCCG CGCTTCTTCG   780
TCCCCGGGCC GCGGGGGCAG CTCGGAGCCC GGCTCCCCGC GTTCCGCCTA CTCGTCGGAC   840
GACAGCGGCT GCGAAGGCGC GCTGAGTCCT GCGGAGCGCG AGCTACTCGA CTTCTCCAGC   900
TGGTTAGGGG GCTACTGAGC GCCCTCGACC TA                                  932

Seq ID NO: C243 Protein Sequence
Protein Accession #: NP_060233.1

1          11         21         31         41         51
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|          |          |          |          |          |
MSGGHQLQLA ALWPWLLMAT LQAGFGRTGL VLAAAVESER SAEQKAVIRV IPLKMDPTGK   60
LNLTLEGVFA GVAEITPAEG KLMQSHPLYL CNASDDDNLE PGFISIVKLE SPRRAPRPCL  120
SLASKARMAG ERGASAVLFD ITEDRAAAEQ LQQPLGLTWP VVLIWGNDAE KLMEFVYKNQ  180
KAHVRIELKE PPAWPDYDVW ILMTVVGTIF VIILASVLRI RCRPRHSRPD PLQQRTAWAI  240
SQLATRRYQA SCRQARGEWP DSGSSCSSAP VCAICLEEFS EGQELRVISC LHEFHRNCVD  300
PWLHQHRTCP LCVFNITEGD SFSQSLGPSR SYQEPGRRLH LIRQHPGHAH YHLPAAYLLG  360
PSRSAVARPP RPGPFLPSQE PGMGPRHHRF PRAAHPRAPG EQQRLAGAQH PYAQGWGMSH  420
LQSTSQHPAA CPVPLRRARP PDSSGSGESY CTERSGYLAD GPASDSSSGP CHGSSSDSVV  480
NCTDISLQGV HGSSSTFCSS LSSDFDPLVY CSPKGDPQRV DMQPSVTSRP RSLDSVVPTG  540
ETQVSSHVHY HRHRHHHYKK RFQWHGRKPG PETGVPQSRP PIPRTQPQPE PPSPDQQVTG  600
SNSAAPSGRL SNPQCPRALP EPAPGPVDAS SICPSTSSLF NLQKSSLSAR HPQRKRRGGP  660
SEPTPGSRPQ DATVHPACQI FPHYTPSVAY PWSPEAHPLI CGPPGLDKRL LPETPGPCYS  720
NSQPVWLCLT PRQPLEPHPP GEGPSEWSSD TAEGRPCPYP HCQVLSAQPG SEEELEELCE  780
QAV                                                                783

Seq ID NO: C244 DNA Sequence
Nucleic Acid Accession #: NM_004289
Coding sequence: 493..1695

1          11         21         31         41         51
|          |          |          |          |          |
GCCGCCGCCT CGTCCACCGG AGGAGCCGGC GCCAGCGTGG ACGGCGGCAG CCAGGCTGTG   60
CAGGGGGGCG GCGGGGACCC CCGAGCGGCT CGCAGTGGCC CCTTCGACGC CGGGGAAGAG  120
GAGAAGGCAC CCGCGGAACC GACGGCTCAG GTGCCGGACG CTGGCGGATG TGCGAGCGAG  180
GAGAATGGGG TACTAAGAGA AAAGCACGAA GCTGTGGATC ATAGTTCCCA GCATGAGGAA  240
AATGAAGAAA GGGTGTCAGC CCAGAAGGAG AACTCACTTC AGCAGAATGA TGATGATGAA  300
AACAAAATAG CAGAGAAACC TGACTGGGAG GCAGAAAAGA CCACTGAATC TAGAAATGAG  360
AGACATCTGA ATGGGACAGA TACTTCTTTC TCTCTGGAAG ACTTATTCCA GTTGCTTTCA  420
TCACACCCTG AAAATTCACT GGAGGGCATC TCATTGGGAG ATATTCCTCT TCCAGGCAGT  480
ATCAGTGATG GCATGAATTC TTCAGCACAT TATCATGTAA ACTTCAGCCA GGCTATAAGT  540
CAGGATGTGA ATCTTCATGA GGCCATCTTG CTTTGTCCCA ACAATACATT TAGAAGAGAT  600
CCAACAGCAA GGACTTCACA GTCACAAGAA CCATTTCTGC AGTTAAATTC TCATACCACC  660
AATCCTGAGC AAACCCTTCC TGGAACTAAT TTGACAGGAT TTCTTTCACC GGTTGACAAT  720
CATATGAGGA ATCTAACAAG CCAAGACCTA CTGTATGACC TTGACATAAA TATATTTGAT  780
GAGATAAACT TAATGTCATT GGCCACAGAA GACAACTTTG ATCCAATCGA TGTTTCTCAG  840
CTTTTTGATG AACCAGATTC TGATTCTGGC CTTTCTTTAG ATTCAAGTCA CAATAATACC  900
TCTGTCATCA AGTCTAATTC CTCTCACTCT GTGTGTGATG AAGGTGCTAT AGGTTATTGC  960
ACTGACCATG AATCTAGTTC CCATCATGAC TTAGAAGGTG CTGTAGGTGG CTACTACCCA 1020
GAACCCAGTA AGCTTTGTCA CTTGGATCAA AGTGATTCTG ATTTCCATGG AGATCTTACA 1080
TTTCAACACG TATTTCATAA CCACACTTAC CACTTACAGC CAACTGCACC AGAATCTACT 1140
TCTGAACCTT TTCCGTGGCC TGGGAAGTCA CAGAAGATAA GGAGTAGATA CCTTGAAGAC 1200
ACAGATAGAA ACTTGAGCCG TGATGAACAG CGTGCTAAAG CTTTGCATAT CCCTTTTTCT 1260
GTAGATGAAA TTGTCGGCAT GCCTGTTGAT TCTTTCAATA GCATGTTAAG TAGATATTAT 1320
CTGACAGACC TACAAGTCTC ACTTATCCGT GACATCAGAC GAAGAGGGAA AAATAAAGTT 1380
GCTGCGCAGA ACTGTCGTAA ACGCAAATTG GACATAATTT TGAATTTAGA AGATGATGTA 1440
TGTAACTTGC AAGCAAAGAA GGAAACTCTT AAGAGAGAGC AAGCACAATG TAACAAAGCT 1500
ATTAACATAA TGAAACAGAA ACTGCATGAC CTTTATCATG ATATTTTTAG TAGATTAAGA 1560
GATGACCAAG GTAGGCCAGT CAATCCCAAC CACTATGCTC TCCAGTGTAC CCATGATGGA 1620
AGTATCTTGA TAGTACCCAA AGAACTGGTG GCCTCAGCCC ACAAAAAGGA AACCCAAAAG 1680
GGAAAGAGAA AGTGAGAAGA AACTGAAGAT GGACTCTATT ATGTGAAGTA GTAATGTTCA 1740
GAAACTGATT ATTTGGATCA GAAACCATTG AAACTGCTTC AAGAATTGTA TCTTTAAGTA 1800
CTGCTACTTG AATAACTCAG TTAACGCTGT TTTGAAGCTT ACATGGACAA ATGTTTAGGA 1860
CTTCAAGATC ACACTTGTGG GCAATCTGGG GGAGCCACAA CTTTTCATGA AGTGCATTGT 1920
ATACAAAATT CATAGTTATG TCCAAAGAAT AGGTTAACAT GAAAACCCAG TAAGACTTTC 1980
CATCTTGGCA GCCATCCTTT TTAAGAGTAA GTTGGTTACT TCAAAAAGAG CAAACACTGG 2040
GGATCAAATT ATTTTAAGAG GTATTTCAGT TTTAAATGCA AAATAGCCTT ATTTTCATTT 2100
AGTTTGTTAG CACTATAGTG AGCTTTTCAA ACACTATTTT AATCTTTATA TTTAACTTAT 2160
AAATTTTGCT TTCT                                                   2174

Seq ID NO: C245 Protein Sequence
Protein Accession #: NP_004433

1          11         21         31         41         51
|          |          |          |          |          |
MALRRLGAAL LLLPLLAAVE ETLMDSTTAT AELGWMVHPP SGWEEVSGYD ENMNTIRTYQ   60
VCNVFESSQN NWLRTKFIRR RGAHRIHVEM KFSVRDCSSI PSVPGSCKET FNLYYYEADF  120
DSATKTFPNW MENPWVKVDT IAADESFSQV DLGGRVMKIN TEVRSFGPVS RSGFYLAFQD  180
YGGCMSLIAV RVFYRKCPRI IQNGAIFQET LSGAESTSLV AARGSCIANA EEVDVPIKLY  240
CNGDGEWLVP IGRCMCKAGF EAVENGTVCR GCPSGTFKAN QGDEACTHCP INSRTTSEGA  300
TNCVCRNGYY RADLDPLDMP CTTIPSAPQA VISSVNETSL MLEWTPPRDS GGREDLVYNI  360
ICKSCGSGRG ACTRCGDNVQ YAPRQLGLTE PRIYISDLLA HTQYTFEIQA VNGVTDQSPF  420
SPQFASVNIT TNQAAPSAVS IMHQVSRTVD SITLSWSQPD QPNGVILDYE LQYYEKELSE  480
YNATAIKSPT NTVTVQGLKA GAIYVFQVRA RTVAGYGRYS GKMYFQTMTE AEYQTSIQEK  540
LPLIIGSSAA GLVFLIAVVV IAIVCNRRRG FERADSEYTD KLQHYTSGHM TPGMKIYIDP  600
FTYEDPNEAV REFAKEIDIS CVKIEQVIGA GEFGEVCSGH LKLPGKREIF VAIKTLKSGY  660
TEKQRRDFLS EASIMGQFDH PNVIHLEGVV TKSTPVMIIT EFMENGSLDS FLRQNDGQFT  720
VIQLVGMLRG IAAGMKYLAD MNYVHRDLAA RNILVNSNLV CKVSDFGLSR FLEDDTSDPT  780
YTSALGGKIP IRWTAPEAIQ YRKFTSASDV WSYGIVMWEV MSYGERPYWD MTNQDVINAI  840
EQDYRLPPPM DCPSALHQLM LDCWQKDRNH RPKFGQIVNT LDKMIRNPNS LKAMAPLSSG  900
INLPLLDRTI PDYTSFNTVD EWLEAIKMGQ YKESFANAGF TSFDVVSQMM MEDILRVGLT  960
LAGHQKKILN SIQVMRAQMN QIQSVEV                                      987

Seq ID NO: C246 Protein Sequence
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Protein Accession #: NP_114148.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDARRVPQKD LRVKKNLKKF RYVKLISMET SSSSDDSCDS FASDNFANTR LQSVREGCRT   60
RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSENSVT DSNSDSEDES GMNFLEKRAL  120
NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL  180
TRSRSRILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSRRSR SSVTLPHIIR  240
PVEEITEGGV GERLQQFSKR RYITVHWALL VINAVRRLLI PKQTAETQTA GAFEASSVAP  300
AFETVMVKRS GMLCWIRTGI ARLVEESATA VSAGSEMDGV RLGSLCI                347
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Seq ID NO: C247 Protein Sequence
Protein Accession #: NP_036577.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MENPSPAAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY   60
PLFRPPAQWS SLLGAAHSSD YSMWRKNQYV SNGLRDFAER GEAWALMKEI EAAGEALQSV  120
HAVFSAPAVP SGTGQTSAEL EVQRRHSLVS FVVRIVPSPD WFVGVDSLDL CDGDRWREQA  180
ALDLYPYDAG TDSGFTFSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT  240
LVRLRQSPRA FIPPAPVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTKS  300
RTRYVRVQPA NNGSPCPELE EEAECVPDNC V                                 331
```

Seq ID NO: C248 Protein Sequence
Protein Accession #: NP_063947.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLQDPDSDQP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY   60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT  120
GNWFSACFDN FTEALAETAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELRMRNSS  180
GPCLSGSLVS LHCLACGKSL KTPRVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV  240
LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIIE FNPMYPKDND IALMKLQFPL  300
TFSGTVRPIC LPFFDEELTP ATPLWIIGWG FTKQNGGKMS DILLQASVQV IDSTRCNADD  360
AYQGEVTEKM MCAGIPEGGV DTCQGDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT  420
KVSAYLNWIY NVWKAEL                                                 437
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Seq ID NO: C249 Protein Sequence
Protein Accession #: NP_003036.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGCKVLLNIG QQMLRRKVVD CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLAGAVARE   60
NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNLILS  120
YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT  180
LGVKESAMVN KIFTCINVLV LGFIMVSGFV KGSVKNWQLT EEDFGNTSGR LCLNNDTKEG  240
KPGVGGFMPF GFSGVLSGAA TCFYAFVGFD CIATTGEEVK NPQKAIPVGI VASLLICFIA  300
YFGVSAALTL MMPYFCLDNN SPLPDAFKHV GWEGAKYAVA VGSLCALSAS LLGSMFPMPR  360
VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLVD LMSIGTLLAY  420
SLVAACVLVL RYQPEQPNLV YQMASTSDEL DPADQNELAS TNDSQLGFLP EAEMFSLKTI  480
LSPKNMEPSK ISGLIVNIST SLIAVLIITF CIVTVLGREA LTKGALWAVF LLAGSALLCA  540
VVTGVIWRQP ESKTKLSFKV PFLPVLPILS IFVNVYLMMQ LDQGTWVRFA VWMLIGFIIY  600
FGYGLWHSEE ASLDADQART PDGNLDQCK                                    629
```

Seq ID NO: C250 Protein Sequence
Protein Accession #: NP_002767.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA PCARGSQPWQ   60
VSLFNGLSFH CAGVLVDQSW VLTAAHCGNK PLWARVGDDH LLLLQGEQLR RTTRSVVHPK  120
YHQGSGPILP RRTDEHDLML LKLARPVVPG PRVRALQLPY RCAQPGDQCQ VAGWGTTAAR  180
RVKYNKGLTC SSITILSPKE CEVFYPGVVT NNMICAGLDR GQDPCQSDSG GPLVCDETLQ  240
GILSWGVYPC GSAQHPAVYT QICKYMSWIN KVIRSN                            276
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Seq ID NO: C251 Protein Sequence
Protein Accession #: XP_095088.3

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1          11         21         31         41         51
|          |          |          |          |          |
MTRAATAEPG RVSPASPARS TAGLPRAFLQ SLRTLLDILD DWQRGCVHLR EIQSLWVEAR   60
ELPSGVLEGL SQRRGPQPGA AVRSRRGCAV PRGARAVPER CAGTETRRGR RCSGLQRLGG  120
GFRGCPADPC ARGEHRRHTI TSGVDCGLLK QMKELEQEKE VLLQGLEMMA QGRDWYQQQL  180
QQVQERQCRL GQSRASADFG AVGSPRPLGR LLPKVQEVAR WLGELLAEAC AGRALPTSSS  240
GPPCSALTST SSPGWQQQII LMLKEQNRLL TQEVTEKSER ITQLEQKSAL IKQLFEARAL  300
SQQDGGLSPA GPHIEPLTRF RLPVLTWAGA LLSPHSPQLL LPLSADSGGP LHELPDTWFP  360
AVLLWVPSPG KRTAHARLHF HQRPAEGAWQ LGCGAEAAPE TCGTLPHFES HKTTCEPDSL  420
GGPCPQEGDR SWSHLGAAFD VAPAVAKVTP NREDAAGSRH GDICPLCPKG LLTFRDIAIE  480
FSLAEWQCLD HAQQNLYRDV MLENYRNLFS LGMTVSKPDL IACLEQNKEP QNIKRNEMAA  540
KHPVTCSHFN QDLQPEQSIK DSLQKVIPRT YGKCGHENLQ LKKCCKRVDE CEVHKGGYND  600
LNQCLSNTQN KIFQTHKCVK VFSKFSNSNR HNARYTGKKH LKCKKYGKSF CMFSHLNQHQ  660
IIHTKEKSYK CEECGKSFNH SSSGTTHKRI LTGEKPYRCE ECGKAFRWPS NLTRHKRIHT  720
GEKPYACEEC GQAFRRSSTL TNHKRIHTGE RPYKCEECGK AFSVSSALIY HKRIHTGEKP  780
YTCEECGKAF NCSSTLKTHK IIHTGEKPYT CEECGRTFNC SSTVKAHKRI HTGEKPYKCE  840
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ECDKAFKWHS SLAKHKIIHT GEKPYKCSDS KALAKSSEVQ KVYSGDGENG IRVHKKKETQ   900
GWLVRNKNEN RTGLFQIRAA VRPNRDPSWG QQEGSLTDPI QRKEEPDLQN HYDHQNALED   960
QRNTGVGGLL TFRDVVIEFS LEEWQCLDHA QQNLYRDVML ENYRNLVSLG IAVSKPDLIT   1020
CLEQNKEPWN IKRNEMVTKH PDLPPELGIK DSLQKVIPRR YGKSGHDNLQ VKTCKSMGEC   1080
EVQKGGCNEV NQCLSTTQNK IFQTHKCVKV FGKFSNSNRH KTRHTGKKHF KCKKYGKSFC   1140
MVSQLHQHQI IHTRENSYQC EECGKPFNCS STLSKHKRIH TGEKPYRCEE CGKAFTWSST   1200
LTKHRRIHTG EKPYTCEECG QAFSRSSTLA NHKRIHTGEK PYTCEECGKA FSLSSSLTYH   1260
KRIHTGEKPY TCEECGKAFN CSSTLKKHKI IHTGEKPYKC KECGKAFAFS STLNTHKRIH   1320
TGEEPYKCEE CDKAFKWSSS LANHKSMHTG EKPYKCE                            1357
```

Seq ID NO: C252 Protein Sequence
Protein Accession #: NP_114433.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSN CYGYFRKLRN WSDAELECQS   60
YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG   120
KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP                           158
```

Seq ID NO: C253 Protein Sequence
Protein Accession #: XP_051860.2

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1          11         21         31         41         51
|          |          |          |          |          |
MDCVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK PVRPKLTVTI DTNVNSTILN   60
LEDNVQSWKP GDTLVIASTD YSMYQAEEFQ VLPCRSCAPN QVKVAGKPMY LHIGEEIDGV   120
DMRAEVGLLS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIKFALGFK AAHLEGTELK   180
HMGQQLVGQY PIHFHLAGDV DERGGYDPPT YIRDLSIHHT FSRCVTVHGS NGLLIKDVVG   240
YNSLGHCFFT EDGPEERNTF DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ   300
DCNAVSTFWM ANPNNNLINC AAAGSEETGF WFIFHHVPTG PSVGMYSPGY SEHIPLGKFY   360
NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLSIISARYS PHQDADPLKP REPAIIRHFI   420
AYKNQDHGAW LRGGDVWLDS CRFADNGIGL TLASGGTFPY DDGSKQEIKN SLFVGESGNV   480
GTEMMDNRIW GPGGLDHSGR TLPIGQNFPI RGIQLYDGPI NIQNCTFRKF VALEGRHTSA   540
LAFRLNNAWQ SCPHNNVTGI AFEDVPITSR VFFGEPGPWF NQLDMDGDKT SVFHDVDGSV   600
SEYPGSYLTK NDNWLVRHPD CINVPDWRGA ICSGCYAQMY IQAYKTSNLR MKIIKNDFPS   660
HPLYLEGALT RSTHYQQYQP VVTLQKGYTI HWDQTAPAEL AIWLINFNKG DWIRVGLCYP   720
RGTTFSILSD VHNRLLKQTS KTGVFVRTLQ MDKVEQSYPG RSHYYWDEDS GLLFLKLKAQ   780
NEREKFAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLFGSQLK   840
TKDHFLEVKM ESSKQHFPHL WNDFAYIEVD GKKYPSSEDG IQVVVIDGNQ GRVVSHTSFR   900
NSILQGIPWQ LFNYVATIPD NSIVLMASKG RYVSRGPWTR VLEKLGADRG LKLKEQMAFV   960
GFKGSFRPIW VTLDTEDHKA KIFQVVPIPV VKKKKL                             996
```

Seq ID NO: C254 Protein Sequence
Protein Accession #: NP_055188.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTALSSENCS FQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT CQNFMEYFCI   60
SLAFVDLLLL VNISIILYFR DFVLLSIRFT KYHICLFTQI ISFTYGFLHY PVFLTACIDY   120
CLNFSKTTKL SFKCQKLFYF FTVILIWISV LAYVLGDPAI YQSLKAQNAY SRHCPFYVSI   180
QSYWLSFFMV MILFVAFITC WEEVTTLVQA IRITSYMNET ILYFPFSSHS SYTVRSKKIF   240
LSKLIVCFLS TWLPFVLLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN   300
LKDIGLPLDP FVNWKCCFIP LTIPNLEQIE KPISIMIC                           338
```

Seq ID NO: C255 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MALVLGSLLL LGLCGNSFSG GQPSSTDAPK AWNYELPATN YETQDSHKAG PIGILFELVH   60
IFLYVVQPRD FPEDTLRKFL QKAYESKIDY DKIVYYEAGI ILCCVLGLLF IILMPLVGYF   120
FCMCRCCNKC GGEMHQRQKE NGPFLRKCFA ISLLVICIII SIGIFYGFVA NHQVRTRIKR   180
SRKLADSNFK DLRTLLNETP EQIKYILAQY NTTKDKAFTD LNSINSVLGG GILDRLRPNI   240
IPVLDEIKSM ATAIKETKEA LENMNSTLKS LHQQSTQLSS SLTSVKTSLR SSLNDPLCLV   300
HPSSETCNSI RLSLSQLNSN PELRQLPPVD AELDNVNNVL RTDLDGLVQQ GYQSLNDIPD   360
RVQRQTTTVV AGIKRVLNSI GSDIDNVTQR LPIQDILSAF SVYVNNTESY IHRNLPTLEE   420
YDSYWWLGGL VICSLLTLIV IFYYLGLLCG VCGYDRHATP TTRGCVSNTG GVFLMVGVGL   480
SFLFCWILMI IVVLTFVFGA NVEKLICEPY TSKELFRVLD TPYLLNEDWE YYLSGKLFNK   540
SKMKLTFEQV YSDCKKNRGT YGTLHLQNSF NISEHLNINE HTGSISSELE SLKVNLNIFL   600
LGAAGRKNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLLS FAYDLEAKAN SLPPGNLRNS   660
LKRDAQTIKT IHQQRVLPIE QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFAQNFITN   720
NTSSVIIEET KKYGRTIIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYIID   780
PLNLFWFGIG KATVFLLPAL IFAVKLAKYY RRMDSEDVYD DVETIPMKNM ENGNNGYHKD   840
HVYGIHNPVM TSPSQH                                                   856
```

Seq ID NO: C256 Protein Sequence
Protein Accession #: NP_149038.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKAIIHLTLL ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT   60
PSFPTATSPA PPIISTHSSS TIPTPAPPII STHSSSTIPI PTAADSESTT NVNSLATSDI   120
ITASSPNDGL ITMVPSETQS NNEMSPTTED NQSSGPPTGT ALLETSTLNS TGPSNPCQDD   180
PCADNSLCVK LHNTSPCLCL EGYYYNSSTC KKGKVFPGKI SVTVSETFDP EEKHSMAYQD   240
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LHSEITSLFK DVFGTSVYGQ TVILTVSTSL SPRSEMRADD KFVNVTIVTI LAETTSDNEK   300
TVTEKINKAI RSSSSNFLNY DLTLRCDYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC   360
VASSLKCPDA CNAQHKQCLI KKSGGAPECA CVPGYQEDAN GNCQKCAFGY SGLDCKDKFQ   420
LILTIVGTIA GIVILSMIIA LIVTARSNNK TKHIEEENLI DEDFQNLKLR STGFTNLGAE   480
GSVFPKVRIT ASRDSQMQNP YSRHSSMPRP DY                                 512

Seq ID NO: C257 Protein Sequence
Protein Accession #: NP_001423.1

1          11         21         31         41         51
|          |          |          |          |          |
MTAGRRMEML CAGRVPALLL CLGFHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV   60
AQVSITKCSS DMNGYCLHGQ CIYLVDMSQN YCRCEVGYTG VRCEHFFLTV HQPLSKEYVA   120
LTVILIILFL ITVVGSTYYF CRWYRNRKSK EPKKEYERVT SGDPELPQV               169

Seq ID NO: C258 Protein Sequence
Protein Accession #: AAC63902.1

1          11         21         31         41         51
|          |          |          |          |          |
MDRSKENCIS GPVKATAPVG GPKRVLVTQQ IPCQNPLPVN SGQAQRVLCP SNSSQRVPLQ   60
AQKLVSSHKP VQNQKQKQLQ ATSVPHPVSR PLNNTQKSKQ PLPSAPENNP EEELASKQKN   120
EESKKRQWAL EDFEIGRPLG KGKFGNVYLA REKQSKFILA LKVLFKAQLE KAGVEHQLRR   180
EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSKFDE QRTATYITEL   240
ANALSYCHSK RVIHRDIKPE NLLLGSAGEL KIADFGWSVH APSSRRTTLC GTLDYLPPEM   300
IEGRMHDEKV DLWSLGVLCY EFLVGKPPFE ANTYQETYKR ISRVEFTFPD FVTEGARDLI   360
SRLLKHNPSQ RPMLREVLEH PWITANSSKP SNCQNKESAS KQS                      403

Seq ID NO: C259 Protein Sequence
Protein Accession #: NP_037504.1

1          11         21         31         41         51
|          |          |          |          |          |
MSRTAYTVGA LLLLLGTLLP AAEGKKKGSQ GAIPPPDKAQ HNDSEQTQSP QQPGSRNRGR   60
GQGRGTAMPG EEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG   120
QCNSFYIPRH IRKEEGSFQS CSFCKPKKFT TMMVTLNCPE LQPPTKKKRV TRVKQCRCIS   180
IDLD                                                                184

Seq ID NO: C260 Protein Sequence
Protein Accession #: Eos sequence

1          11         21         31         41         51
|          |          |          |          |          |
MKVGVLWLIS FFTFTDGHGG FLGKNDGIKT KKELIVNKKK HLGPVEEYQL LLQVTYRDSK   60
EKRDLRNFLK LLKPPLLWSH GLIRIIRAKA TTDCNSLNGV LQCTCEDSYT WFPPSCLDPQ   120
NCYLHTAGAL PSCECHLNNL SQSVNFCERT KIWGTFKINE RFTNDLLNSS SAIYSKYANG   180
IEIQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK   240
LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV   300
LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNISSLSL   360
ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLETLEN ISTLVPPTAL   420
PLNFSRKFID WKGIPVNKSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRSLPETII   480
SMASLTLGNI LPVSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDFS   540
HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPST IFPVVKWITY VGLGISIGSL   600
ILCLIIEALF WKQIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPSGVCTAA   660
VFFTHFFYLS LFFWMLMLGI LLAYRIILVF HHMAQHLMMA VGFCLGYGCP LIISVITIAV   720
TQPSNTYKRK DVCWLNWSNG SKPLLAFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR   780
DDKATIIRVG KSLLILTPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL   840
LDSKLRQLLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGHYA FSHTGDSSDN   900
IMLTQFVSNE                                                          910

Seq ID NO: C261 Protein Sequence
Protein Accession #: NP_000575.1

1          11         21         31         41         51
|          |          |          |          |          |
MTSKLAVALL AAFLISAALC EGAVLPRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH   60
CANTEIIVKL SDGRELCLDP KENWVQRVVE KFLKRAENS                          99

Seq ID NO: C262 Protein Sequence
Protein Accession #: NP_005594.1

1          11         21         31         41         51
|          |          |          |          |          |
MSTERDSETT FDEDSQPNDE VVPYSDDETE DELDDQGSAV EPEQNRVNRE AEENREPFRK   60
ECTWQVKAND RKYHEQPHFM NTKFLCIKES KYANNAIKTY KYNAFTFIPM NLFEQFKRAA   120
NLYFLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTCEV   180
IKDGRFKVAK WKEIQVGDVI RLKKNDFVPA DILLLSSSEP NSLCYVETAE LDGETNLKFK   240
MSLEITDQYL QREDTLATFD GFIECEEPNN RLDKFTGTLF WRNTSFPLDA DKILLRGCVI   300
RNTDPCHGLV IFAGADTKIM KNSGKTRFKR TKIDYLMNYM VYTIFVVLIL LSAGLAIGHA   360
YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN   420
WDLQMYYAEK DTPAKARTTT LNEQLGQIHY IFSDKTGTLT QNIMTFKKCC INGQIYGDHR   480
DASQHNHNKI EQVDFSWNTY ADGKLAFYDH YLIEQIQSGK EPEVRQFFFL LAVCHTVMVD   540
RTDGQLNYQA ASPDEGALVN AARNFGFAFL ARTQNTITIS ELGTERTYNV LAILDFNSDR   600
KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETQ DALDIFANET LRTLCLCYKE   660
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IEEKEFTEWN KKFMAASVAS TNRDEALDKV YEEIEKDLIL LGATAIEDKL QDGVPETISK   720
LAKADIKIWV LTGDKKETAE NIGFACELLT EDTTICYGED INSLLHARME NQRNRGGVYA   780
KFAPPVQESF FPPGGNRALI ITGSWLNEIL LEKKTKRNKI LKLKFPRTEE ERRMRTQSKR   840
RLEAKKEQRQ KNFVDLACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVNM   900
IKTAHIGVGI SGQEGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRYFFYKNFA   960
FTLVHFWYSF FNGYSAQTAY EDWFITLYNV LYTSLPVLLM GLLDQDVSDK LSLRFPGLYI  1020
VGQRDLLFNY KRFFVSLLHG VLTSMILFFI PLGAYLQTVG QDGEAPSDYQ SFAVTIASAL  1080
VITVNFQIGL DTSYWTFVNA FSIFGSIALY FGIMFDFHSA GIHVLFPSAF QFTGTASNAL  1140
RQPYIWLTII LTVAVCLLPV VAIRFLSMTI WPSESDKIQK HRKRLKAEEQ WQRRQQVFRR  1200
GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPLDAIVAD GTAEYRRTGD S           1251
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Seq ID NO: C263 Protein Sequence
Protein Accession #: XM_044533

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1          11         21         31         41         51
|          |          |          |          |          |
MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL   60
RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC   120
SFKGKDPQRD CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED   180
GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF   240
VASAYIPESL GSLQGDDDKI YFFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW   300
TSFLKAQLLC SRPDDGFPFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV   360
FTMKDVQRVF SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL   420
NFLKDHFLMD GQVRSRMLLL QPQARYQRVA VHRVPGLHHT YDVLFLGTGD GRLHKAVSVG   480
PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD   540
PYCAWSGSSC KHVSLYQPQL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCEQVQ   600
FQPNTVNTLA CPLLSNLATR LWLRNGAPVN ASASCHVLPT GDLLLVGTQQ LGEFQCWSLE   660
EGFQQLVASY CPEVVEDGVA DQTDEGGSVP VIISTSRVSA PAGGKASWGA DRSYWKEFLV   720
MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST   780
PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV      837
```

Seq ID NO: C264 Protein Sequence
Protein Accession #: NP_008950.1

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1          11         21         31         41         51
|          |          |          |          |          |
MASQNRDPAA TSVAAARKGA EPSGGAARGP VGKRLQQELM TLMMSGDKGI SAFPESDNLF   60
KWVGTIHGAA GTVYEDLRYK LSLEFPSGYP YNAPTVKFLT PCYHPNVDTQ GNICLDILKE   120
KWSALYDVRT ILLSIQSLLG EPNIDSPLNT HAAELWKNPT AFKKYLQETY SKQVTSQEP    179
```

Seq ID NO: C265 Protein Sequence
Protein Accession #: NP_055399.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGRGWGFLFG LLGAVWLLSS GHGEEQPPET AAQRCFCQVS GYLDDCTCDV ETIDRFNNYR   60
LFPRLQKLLE SDYFRYYKVN LKRPCPFWND ISQCGRRDCA VKPCQSDEVP DGIKSASYKY   120
SEEANNLIEE CEQAERLGAV DESLSEETQK AVLQWTKHDD SSDNFCEADD IQSPEAEYVD   180
LLLNPERYTG YKGPDAWKIW NVIYEENCFK PQTIKRPLNP LASGQGTSEE NTFYSWLEGL   240
CVEKRAFYRL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITEFQQRFDG ILTEGEGPRR   300
LKNLYFLYLI ELRALSKVLP FFERPDFQLF TGNKIQDEEN KMLLLEILHE IKSFPLHFDE   360
NSFFAGDKKE AHKLKEDFRL HFRNISRIMD CVGCFKCRLW GKLQTQGLGT ALKILFSEKL   420
IANMPESGPS YEPHLTRQEI VSLFNAFGRI STSVKELENF RNLLQNIH               468
```

Seq ID NO: C266 Protein Sequence
Protein Accession #: NP_002879.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQPRRQRLPA PWSGPRGPRP TAPLLALLLL LAPVAAPAGS GGPDDPGQPQ DAGVPRRLLQ   60
QKARAALHFF NFRSGSPSAL RVLAEVQEGR AWINPKEGCK VHVVFSTERY NPESLLQEGE   120
GRLGKCSARV FFKNQKPRPT INVTCTRLIE KKKRQQEDYL LYKQMKQLKN PLEIVSIPDN   180
HGHIDPSLRL IWDLAFLGSS YVMWEMTTQV SHYYLAQLTS VRQWVRKT               228
```

Seq ID NO: C267 Protein Sequence
Protein Accession #: NP_005400.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI   60
EVIITLKENK GQRCLNPKSK QARLIIKKVE RKNF                               94
```

Seq ID NO: C268 Protein Sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MLRQVLRRGL QSFCHRLGLC VSRHPVFFLT VPAVLTITFG LSALNRFQPE GDLERLVAPS   60
HSLAKIERSL ASSLFPLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA   120
VLEMKVNHKG YNYTFSHLCV LRNQDKKCVL DDIISVLEDL RQAAVSNKTT ARVQVRYPNT   180
KLKVCSFCML LPIKEAALHF LP                                            202
```

Seq ID NO: C269 Protein Sequence
Protein Accession #: NP_002429.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRLPLLLVFA SVIPGAVLLL DTRQFLIYNE DHKRCVDAVS PSAVQTAACN QDAESQKFRW   60
VSESQIMSVA FKLCLGVPSK TDWVAITLYA CDSKSEFQKW ECKNDTLLGI KGEDLFFNYG   120
NRQEKNIMLY KGSGLWSRWK IYGTTDNLCS RGYEAMYTLL GNANGATCAF PFKFENKWYA   180
DCTSAGRSDG WLWCGTTTDY DTDKLFGYCP LKFEGSESLW NKDPLTSVSY QINSKSALTW   240
HQARKSCQQQ NAELLSITEI HEQTYLTGLT SSLTSGLWIG LNSLSFNSGW QWSDRSPFRY   300
LNWLPGSPSA EPGKSCVSLN PGKNAKWENL ECVQKLGYIC KKGNTTLNSF VIPSESDVPT   360
HCPSQWWPYA GHCYKIHRDE KKIQRDALTT CRKEGGDLTS IHTIEELDFI ISQLGYEPND   420
ELWIGLNDIK IQMYFEWSDG TPVTFTKWLR GEPSHENNRQ EDCVVMKGKD GYWADRGCEW   480
PLGYICKMKS RSQGPEIVEV EKGCRKGWKK HHFYCYMIGH TLSTFAEANQ TCNNENAYLT   540
TIEDRYEQAF LTSFVGLRPE KYFWTGLSDI QTKGTFQWTI EEEVRFTHWN SDMPGRKPGC   600
VAMRTGIAGG LWDVLKCDEK AKFVCKHWAE GVTHPPKPTT TPEPKCPEDW GASSRTSLCF   660
KLYAKGKHEK KTWFESRDFC RALGGDLASI NNKEEQQTIW RLITASGSYH KLFWLGLTYG   720
SPSEGFTWSD GSPVSYENWA YGEPNNYQNV EYCGELKGDP TMSWNDINCE HLNNWICQIQ   780
KGQTPKPEPT PAPQDNPPVT EDGWVIYKDY QYYFSKEKET MDNARAFCKR NFGDLVSIQS   840
ESEKKFLWKY VNRNDAQSAY FIGLLISLDK KFAWMDGSKV DYVSWATGEP NFANEDENCV   900
TMYSNSGFWN DINCGYPNAF ICQRHNSSIN ATTVMPTMPS VPSGCKEGWN FYSNKCFKIF   960
GFMEEERKNW QEARKACIGF GGNLVSIQNE KEQAFLTYHM KDSTFSAWTG LNDVNSEHTF   1020
LWTDGRGVHY TNWGKGYPGG RRSSLSYEDA DCVVIIGGAS NEAGKWMDDT CDSKRGYICQ   1080
TRSDPSLTNP PATIQTDGFV KYGKSSYSLM RQKFQWHEAE TYCKLHNSLI ASILDPYSNA   1140
FAWLQMETSN ERVWIALNSN LTDNQYTWTD KWRVRYTNWA ADEPKLKSAC VYLDLDGYWK   1200
TAHCNESFYF LCKRSDEIPA TEPPQLPGRC PESDHTAWIP FHGHCYYIES SYTRNWGQAS   1260
LECLRMGSSL VSIESAAESS FLSYRVEPLK SKTNFWIGLF RNVEGTWLWI NNSPVSFVNW   1320
NTGDPSGERN DCVALHASSG FWSNIHCSSY KGYICKRPKI IDAKPTHELL TTKADTRKMD   1380
PSKPSSNVAG VVIIVILLIL TGAGLAAYFF YKKRRVHLPQ EGAFENTLYF NSQSSPGTSD   1440
MKDLVGNIEQ NEHSVI                                                   1456
```

Seq ID NO: C270 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MVLLHWCLLW LLFPLSSRTQ KLPTRDEELF QMQIRDKAFF HDSSVIPDGA EISSYLFRDT   60
PKRYFFVVEE DNTPLSVTVT PCDAPLEWKL SLQELPEDRS GEGSGDLEPL EQQKQQIINE   120
EGTELFSYKG NDVEYFISSS SPSGLYQLDL LSTEKDTHFK VYATTTPESD QPYPELPYDP   180
RVDVTSLGRT TVTLAWKPSP TASLLKQPIQ YCVVINKEHN FKSLCAVEAK LSADDAFMMA   240
PKPGLDFSPF DFAHFGFPSD NSGKERSFQA KPSPKLGRHV YSRPKVDIQK ICIGNKNIFT   300
VSDLKPDTQY YFDVFVVNIN SNMSTAYVGT FARTKEEAKQ KTVELKDGKI TDVFVKRKGA   360
KFLRFAPVSS HQKVTFFIHS CLDAVQIQVR RDGKLLLSQN VEGIQQFQLR GKPKAKYLVR   420
LKGNKKGASM LKILATTRPT KQSFPSLPED TRIKAFDKLR TCSSATVAWL GTQERNKFCI   480
YKKEVDDNYN EDQKKREQNQ CLGPDIRKKS EKVLCKYFHS QNLQKAVTTE TIKGLQPGKS   540
YLLDVYVIGH GGHSVKYQSK VVKTRKFC                                      568
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Seq ID NO: C271 Protein Sequence
Protein Accession #: AAH34229.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEKVQLEFEN QEMEKKLQEF RSTRNKEKED RESSEYYWKS GKVGKLVNQS YMMSQNKGNV   60
VKFSAGKVKL KLLKEQIQEP VKPTVNYKMA NSSECEKPKI NGKVCGQCEN KAALLVCLEC   120
GEDYCSGCFA NVHQKGALKL HRTTLLQARS QILFNVLDVA HQFIKDVNPD EPKEENNSTK   180
ETSKIQHKPK SVLLQRSSSE VEITTMKRAQ RTKPRKSLLC EGSFDEEASA QSFQEVLSQW   240
RTGNHDDNKK QNLHAAVKDS LEECEVQTNL KIWREPLNIE LKEDILSYME KLWLKKHRRT   300
PQEQLFKCYQ IRSHIHMKPL VMHSVLKMKT MKIVMVRRPK YNTQLFYCQ               349
```

Seq ID NO: C272 Protein Sequence
Protein Accession #: NP_078963.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEKLWLKKHR RTPQEQLFKM LSDTFPHPHE TTGDAQCSQN ENDEDSDGEE TKVQHTALLL   60
PVETLNIERP EPSLKIVELD DTYEEEFEEA ENIVPYKVKL ADADSQRSCA FHDCQKNSFP   120
YENGIHQHHV FDKGKRDFLN LCLRNSSTYY KDNSKGETSN TDFDNIVDPD VYSSDIEKIE   180
ESTSFERNLK EKNIGLESNQ KSDDSCVSLE SKDTLLGRDL EKAPIEEKLS QDIKESLELS   240
NLYKRPSFEE SKTTKSSLLL QEIACRSKPI TKQYQGLERF FIFDTNERLN LLPSHRLECN   300
NSSTRITLAE DREWIPDHSL SEYADNAIVL GVLQGAQSPS SSRKQQKMGQ KSQRPSTANF   360
PLSNSVKESS SCLSSSHPRS RSAAAQSSSR AASEISEIEY IDITDQNELS LDDTTDQHTL   420
DNLEKELQVL RSLADTSEKL YSLTSEEPPD FSSQSLNISQ ISTDFLKTSH VRGPCGVEEL   480
SCSGRDTKIQ SLLSLSESST DEEEEDFLNK QHVITLPWSK ST                      522
```

Seq ID NO: C273 Protein Sequence
Protein Accession #: NP_005399.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKVSAVLLCL LLMTAAFNPQ GLAQPDALNV PSTCCFTFSS KKISLQRLKS YVITTSRCPQ   60
KAVIFRTKLG KEICADPKEK WVQNYMKHLG RKAHTLKT                           98
```

Seq ID NO: C274 Protein Sequence
Protein Accession #: BAC05158.1

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1          11         21         31         41         51
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MFLLTGGVSL KSAEKNPDPT WLQDKSWEEI CRASEFPAFR GLRQHFCEHI YEWREIYDSK   60
EPHNAKFPAP MDKNLNELQK IIILRCLRPD KITPAITNYV TDKLGKKFVE PPPFDLTKSY  120
LDSNCTIPLI FVLSPGADPM ASLLKFANDK SMSGNKFQAI SLGQGQGPIA AKMIKAAIEE  180
GTWVCLQNCH LAVSWMPMLE KICEDFTSET CNSSFRLWLT SYPSSKFPVT ILQNGVKMTN  240
EPPTGLRLNL LQSYLTDPVS DPEFFKGCRG KELLFINEYD TIPFEAISYL TGECNYGGRV  300
TDDWDRRLLL TMLADFYNLY IVENPHYKFS PSGNYFAPPK GTYEDYIEFI KKLPFTQHPE  360
IFGLHENVDI SKDLQQTKTL FESLLLTQGG SKQTGASGST DQILLEITKD ILNKLPSDFD  420
IEMALRKYPV RYEESMNTVL VQEMERFNNL IITIRNTLRD LEKAIKGVVV MDSALEALSS  480
SLLVGKVPEI WAKRSYPSLK PLGSYITDFL ARLNFLQDWY NSGKPCVFWL SGFFFTQAFL  540
TGAMQNYARK YTTPIDLLGY EFEVIPSDTS DTSPEDGVYI HGLYLDGARW DRESGLLAEQ  600
YPKLLFDLMP IIWIKPTQKS RIIKSDAYVC PLYKTSERKG TLSTTGHSTN FVIAMLLKTD  660
QPTRHWIKRG VALLCQLDD                                               679
```

Seq ID NO: C275 Protein Sequence
Protein Accession #: AAA60212.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAESHLLQWL LLLLPTLCGP GTAAWTTSSL ACAQGPEFWC QSLEQALQCR ALGHCLQEVW   60
GHVGADDLCQ ECEDIVHILN KMAKEAIFQD TMRKFLEQEC NVLPLKLLMP QCNQVLDDYF  120
PLVIDYFQNQ TDSNGICMHL GLCKSRQPEP EQEPGMSDPL PKPLRDPLPD PLLDKLVLPV  180
LPGALQARPG PHTQDLSEQQ FPIPLPYCWL CRALIKRIQA MIPKGALAVA VAQVCRVVPL  240
VAGGICQCLA ERYSVILLDT LLGRMLPQLV CRLVLRCSMD DSAGPRSPTG EWLPRDSECH  300
LCMSVTTQAG NSSEQAIPQA MLQACVGSWL DREKCKQFVE QHTPQLLTLV PRGWDAHTTC  360
QALGVCGTMS SPLQCIHSPD L                                            381
```

Seq ID NO: C276 Protein Sequence
Protein Accession #: NP_631911.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLGCGIPALG LLLLLQGSAD GNGIQGFFYP WSCEGDIWDR ESCGGQAAID SPNLCLRLRC   60
CYRNGVCYHQ RPDENVRRKH MWALVWTCSG LLLLSCSICL FWWAKRRDVL HMPGFLAGPC  120
DMSKSVSLLS KHRGTKKTPS TGSVPVALSK ESRDVEGGTE GEGTEEGEET EGEEEED     177
```

Seq ID NO: C277 Protein Sequence
Protein Accession #: NP_473364.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKLVTIFLLV TISLCSYSAT AFLINKVPLP VDKLAPLPLD NILPFMDPLK LLLKTLGISV   60
EHLVEGLRKC VNELGPEASE AVKKLLEALS HLV                               93
```

Seq ID NO: C278 Protein Sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MPLSYAYKNA ETLAGRHTSS WMSRGAYQRR NTRAAGRPEE CTDRNWHAGR TRGIWLGQLE   60
ERCSDVFGVS FFWWVRGLAG SGAKLQTFTP AQEGAPTVQR QAEALLKCRQ SGRPGRGGAE  120
SERARDASML SPLSAAMRNY PTSSTIPPRR SYSPTEIAHK SYSCSLPDMK ISMAESGPSL  180
DSLDILEDGE SGSPFLVTHL YFLGVVTTGM EQLDFETGPN IFDLQIYVKD EVGVTDLQVL  240
TVQVTDVNEP PQFQGNLAED HLRADQPHFN AHSHTYVRVV ATALARHRLR SSIGSPFLGT  300
FCVVVGMQYF LISPPKSFRM SANGTLFSTT ELDFEAGHRS FHLIVEVRDS GGLKASTELQ  360
VNIVNLNDEV PRFTSPTRVY TVLEELSPGT IVANITAEDP DDEGFPSHLL YSITTVSKYF  420
MINQLTGTIQ VAQRIDRDAG ELRQNPTISL EVLVKDRPYG GQENRIQITF IVEDVNDNPA  480
TCQKFTFRSS LHPALCSKTL TWMDTVLDCF HAADKDIPVT GRFTKERGLI GLTVPHGWGS  540
LTIMAEGKEE QVTSYMDGSR QRDRACVGKL LLIKPSDLMR LSHYHENNSG KTCPHDSISS  600
YQVPPTTCRN SRIQATNNED TSSVTVTVNI LEENDEKPIC TPNSYFLALP VDLKVGTNIQ  660
NFKLTCTDLD SSPRSFRYSI GPGNVNNHFT FSPNAGSNVT RLLLTSRFDY AGGFDKIWDY  720
KLLVYVTDDN LMSDRKKAEA LVETGTVTLS IKVIPHPTTI ITTTPRPRVT YQVLRKNVYS  780
PSAWYVPFVI TLGSILLLGL LVYLVVLLAK AIHRHCPCKT GKNKEPLTKK GETKTAERDV  840
VVETIQMNTI FDGEAIDPEP EQASLELYAL LPSCCDPSPV TLRKVQVCGE SEETGQCSGH  900
ITLPGKIPVD DPRKQETGLQ GDFEVWTLCP AVKVVVGSPQ AERCIRLALS LKKYSSD     957
```

Seq ID NO: C279 Protein Sequence
Protein Accession #: XP_168571.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MINQLTGTIQ VAQRIDRDAG ELRQNPTISL EVLVKDRPYG GQENRIQITF IVEDVNDNPA   60
TCQKFTFSIM VPERTAKGTL LLDLNKFCFD DDSEAPNNRF NFTMPSGVGS GSRFLQDPAG  120
SGKIVLIGDL DYENPSNLAA GNKYTVIIQV QDVAPPYYKN NVYVYILTSP ENEFPLIFDR  180
PSYVFDVSER RPAQGHLSGP EEKRLLSICM VRAVCHHFGL HIASGSPRVP GRPIGQSHPQ  240
TLPLQDWEEQ GTSDKERRNE DCRERRRGGN YPDEHYL                           277
```

Seq ID NO: C280 Protein Sequence
Protein Accession #: NP_005257.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MGDWSFLGNF LEEVHKHSTV VGKVWLTVLF IFRMLVLGTA AESSWGDEQA DFRCDTIQPG   60
CQNVCYDQAF PISHIRYWVL QIIFVSTPSL VYMGHAMHTV RMQEKRKLRE AERAKEVRGS  120
```

```
GSYEYPVAEK AELSCWEEGN GRIALQGTLL NTYVCSILIR TTMEVGFIVG QYFIYGIFLT   180
TLHVCRRSPC PHPVNCYVSR PTEKNVFIVF MLAVAALSLL LSLAELYHLG WKKIRQRFVK   240
PRQHMAKCQL SGPSVGIVQS CTPPPDFNQC LENGPGGKFF NPFSNNMASQ QNTDNLVTEQ   300
VRGQEQTPGE GFIQVRYGQK PEVPNGVSPG HRLPHGYHSD KRRLSKASSK ARSDDLSV     358
```

Seq ID NO: C281 Protein Sequence
Protein Accession #: NP_055274.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MYLSICCCFL LWAPALTLKN LNYSVPEEQG AGTVIGNIGR DARLQPGLPP AERGGGGRSK   60
SGSYRVLENS APHLLDVDAD SGLLYTKQRI DRESLCRHNA KCQLSLEVFA NDKEICMIKV   120
EIQDINDNAP SFSSDQIEMD ISENAAPGTR FPLTSAHDPD AGENGLRTYL LTRDDHGLFG   180
LDVKSRGDGT KFPELVIQKA LDREQQNHHT LVLTALDGGE PPRSATVQIN VKVIDSNDNS   240
PVFEAPSYLV ELPENAPLGT VVIDLNATDA DEGPNGEVLY SFSSYVPDRV RELFSIDPKT   300
GLIRVKGNLD YEENGMLEID VQARDLGPNP IPAHCKVTVK LIDRNDNAPS IGFVSVRQGA   360
LSEAAPPGTV IALVRVTDRD SGKNGQLQCR VLGGGGTGGG GGLGGPGGSV PFKLEENYDN   420
FYTVVTDRPL DRETQDEYNV TIVARDGGSP PLNSTKSFAI KILDENDNPP RFTKGLYVLQ   480
VHENNIPGEY LGSVLAQDPD LGQNGTVSYS ILPSHIGDVS IYTYVSVNPT NGAIYALRSF   540
NFEQTKAFEF KVLAKDSGAP AHLESNATVR VTVLDVNDNA PVIVLPTLQN DTAELQVPRN   600
AGLGYLVSTV RALDSDFGES GRLTYEIVDG NDDHLFEIDP SSGEIRTLHP FWEDVTPVVE   660
LVVKVTDHGK PTLSAVAKLI IRSVSGSLPE GVPRVNGEQH HWDMSLPLIV TLSTISIILL   720
AAMITIAVKC KRENKEIRTY NCRIAEYSHP QLGGGKGKKK KINKNDIMLV QSEVEERNAM   780
NVMNVVSSPS LATSPMYFDY QTRLPLSSPR SEVMYLKPAS NNLTVPQGHA GCHTSFTGQG   840
TNASETPATR MSIIQTDNFP AEPNYMGSRQ QFVQSISVAP RLRTQKEPA               889
```

Seq ID NO: C282 Protein Sequence
Protein Accession #: NP_005592.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MELCRSLALL GGSLGLMFCL IALSTDFWFE AVGPTHSAHS GLWPTGHGDI ISGYIHVTQT   60
FSIMAVLWAL VSVSFLVLSC FPSLFPPGHG PLVSTTAAFA AAISMVVAMA VYTSERWDQP   120
PHPQIQTFFS WSFYLGWVSA ILLLCTGALS LGAHCGGPRP GYETL                   165
```

Seq ID NO: C283 Protein Sequence
Protein Accession #: NP_006424.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MATWALLLLA AMLLGNPGLV FSRLSPEYYD LARAHLRDEE KSCPCLAQEG PQGDLLTKTQ   60
ELGRDYRTCL TIVQKLKKMV DKPTQRSVSN AATRVCRTGR SRWRDVCRNF MRRYQSRVTQ   120
GLVAGETAQQ ICEDLRLCIP STGPL                                         145
```

Seq ID NO: C284 Protein Sequence
Protein Accession #: NP_005594.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKVSAAALAV ILIATALCAP ASASPYSSDT TPCCFAYIAR PLPRAHIKEY FYTSGKCSNP   60
AVVFVTRKNR QVCANPEKKW VREYINSLEM S                                   91
```

Seq ID NO: C285 Protein Sequence
Protein Accession #: NP_071437.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAPGRAVAGL LLLAAAGLGG VAEGPGLAFS EDVLSVFGAN LSLSAAQLQH LLEQMGAASR   60
VGVPEPGQLH FNQCLTAEEI FSLHGFSNAT QITSSKFSVI CPAVLQQLNF HPCEDRPKHK   120
TRPSHSEVWG YGFLSVTIIN LASLLGLILT PLIKKSYFPK ILTFFVGLAI GTLFSNAIFQ   180
LIPEAPGFDP KVDSYVEKAV AVFGGFYLLF FFERMLKMLL KTYGQNGHTH FGNDNFGPQE   240
KTHQPKALPA INGVTCYANP AVTEANGHIH FDNVSVVSLQ DGKKEPSSCT CLKGPKLSEI   300
GTIAWMITLC DALHNFIDGL AIGASCTLSL LQGLSTSIAI LCEEFPHELG DFVILLNAGM   360
STRQALLFNF LSACSCYVGL AFGILVGNNF APNIIFALAG GMFLYISLAD MFPEMNDMLR   420
EKVTGRKTDF TFFMIQNAGM LTGFTAILLI TLYAGEIELE                         460
```

Seq ID NO: C286 Protein Sequence
Protein Accession #: NP_004175.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPNSEPASLL ELFNSIATQG ELVRSLKAGN ASKDEIDSAV KMLVSLKMSY KAAAGEDYKA   60
DCPPGNPAPT SNHGPDATEA EEDFVDPWTV QTSSAKGIDY DKLIVRFGSS KIDKELINRI   120
ERATGQRPHH FLRRGIFFSH RDMNQVLDAY ENKKPFYLYT GRGPSSEAMH VGHLIPFIFT   180
KWLQDVFNVP LVIQMTDDEK YLWKDLTLDQ AYGDAVENAK DIIACGFDIN KTFIFSDLDY   240
MGMSSGFYKN VVKIQKHVTF NQVKGIFGFT DSDCIGKISF PAIQAAPSFS NSFPQIFRDR   300
TDIQCLIPCA IDQDPYFRMT RDVAPRIGYP KPALLHSTFF PALQGAQTKM SASDPNSSIF   360
LTDTAKQIKT KVNKHAFSGG RDTIEEHRQF GGNCDVDVSF MYLTFFLEDD DKLEQIRKDY   420
TSGAMLTGEL KKALIEVLQP LIAEHQARRK EVTDEIVKEF MTPRKLSFDF Q            471
```

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP_004929.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTVFRQENVD DYYDTGEELG SGQFAVVKKC REKSTGLQYA AKFIKKRRTK SSRRGVSRED   60
IEREVSILKE IQHPNVITLH EVYENKTDVI LILELVAGGE LFDFLAEKES LTEEEATEFL   120
KQILNGVYYL HSLQIAHFDL KPENIMLLDR NVPKPRIKII DFGLAHKIDF GNEFKNIFGT   180
PEFVAPEIVN YEPLGLEADM WSIGVITYIL LSGASPFLGD TKQETLANVS AVNYEFEDEY   240
FSNTSALAKD FIRRLLVKDP KKRMTIQDSL QHPWIKPKDT QQALSRKASA VNMEKFKKFA   300
ARKKWKQSVR LISLCQRLSR SFLSRSNMSV ARSDDTLDEE DSFVMKAIIH AINDDNVPGL   360
QHLLGSLSNY DVNQPNKHGT PPLLIAAGCG NIQILQLLIK RGSRIDVQDK GGSNAVYWAA   420
RHGHVDTLKF LSENKCPLDV KDKSGEMALH VAARYGHADV AQVTCAASAQ IPISRTKEEE   480
TPLHCAAWHG YYSVAKALCE AGCNVNIKNR EGETPLLTAS ARGYHDIVEC LAEHGADLNA   540
CDKDGHIALH LAVRRCQMEV IKTLLSQGCF VDYQDRHGNT PLHVACKDGN MPIVVALCEA   600
NCNLDISNKY GRTPLHLAAN NGILDVVRYL CLMGASVEAL TTDGKTAEDL ARSEQHEHVA   660
GLLARLRKDT HRGLFIQQLR PTQNLQPRIK LKLFGHSGSG KTTLVESLKC GLLRSFFRRR   720
RPRLSSTNSS RFPPSPLASK PTVSVSINNL YPGCENVSVR SRSMMFEPGL TKGMLEVFVA   780
PTHHPHCSAD DQSTKAIDIQ NAYLNGVGDF SVWEFSGNPV YFCCYDYFAA NDPTSIHVVV   840
FSLEEPYEIQ LNPVIFWLSF LKSLVPVEEP IAFGGKLKNP LQVVLVATHA DIMNVPRPAG   900
GEFGYDKDTS LLKEIRNRFG NDLHISNKLF VLDAGASGSK DMKVLRNHLQ EIRSQIVSVC   960
PPMTHLCEKI ISTLPSWRKL NGPNQLMSLQ QFVYDVQDQL NPLASEEDLR RIAQQLHSTG  1020
EINIMQSETV QDVLLLDPRW LCTNVLGKLL SVETPRALHH YRGRYTVEDI QRLVPDSDVE  1080
ELLQILDAMD ICARDLSSGT MVDVPALIKT DNLHRSWADE EDEVMVYGGV RIVPVEHLTP  1140
FPCGIFHKVQ VNLCRWIHQQ STEGDADIRL WVNGCKLANR GAELLVLLVN HGQGIEVQVR  1200
GLETEKIKCC LLLDSVCSTI ENVMATTLPG LLTVKHYLSP QQLREHHEPV MIYQPRDFFR  1260
AQTLKETSLT NTMGGYKESF SSIMCFGCHD VYSQASLGMD IHASDLNLLT RRKLSRLLDP  1320
PDPLGKDWCL LAMNLGLPDL VAKYNTNNGA PKDFLPSPLH ALLREWTTYP ESTVGTLMSK  1380
LRELGRRDAA DLLLKASSVF KINLDGNGQE AYASSCNSGT SYNSISSVVS R            1431
```

Seq ID NO: C288 Protein Sequence
Protein Accession #: NP_002072.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MELRARGWWL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSDVP QAEISGEHLR   60
ICPQGYTCCT SEMEENLANR SHAELETALR DSSRVLQAML ATQLRSFDDH FQHLLNDSER   120
TLQATFPGAF GELYTQNARA FRDLYSELRL YYRGANLHLE ETLAEFWARL LERLFKQLHP   180
QLLLPDDYLD CLGKQAEALR PFGEAPRELR LRATRAFVAA RSFVQGLGVA SDVVRKVAQV   240
PLGPECSRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVLI   300
TDKFWGTSGV ESVIGSVHTW LAEAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR   360
RGKLAPRERP PSGTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNGMA   420
RGRYLPEVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFQD   480
ASDDGSGSGS                                                          490
```

Seq ID NO: C289 Protein Sequence
Protein Accession #: AAH30205.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MIILIYLFLL LWEDTQGWGF KDGIPHNSIW LERAAGVYHR EARSGKYKLT YAEAKAVCEF   60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFGKTGI IDYGIRLNRS   120
ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF   180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF   240
QIKYVAMDPV SKSSQGKNTS TTSTGNKNFL AGRFSHL                            277
```

Seq ID NO: C290 Protein Sequence
Protein Accession #: NP_001973.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRANDALQVL GLLFSLARGS EVGNSQAVCP GTLNGLSVTG DAENQYQTLY KLYERCEVVM   60
GNLEIVLTGH NADLSFLQWI REVTGYVLVA MNEFSTLPLP NLRVVRGTQV YDGKFAIFVM   120
LNYNTNSSHA LRQLRLTQLT EILSGGVYIE KNDKLCHMDT IDWRDIVRDR DAEIVVKDNG   180
RSCPPCHEVC KGRCWGPGSE DCQTLTKTIC APQCNGHCFG PNPNQCCHDE CAGGCSGPQD   240
TDCFACRHFN DSGACVPRCP QPLVYNKLTF QLEPNPHTKY QYGGVCVASC PHNFVVDQTS   300
CVRACPPDKM EVDKNGLKMC EPCGGLCPKA CEGTGSGSRF QTVDSSNIDG FVNCTKILGN   360
LDFLITGLNG DPWHKIPALD PEKLNVFRTV REITGYLNIQ SWPPHMHNFS VFSNLTTIGG   420
RSLYNRGFSL LIMKNLNVTS LGFRSLKEIS AGRIYISANR QLCYHHSLNW TKVLRGPTEE   480
RLDIKHNRPR RDCVAEGKVC DPLCSSGGCW GPGPGQCLSC RNYSRGGVCV THCNFLNGEP   540
REFAHEAECF SCHPECQPMG GTATCNGSGS DTCAQCAHFR DGPHCVSSCP HGVLGAKGPI   600
YKYPDVQNEC RPCHENCTQG CKGPELQDCL GQTLVLIGKT HLTMALTVIA GLVVIFMMLG   660
GTFLYWRGRR IQNKRAMRRY LERGESIEPL DPSEKANKVL ARIFKETELR KLKVLGSGVF   720
GTVHKGVWIP EGESIKIPVC IKVIEDKSGR QSFQAVTDHM LAIGSLDHAH IVRLLGLCPG   780
SSLQLVTQYL PLGSLLDHVR QHRGALGPQL LLNWGVQIAK GMYYLEEHGM VHRNLAARNV   840
LLKSPSQVQV ADFGVADLLP PDDKQLLYSE AKTPIKWMAL ESIHFGKYTH QSDVWSYGVT   900
VWELMTFGAE PYAGLRLAEV PDLLEKGERL AQPQICTIDV YMVMVKCWMI DENIRPTFKE   960
LANEFTRMAR DPPRYLVIKR ESGPGIAPGP EPHGLTNKKL EEVELEPELD LDLDLEAEED  1020
NLATTTLGSA LSLPVGTLNR PRGSQSLLSP SSGYMPMNQG NLGGSCQESA VSGSSERCPR  1080
PVSLHPMPRG CLASESSEGH VTGSEAELQE KVSMCRSRSR SRSPRPRGDS AYHSQRHSLL  1140
TPVTPLSPPG LEEEDVNGYV MPDTHLKGTP SSREGTLSSV GLSSVLGTEE EDEDEEYEYM  1200
NRRRRHSPPH PPRPSSLEEL GYEYMDVGSD LSASLGSTQS CPLHPVPIMP TAGTTPDEDY  1260
EYMNRQRDGG GPGGDYAAMG ACPASEQGYE EMRAFQGPGH QAPHVHYARL KTLRSLEATD  1320
SAFDNPDYWH SRLFPKANAQ RT                                            1342
```

Seq ID NO: C291 Protein Sequence
Protein Accession #: NP_001207.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAPLCPSPWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL   60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG   120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL   180
ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT   240
VEGHRFPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPEENSAYE QLLSRLEEIA   300
EEGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS   360
DTLWGPGDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF   420
GLLFAVTSVA FLVQMRRQHR RGTKGGVSYR PAEVAETGA                          459
```

Seq ID NO: C292 Protein Sequence
Protein Accession #: NP_004198.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGGAVVDEGP TGVKAPDGGW GWAVLFGCFV ITGFSYAFPK AVSVFFKELI QEFGIGYSDT   60
AWISSILLAM LYGTGPLCSV CVNRFGCRPV MLVGGLFASL GMVAASFCRS IIQVYLTTGV   120
ITGLGLALNF QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPLGQLL QDRYGWRGGF   180
LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLLDL SVFRDRGFVL YAVAASVMVL   240
GLFVPPVFVV SYAKDLGVPD TKAAFLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSF   300
SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGMVGALQF EVLMAIVGTH KFSSAIGLVL   360
LMEAVAVLVG PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLLGNFFCI RKKPKEPQPE   420
VAAAEEEKLH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV                   465
```

Seq ID NO: C293 Protein Sequence
Protein Accession #: NP_000349.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MALFVRLLAL ALALALGPAA TLAGPAKSPY QLVLQHSRLR GRQHGPNVCA VQKVIGTNRK   60
YFTNCKQWYQ RKICGKSTVI SYECCPGYEK VPGEKGCPAA LPLSNLYETL GVVGSTTTQL   120
YTDRTEKLRP EMEGPGSFTI FAPSNEAWAS LPAEVLDSLV SNVNIELLNA LRYHMVGRRV   180
LTDELKHGMT LTSMYQNSNI QIHHYPNGIV TVNCARLLKA DHHATNGVVH LIDKVISTIT   240
NNIQQIIEIE DTFETLRAAV AASGLNTMLE GNGQYTLLAP TNEAFEKIPS ETLNRILGDP   300
EALRDLLNNH ILKSAMCAEA IVAGLSVETL EGTTLEVGCS GDMLTINGKA IISNKDILAT   360
NGVIHYIDEL LIPDSAKTLF ELAAESDVST AIDLFRQAGL GNHLSGSERL TLLAPLNSVF   420
KDGTPPIDAH TRNLLRNHII KDQLASKYLY HGQTLETLGG KKLRVFVYRN SLCIENSCIA   480
AHDKRGRYGT LFTMDRVLTP PMGTVMDVLK GDNRFSMLVA AIQSAGLTET LNREGVYTVF   540
APTNEAFRAL PPRERSRLLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS   600
LKNNVVSVNK EPVAEPDIMA TNGVVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF   660
SRASQRSVRL APVYQKLLER MKH                                          683
```

Seq ID NO: C294 Protein Sequence
Protein Accession #: NP_006527.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTQRSIAGPI CNLKFVTLLV ALSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISN   60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH   120
GDDPYTLQYR GCGKEGKYIH FTPNFLLNDN LTAGYGSRGR VFVHEWAHLR WGVFDEYNND   180
KPFYINGQNQ IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI   240
MFMQSLSSVV EFCNASTHNQ EAPNLQNQMC SLRSAWDVIT DSADFHHSFP MNGTELPPPP   300
TFSLVQAGDK VVCLVLDVSS KMAEADRLLQ LQQAAEFYLM QIVEIHTFVG IASFDSKGEI   360
RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNGKA YGSVMILVTS   420
GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKFFVPDI SNSNSMIDAF   480
SRISSGTGDI FQQHIQLEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL   540
FDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWTYTLN NTHHSLQALK VTVTSRASNS   600
AVPPATVEAF VERDSLHFPH PVMIYANVKQ GFYPILNATV TATVEPETGD PVTLRLLDDG   660
AGADVIKNDG IYSRYFFSFA ANGRYSLKVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN   720
IQMNAPRKSV GRNEEERKWG FSRVSSGGSF SVLGVPAGPH PDVFPPCKII DLEAVKVEEE   780
LTLSWTAPGE DFDQGQATSY EIRMSKSLQN IQDDFNNAIL VNTSKRNPQQ AGIREIFTFS   840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY   900
LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENGT KLL                     943
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Seq ID NO: C295 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MKFLLILLLQ ATASGALPLN SSTSLEKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM   60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHHF REMPGGPVWR KHYITYRINN   120
YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD FHAFDGKGGI   180
LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY   240
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF   300
FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP   360
EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK   420
NFQGIGPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC .            470
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Seq ID NO: C296 Protein Sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MKFLLILLLQ ATASGALPLN SSTSLEKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM   60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHHF REMPGGPVWR KHYITYRINN  120
YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD FHAFDGKGGI  180
LAHAFGPGSG IGGDAHFDED EFWTTHSGGT NLFLTAVHAI GHSLGLGHSS DPKAVMFPTY  240
KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF  300
FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP  360
EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK  420
NFQGIGPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC             470

Seq ID NO: C297 Protein Sequence
Protein Accession #: NP_008883.1

1          11         21         31         41         51
|          |          |          |          |          |
MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW   60
IGIFVGICLF CLSVLGIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL  120
FLKQMLERYQ NNSPPNNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN  180
DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI  240
LCWTFWVLLG TMFYWSRIEY                                              260

Seq ID NO: C298 Protein Sequence
Protein Accession #: NP_001784.2

1          11         21         31         41         51
|          |          |          |          |          |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG   60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG  120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK  180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT  240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA  300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP  360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL  420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR  480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID  540
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD  600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL  660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR  720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF  780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD              829

Seq ID NO: C299 Protein Sequence
Protein Accession #: NP_005620.1

1          11         21         31         41         51
|          |          |          |          |          |
MAKKSAENGI YSVSGDEKKG PLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTRQMD   60
FIMSCVGFAV GLGNVWRFPY LCYKNGGGVF LIPYVLIALV GGIPIFFLEI SLGQFMKAGS  120
INVWNICPLF KGLGYASMVI VFYCNTYYIM VLAWGFYYLV KSFTTTLPWA TCGHTWNTPD  180
CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVLR LSGGLEVPGA LNWEVTLCLL  240
ACWVLVYFCV WKGVKSTGKI VYFTATFPYV VLVVLLVRGV LLPGALDGII YYLKPDWSKL  300
GSPQVWIDAG TQIFFSYAIG LGALTALGSY NRFNNNCYKD AIILALINSG TSFFAGFVVF  360
SILGFMAAEQ GVHISKVAES GPGLAFIAYP RAVTLMPVAP LWAALFFFML LLLGLDSQFV  420
GVEGFITGLL DLLPASYYFR FQREISVALC CALCFVIDLS MVTDGGMYVF QLFDYYSASG  480
TTLLWQAFWE CVVVAWVYGA DRFMDDIACM IGYRPCPWMK WCWSFFTPLV CMGIFIFNVV  540
YYEPLVYNNT YVYPWWGEAM GWAFALSSML CVPLHLLGCL LRAKGTMAER WQHLTQPIWG  600
LHHLEYRAQD ADVRGLTTLT PVSESSKVVV VESVM                             635

Seq ID NO: C300 Protein Sequence
Protein Accession #: NP_006507.1

1          11         21         31         41         51
|          |          |          |          |          |
MEPSSKKLTG RLMLAVGGAV LGSLQFGYNT GVINAPQKVI EEFYNQTWVH RYGESILPTT   60
LTTLWSLSVA IFSVGGMIGS FSVGLFVNRF GRRNSMLMMN LLAFVSAVLM GFSKLGKSFE  120
MLILGRFIIG VYCGLTTGFV PMYVGEVSPT AFRGALGTLH QLGIVVGILI AQVFGLDSIM  180
GNKDLWPLLL SIIFIPALLQ CIVLPFCPES PRFLLINRNE ENRAKSVLKK LRGTADVTHD  240
LQEMKEESRQ MMREKKVTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYYSTSIFEK  300
AGVQQPVYAT IGSGIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ  360
LPWMSYLSIV AIFGFVAFFE VGPGPIPWFI VAELFSQGPR PAAIAVAGFS NWTSNFIVGM  420
CFQYVEQLCG PYVFIIFTVL LVLFFIFTYF KVPETKGRTF DEIASGFRQG GASQSDKTPE  480
ELFHPLGADS QV                                                      492

Seq ID NO: C301 Protein Sequence
Protein Accession #: XP_035292.2

1          11         21         31         41         51
|          |          |          |          |          |
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV   60
GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAELGTTI SKSGGDYAYM  120
LEVYGSLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCVL  180
LLTAVNCYSV KAATRVQDAF AAAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV  240
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GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL   300
STEQMLSSEA VAVDFGNYHL GVMSWIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP   360
SILSMIHPQL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCVAL AIIGMIWLRH   420
RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWWKN   480
KPKWLLQGIF STTVLCQKLM QVVPQET                                       507

Seq ID NO: C302 Protein Sequence
Protein Accession #: NP_005259.1

1          11         21         31         41         51
|          |          |          |          |          |
MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVTA ERVWSDDHKD FDCNTRQPGC   60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP   120
GKKRGGLWWT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP   180
SEKNIFTLFM VATAAICILL NLVELIYLVS KRCHECLAAR KAQAMCTGHH PHGTTSSCKQ   240
DDLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL                                273

Seq ID NO: C303 Protein Sequence
Protein Accession #: NP_005121.1

1          11         21         31         41         51
|          |          |          |          |          |
MKICSLTLLS FLLLAAQVLL VEGKKKVKNG LHSKVVSEQK DTLGNTQIKQ KSRPGNKGKF   60
VTKDQANCRW AATEQEEGIS LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL   120
RSQKDICRYS KTAVKTRVCR KDFPESSLKL VSSTLFGNTK PRKEKTEMSP REHIKGKETT   180
PSSLAVTQTM ATKAPECVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC          234

Seq ID NO: C304 Protein Sequence
Protein Accession #: AAH22542

1          11         21         31         41         51
|          |          |          |          |          |
MCSEIILRQE VLKDGFHRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE   60
RNITEAVMVS ENFDIEAPNY LSKESEVLIY ARRDSQCIDC FQAFLPVHCR YHRPHSEDGE   120
ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ   180
WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLLITILCS KKKKK                   225

Seq ID NO: C305 Protein Sequence
Protein Accession #: NP_004985.1

1          11         21         31         41         51
|          |          |          |          |          |
MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEEYLY RYGYTRVAEM   60
RGESKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLKWHHHN   120
ITYWIQNYSE DLPRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP   180
FDGKDGLLAH AFPPGPGIQG DAHFDDDELW SLGKGVVVPT RFGNADGAAC HFPFIFEGRS   240
YSACTTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS   300
ACTTDGRSDG YRWCATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST   360
CTSEGRGDGR LWCATTSNFD SDKKWGFCPD QGYSLFLVAA HEFGHALGLD HSSVPEALMY   420
PMYRFTEGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER   480
PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFKDGKYW   540
RFSEGRGSRP QGPFLIADKW PALPRKLDSV FEEPLSKKLF FFSGRQVWVY TGASVLGPRR   600
LDKLGLGADV AQVTGALRSG RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD   660
THDVFQYREK AYFCQDRFYW RVSSRSELNQ VDQVGYVTYD ILQCPED                  707

Seq ID NO: C306 Protein Sequence
Protein Accession #: NP_000204

1          11         21         31         41         51
|          |          |          |          |          |
MAGPRPSPWA RLLLAALISV SLSGTLANRC KKAPVKSCTE CVRVDKDCAY CTDEMFRDRR   60
CNTQAELLAA GCQRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL   120
EVFEPLESPV DLYILMDFSN SMSDDLDNLK KMGQNLARVL SQLTSDYTIG FGKFVDKVSV   180
PQTDMRPEKL KEPWPNSDPP FSFKNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL   240
QTAVCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLAGI MSRNDERCHL DTTGTYTQYR   300
TQDYPSVPTL VRLLAKHNII PIFAVTNYSY SYYEKLHTYF PVSSLGVLQE DSSNIVELLE   360
EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGEVGIYQV QLRALEHVDG   420
THVCQLPEDQ KGNIHLKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV   480
CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN   540
FQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR   600
CHCHQQSLYT DTICEINYSA IHPGLCEDLR SCVQCQAWGT GEKKGRTCEE CNFKVKMVDE   660
LKRAEEVVVR CSFRDEDDDC TYSYTMEGDG APGPNSTVLV HKKKDCPPGS FWWLIPLLLL   720
LLPLLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFKED HYMLRENLMA SDHLDTPMLR   780
SGNLKGRDVV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKFDTREC   840
AQLRQEVEEN LNEVYRQISG VHKLQQTKFR QQPNAGKKQD HTIVDTVLMA PRSAKPALLK   900
LTEKQVEQRA FHDLKVAPGY YTLTADQDAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL   960
LVEAIDVPAG TATLGRRLVN ITIIKEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG   1020
KSQVSYRTQD GTAQGNRDYI PVEGELLFQP GEAWKELQVK LLELQEVDSL LRGRQVRRFH   1080
VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLGAP QNPNAKAAGS   1140
RKIHFNWLPP SGKPMGYRVK YWIQGDSESE AHLLDSKVPS VELTNLYPYC DYEMKVCAYG   1200
AQGEGPYSSL VSCRTHQEVP SEPGRLAFNV VSSTVTQLSW AEPAETNGEI TAYEVCYGLV   1260
NDDNRPIGPM KKVLVDNPKN RMLLIENLRE SQPYRYTVKA RNGAGWGPER EAIINLATQP   1320
KRPMSIPIIP DIPIVDAQSG EDYDSFLMYS DDVLRSPSGS QRPSVSDDTG CGWKFEPLLG   1380
EELDLRRVTW RLPPELIPRL SASSGRSSDA EAPTAPRTTA ARAGRAAAVP RSATPGPPGE   1440
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HLVNGRMDFA FPGSTNSLHR MTTTSAAAYG THLSPHVPHR VLSTSSTLTR DYNSLTRSEH   1500
SHSTTLPRDY STLTSVSSHD SRLTAGVPDT PTRLVFSALG PTSLRVSWQE PRCERPLQGY   1560
SVEYQLLNGG ELHRLNIPNP AQTSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES   1620
QVHPQSPLCP LPGSAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEM   1680
AQGGGPATAF RVDGDSPESR LTVPGLSENV PYKFKVQART TEGFGPEREG IITIESQDGG   1740
PFPQLGSRAG LFQHPLQSEY SSITTTHTSA TEPFLVDGLT LGAQHLEAGG SLTRHVTQEF   1800
VSRTLTTSGT LSTHMDQQFF QT                                            1822

Seq ID NO: C307 Protein Sequence
Protein Accession #: NP_076404.1

1          11         21         31         41         51
|          |          |          |          |          |
MGFNLTLAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN   60
GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPFRIVH DAGFGPWYFK FILCRYTSVL   120
FYANMYTSIV FLGLISIDRY LKVVKPFGDS RMYSITFTKV LSVCVWVIMA VLSLPNIILT   180
NGQPTEDNIH DCSKLKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF   240
ISQSSRKRKH NQSIRVVVAV FFTCFLPYHL CRIPFTFSHL DRLLDESAQK ILYYCKEITL   300
FLSACNVCLD PIIYFFMCRS FSRRLFKKSN IRTRSESIRS LQSVRRSEVR IYYDYTDV     358

Seq ID NO: C308 Protein Sequence
Protein Accession #: NP_065840.1

1          11         21         31         41         51
|          |          |          |          |          |
MVWCLGLAVL SLVISQGADG RGKPEVVSVV GRAEESVVLG CDLLPPAGRP PLHVIEWLRF   60
GFLLPIFIQF GLYSPRIDPD YVGRVRLQKG ASLQIEGLRV EDQGWYECRV FFLDQHIPED   120
DFANGSWVHL TVNSPPQFQE TPPAVLEVQE LEPVTLRCVA RGSPLPHVTW KLRGKDLGQG   180
QGQVQVQNGT LRIRRVERGS SGVYTCQASS TEGSATHATQ LLVLGPPVIV VPPKNSTVNA   240
SQDVSLACHA EAYPANLTYS WFQDNININVFH ISRLQPRVQI LVDGSLRLLA TQPDDAGCYT   300
CVPSNGLLHP PSASAYLTVL CMPGVIRCPV RANPPLLFVS WTKDGKALQL DKFPGWSQGT   360
EGSLIIALGN EDALGEYSCT PYNSLGTAGP SPVTRVLLKA PPAFIERPKE EYFQEVGREL   420
LIPCSAQGDP PPVVSWTKVG RGLQGQAQVD SNSSLILRPL TKEAHGHWEC SASNAVARVA   480
TSTNVYVLGT SPHVVTNVSV VALPKGANVS WEPGFDGGYL QRFSVWYTPL AKRPDRMHHD   540
WVSLAVPVGA AHLLVPGLQP HTQYQFSVLA QNKLGSGPFS EIVLSAPEGL PTTPAAPGLP   600
PTEIPPPLSP PRGLVAVRTP RGVLLHWDPP ELVPKRLDGY VLEGRQGSQG WEVLDPAVAG   660
TETELLVPGL IKDVLYEFRL VAFAGSFVSD PSNTANVSTS GLEVYPSRTQ LPGLLPQPVL   720
AGVVGGVCFL GVAVLVSILA GCLLNRRRAA RRRRKRLRQD PPLIFSPTGK SAAPSALGSG   780
SPDSVAKLKL QGSPVPSLRQ SLLWGDPAGT PSPHPDPPSS RGPLPLEPIC RGPDGRFVMG   840
PTVAAPQERS GREQAEPRTP AQRLARSFDC SSSSPSGAPQ PLCIEDISPV APPPAAPPSP   900
LPGPGPLLQY LSLPFFREMN VDGDWPPLEE PSPAAPPDYM DTRRCPTSSF LRSPETPPVS   960
PRESLPGAVV GAGATAEPPY TALADWTLRE RLLPGLLPAA PRGSLTSQSS GRGSASFLRP   1020
PSTAPSAGGS YLSPAPGDTS SWASGPERWP RREHVVTVSK RRNTSVDENY EWDSEFPGDM   1080
ELLETLHLGL ASSRLRPEAE TELGVKTPEE GCLLNTAHVT GPEARCAALR EEFLAFRRRR   1140
DATRARLPAY RQPVPHPEQA TLL                                           1163

Seq ID NO: C309 Protein Sequence
Protein Accession #:

1          11         21         31         41         51
|          |          |          |          |          |
MLTKPLQGPP APPGTPTPPP GGKDREAFEA EYRLGPLLGK GGFGTVFAGH RLTDRLQVAI   60
KVIPRNRVLG WSPLSDSVTC PLEVALLWKV GAGGGHPGVI RLLDWFETQE GFMLVLERPL   120
PAQDLFDYIT EKGPLGEGPS RCFFGQVVAA IQHCHSRGVV HRDIKDENIL IDLRRGCAKL   180
IDFGSGALLH DEPYTDFDGT RVYSPPEWIS RHQYHALPAT VWSLGILLYD MVCGDIPFER   240
DQEILEAELH FPAHVSPDCC ALIRRCLAPK PSSRPSLEEI LLDPWMQTPA EDVTPQPLQR   300
RPCPFGLVLA TLSLAWPGLA PNGQKSHPMA MSQG                               334

Seq ID NO: C310 Protein Sequence
Protein Accession #: NP_002501.1

1          11         21         31         41         51
|          |          |          |          |          |
MECLYYFLGF LLLAARLPLD AAKRFHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP   60
VWKRGDMRWK NSWKGGRVQA VLTSDSPALV GSNITFAVNL IFPRCQKEDA NGNIVYEKNC   120
RNEAGLSADP YVYNWTAWSE DSDGENGTGQ SHHNVFFDGK PFPHHPGWRR WNFIYVFHTL   180
GQYFQKLGRC SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPIAQVKDVY VVTDQIPVFV   240
TMFQKNDRNS SDETFLKDLP IMFDVLIHDP SHFLNYSTIN YKWSFGDNTG LFVSTNHTVN   300
HTYVLNGTFS LNLTVKAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENCQIN   360
RYGHFQATIT IVEGILEVNI IQMTDVLMEV PWPESSLIDF VVTCQGSIPT EVCTIISDPT   420
CEITQNTVCS PVDVDEMCLL TVRRTFNGSG TYCVNLTLGD DTSLALTSTL ISVPDRDPAS   480
PLRMANSALI SVGCLAIFVT VISLLVYKKH KEYNPIENSP GNVVRSKGLS VFLNRAKAVF   540
FPGNQEKDPL LKNQEFKGVS                                               560

Seq ID NO: C311 Protein Sequence
Protein Accession #: Eos seq

1          11         21         31         41         51
|          |          |          |          |          |
MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK   60
QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV   120
FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS   180
ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC   240
TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY   300
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TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK   360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE   420
LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN   480
RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND   540
GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS   600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI   660
TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP   720
TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP   780
LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP   840
IKHFPKHVAD LHASSGFTEE FEEVQSCTVD LGITADSSNH PDNKHKNRYI NIVAYDHSRV   900
KLAQLAEKDG KLTDYINANY VDGYNRPKAY IAAQGPLKST AEDFWRMIWE HNVEVIVMIT   960
NLVEKGRRKC DQYWPADGSE EYGNFLVTQK SVQVLAYYTV RNFTLRNTKI KKGSQKGRPS   1020
GRVVTQYHYT QWPDMGVPEY SLPVLTFVRK AAYAKRHAVG PVVVHCSAGV GRTGTYIVLD   1080
SMLQQIQHEG TVNIFGFLKH IRSQRNYLVQ TEEQYVFIHD TLVEAILSKE TEVLDSHIHA   1140
YVNALLIPGP AGKTKLEKQF QLLSQSNIQQ SDYSAALKQC NREKNRTSSI IPVERSRVGI   1200
SSLSGEGTDY INASYIMGYY QSNEFIITQH PLLHTIKDFW RMIWDHNAQL VVMIPDGQNM   1260
AEDEFVYWPN KDEPINCESF KVTLMAEEHK CLSNEEKLII QDFILEATQD DYVLEVRHFQ   1320
CPKWPNPDSP ISKTFELISV IKEEAANRDG PMIVHDEHGG VTAGTFCALT TLMHQLEKEN   1380
SVDVYQVAKM INLMRPGVFA DIEQYQFLYK VILSLVSTRQ EENPSTSLDS NGAALPDGNI   1440
AESLESLV                                                            1448
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Seq ID NO: C312 Protein Sequence
Protein Accession #: XP_031379

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1          11         21         31         41         51
|          |          |          |          |          |
MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK   60
QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV   120
FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS   180
ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC   240
TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY   300
TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK   360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE   420
LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN   480
RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND   540
GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS   600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI   660
TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP   720
TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNGETPLQ PSYSSEVFPL VTPLLLDNQI   780
LNTTPAASSS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSSE LFRHLHTVSQ   840
ILPQVTSATE SDKVPLHASL PVAGCDLLLE PSLAQYSDVL STTHAASETL EFGSESGVLY   900
KTLMFSQVEP PSSDAMMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVTYQG   960
SLFSGPSHIP IPKSSLITPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS   1020
PVSVAEFTYT TSVPGDDNKA LSKSEIIYGN ETELQIPSFN EMVYPSESTV MPNMYDNVNK   1080
LNASLQETSV SISSTKGMFP GSLAHTTTKV FDHEISQVPE NNFSVQPTHT VSQASGDTSL   1140
KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP   1200
AVPSDPILVE TPKVDKISST MLHLIVSNSA SSENMLHSTS VPVFDVSPTS HMHSASLQGL   1260
TISYASEKYE PVLLKSESSH QVVPSLYSND ELFQTANLEI NQAHPPKGRH VFATPVLSID   1320
EPLNTLINKL IHSDEILTST KSSVTGKVFA GIPTVASDTF VSTDHSVPIG NGHVAITAVS   1380
PHRDGSVTST KLLFPSKATS ELSHSAKSDA GLVGGGEDGD TDDDGDDDDD DRGSDGLSIH   1440
KCMSCSSYRE SQEKVMNDSD THENSLMDQN NPISYSLSEN SEEDNRVTSV SSDSQTGMDR   1500
SPGKSPSANG LSQKHNDGKE ENDIQTGSAL LPLSPESKAW AVLTSDEESG SGQGTSDSLN   1560
ENETSTDFSF ADTNEKDADG ILAAGDSEIT PGFPQSPTSS VTSENSEVFH VSEAEASNSS   1620
HESRIGLAEG LESEKKAVIP LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR   1680
VISTPPTPIF PISDDVGAIP IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCTVDLGI   1740
TADSSNHPDN KHKNRYINIV AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA   1800
QGPLKSTAED FWRMIWEHNV EVIVMITNLV EKGRRKCDQY WPADGSEEYG NFLVTQKSVQ   1860
VLAYYTVRNF TLRNTKIKKG SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFVRKAAY   1920
AKRHAVGPVV VHCSAGVGRT GTYIVLDSML QQIQHEGTVN IFGFLKHIRS QRNYLVQTEE   1980
QYVFIHDTLV EAILSKETEV LDSHIHAYVN ALLIPGPAGK TKLEKQFQLL SQSNIQQSDY   2040
SAALKQCNRE KNRTSSIIPV ERSRVGISSL SGEGTDYINA SYIMGYYQSN EFIITQHPLL   2100
HTIKDFWRMI WDHNAQLVVM IPDGQNMAED EFVYWPNKDE PINCESFKVT LMAEEHKCLS   2160
NEEKLIIQDF ILEATQDDYV LEVRHFQCPK WPNPDSPISK TFELISVIKE EAANRDGPMI   2220
VHDEHGGVTA GTFCALTTLM HQLEKENSVD VYQVAKMINL MRPGVFADIE QYQFLYKVIL   2280
SLVSTRQEEN PSTSLDSNGA ALPDGNIAES LESLV                              2315
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Seq ID NO: C313 Protein Sequence
Protein Accession #: NP_002842

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QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV   120
FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS   180
ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC   240
TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY   300
TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK   360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE   420
LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN   480
RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND   540
GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS   600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI   660
TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP   720
TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNAEASNS SHESRIGLAE GLESEKKAVI   780
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PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI   840
PIKHFPKHVA DLHASSGFTE EFETLKEFYQ EVQSCTVDLG ITADSSNHPD NKHKNRYINI   900
VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQCPLKSTAE DFWRMIWEHN   960
VEVIVMITNL VEKGRRKCDQ YWPADGSEEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK  1020
GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR  1080
TGTYIVLDSM LQQIQHEGTV NIFGFLKHIR SQRNYLVQTE EQYVFIHDTL VEAILSKETE  1140
VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP  1200
VERSRVGISS LSGEGTDYIN ASYIMGYYQS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV  1260
MIPDGQNMAE DEFVYWPNKD EPINCESFKV TLMAEEHKCL SNEEKLIIQD FILEATQDDY  1320
VLEVRHFQCP KWPNPDSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL  1380
MHQLEKENSV DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG  1440
AALPDGNIAE SLESLV                                                  1456
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Seq ID NO: C314 Protein Sequence
Protein Accession #: Eos sequence

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MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK   60
QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV   120
MVFKASKITF HWGKCNMSSD GSEHSLEGQK FPLEMQIYCF DADRFSSFEE AVKGKGKLRA   180
LSILFEVGTE ENLDFKAIID GVESVSRFGK QAALDPFILL NLLPNSTDKY YIYNGSLTSP   240
PCTDTDWIVF KDTVSISESQ LAVFCEVLTM QQSGYVMLMD YLQNNFREQQ YKFSRQVFSS   300
YTGKEEIHEA VCSSEPENVQ ADPENYTSLL VTWERPRVVY DTMIEKFAVL YQQLDGEDQT   360
KHEFLTDGYQ DLGAILNNLL PNMSYVLQIV AICTNGLYGK YSDQLIVDMP TDNPELDLFP   420
ELIGTEEIIK EEEEGKDIEE GAIVNPGRDS ATNQIRKKEP QISTTTHYNR IGTKYNEAKT   480
NRSPTRGSEF SGKGDVPNTS LNSTSQPVTK LATEKDISLT SQTVTELPPH TVEGTSASLN   540
DGSKTVLRSP HMNLSGTAES LNTVSITEYE EESLLTSFKL DTGAEDSSGS SPATSAIPFI   600
SENISQGYIF SSENPETITY DVLIPESARN ASEDSTSSGS EESLKDPSME GNVWFPSSTD   660
ITAQPDVGSG RESFLQTNYT EIRVDESEKT TKSFSAGPVM SQGPSVTDLE MPHYSTFAYF   720
PTEVTPHAPT PSSRQQDLVS TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAVI   780
PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI   840
PIKHFPKHVA DLHASSGFTE EFETLKEFYQ EVQSCTVDLG ITADSSNHPD NKHKNRYINI   900
VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN   960
VEVIVMITNL VEKGRRKCDQ YWPADGSEEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK  1020
GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR  1080
TGTYIVLDSM LQQIQHEGTV NIFGFLKHIR SQRNYLVQTE EQYVFIHDTL VEAILSKETE  1140
VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP  1200
VERSRVGISS LSGEGTDYIN ASYIMGYYQS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV  1260
MIPDGQNMAE DEFVYWPNKD EPINCESFKV TLMAEEHKCL SNEEKLIIQD FILEATQDDY  1320
VLEVRHFQCP KWPNPDSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL  1380
MHQLEKENSV DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG  1440
AALPDGNIAE SLESLV                                                  1456
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Seq ID NO: C315 Protein Sequence
Protein Accession #: Eos sequence

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QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV   120
FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS   180
ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC   240
TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY   300
TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK   360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE   420
LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN   480
RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND   540
GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS   600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI   660
TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP   720
TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP   780
LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP   840
IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCTVDLGI TADSSNHPDN KHKNRYINIV   900
AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV   960
EVIVMITNLV EKGRRKCDQY WPADGSEEYG NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG  1020
SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFVRKAAY AKRHAVGPVV VHCSAGVGRT  1080
GTYIVLDSML QQIQHEGTVN IFGFLKHIRS QRNYLVQTEE QYVFIHDTLV EAILSKETEV  1140
LDSHIHAYVN ALLIPGPAGK TKLEKQFQGL TLSPRLECRG TISAHCNLPL PGLTDPPTSA  1200
SRVAGTILLS QSNIQQSDYS AALKQCNREK NRTSSIIPVE RSRVGISSLS GEGTDYINAS  1260
YIMGYYQSNE FIITQHPLLH TIKDFWRMIW DHNAQLVVMI PDGQNMAEDE FVYWPNKDEP  1320
INCESFKVTL MAEEHKCLSN EEKLIIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT  1380
FELISVIKEE AANRDGPMIV HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM  1440
RPGVFADIEQ YQFLYKVILS LVGTRQEENP STSLDSNGAA LPDGNIAESL ESLV        1494
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Seq ID NO: C316 Protein Sequence
Protein Accession #: Eos sequence

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QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV   120
FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS   180
ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC   240
```

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TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY   300
TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK   360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPEASNSSH   420
ESRIGLAEGL ESEKKAVIPL VIVSALTFIC LVVLVGILIY WRKCFQTAHF YLEDSTSPRV   480
ISTPPTPIFP ISDDVGAIPI KHFPKHVADL HASSGFTEEF ETLKEFYQEV QSCTVDLGIT   540
ADSSNHPDNK HKNRYINIVA YDHSRVKLAQ LAEKDGKLTD YINANYVDGY NRPKAYIAAQ   600
GPLKSTAEDF WRMIWEHNVE VIVMITNLVE KGRRKCDQYW PADGSEEYGN FLVTQKSVQV   660
LAYYTVRNFT LRNTKIKKGS QKGRPSGRVV TQYHYTQWPD MGVPEYSLPV LTFVRKAAYA   720
KRHAVGPVVV HCSAGVGRTG TYIVLDSMLQ QIQHEGTVNI FGFLKHIRSQ RNYLVQTEEQ   780
YVFIHDTLVE AILSKETEVL DSHIHAYVNA LLIPGPAGKT KLEKQFQLLS QSNIQQSDYS   840
AALKQCNREK NRTSSIIPVE RSRVGISSLS GEGTDYINAS YIMGYYQSNE FIITQHPLLH   900
TIKDFWRMIW DHNAQLVVMI PDGQNMAEDE FVYWPNKDEP INCESFKVTL MAEEHKCLSN   960
EEKLIIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT FELISVIKEE AANRDGPMIV   1020
HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM RPGVFADIEQ YQFLYKVILS   1080
LVSTRQEENP STSLDSNGAA LPDGNIAESL ESL                               1113
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Seq ID NO: C317 Protein Sequence
Protein Accession #: Eos sequence

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MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK   60
QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV   120
FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS   180
ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC   240
TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY   300
TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK   360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE   420
LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN   480
RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND   540
GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS   600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI   660
TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP   720
TEVTPHAFIP SSRQQDLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP   780
LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP   840
IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCTVDLGI TADSSNHPDN KHKNRYINIV   900
AHDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV   960
EVIVMITNLV EKGRRKCDQY WPADGSEEYG NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG   1020
SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFVRKAAY AKRHAVGPVV VHCSAGVGRT   1080
GTYIVLDSML QQIQHEGTVN IFGFLKHIRS QRNYLVQTEE QYVFIHDTLV EAILSKETEV   1140
LDSHIHAYVN ALLIPGPAGK TKLEKQFQLL SQSNIQQSDY SAALKQCNRE KNRTSSIIPV   1200
SRVARTILLS QSNIQQSDYS AALKQCNREK NRTSSIIPVE RSRVGISSLS GEGTDYINAS   1260
YIMGYYQSNE FIITQHPLLH TIKDFWRMIW DHNAQLVVMI PDGQNMAEDE FVYWPNKDEP   1320
INCESFKVTL MAEEHKCLSN EEKLIIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT   1380
FELISVIKEE AANRDGPMIV HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM   1440
RPGVFADIEQ YQFLYKVILS LVSTRQEENP STSLDSNGAA LPDGNIAESL ESL         1493
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Seq ID NO: C318 Protein Sequence
Protein Accession #: Eos sequence

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QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV   120
FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEEAV KGKGKLRALS   180
ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC   240
TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY   300
TGKEEIHEAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLY QQLDGEDQTK   360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE   420
LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN   480
RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPHT VEGTSASLND   540
GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS   600
ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSTDI   660
TAQPDVGSGR ESFLQTNYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP   720
TEVTPHAFTP SSRQQDLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP   780
LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP   840
IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCTVDLGI TADSSNHPDN KHKNRYINIV   900
AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV   960
EVIVMITNLV EKGRRKCDQY WPADGSEEYG NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG   1020
SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFVRKAAY AKRHAVGPVV VHCSAGVGRT   1080
GTYIVLDSML QQIQHEGTVN IFGFLKHIRS QRNYLVQTEE QYVFIHDTLV EAILSKETEV   1140
LDSHIHAYVN ALLIPGPAGK TKLEKQFQLL SQSNIQQSDY SAALKQCNRE KNRTSSIIPV   1200
ERSRVGISSL SGEGTDYINA SYIMGYYQSN EFIITQHPLL HTIKDFWRMI WDHNAQLVVM   1260
IPDGQNMAED EFVYWPNKDE PINCESFKVT LMAEEHKCLS NEEKLIIQDF ILEATQAWRS   1320
DGRNFLCSDN PYAPTRKRKF RGCLPGSQDD QSDEARSLC                         1359
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Seq ID NO: C319 Protein Sequence
Protein Accession #: XP_002914.4

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LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR   120
VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI   180
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LSIVCLMITQ LAGFSGPAFM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW   240
ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG   300
PVVAILGMIY NVIILGPTGP LGSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE   360
VLTYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQS ITVGVAPIVV VIASVVTFSV   420
HMTLGFDLTA AQAFTVVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK   480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA   540
VLAEQKGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVGSG   600
KTSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS   660
CCLRPDLAIL PSSDLTEIGE RGANLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG   720
NHIFNSAIRK HLKSKTVLFV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI   780
FNNLLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS   840
VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQGSGN TTVTRGNETS   900
VSDSMKDNPH MQYYASIYAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRILRSPM   960
KFFDTTPTGR ILNRFSKDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP  1020
LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL  1080
LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT  1140
GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM  1200
RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD  1260
IGLADLRSKL SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKE CIAQLPLKLE  1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT  1380
MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG    1437
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Seq ID NO: C320 Protein Sequence
Protein Accession #: NP_005679.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECQDAL ETAARAEGLS   60
LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR   120
VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI   180
LSIVCLMITQ LAGFSGPAFM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW   240
ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG   300
PVVAILGMIY NVIILGPTGP LGSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE   360
VLTYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV   420
HMTLGFDLTA AQAFTVVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK   480
NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA   540
VLAEQKGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVGSG   600
KTSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS   660
CCLRPDLAIL PSSDLTEIGE RGANLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG   720
NHIFNSAIRK HLKSKTVLFV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI   780
FNNLLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS   840
VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQGSGN TTVTRGNETS   900
VSDSMKDNPH MQYYASIYAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRILRSPM   960
KFFDTTPTGR ILNRFSKDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP  1020
LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL  1080
LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT  1140
GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM  1200
RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD  1260
IGLADLRSKL SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKE CIAQLPLKLE  1320
SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT  1380
MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG    1437
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Seq ID NO: C321 Protein Sequence
Protein Accession #: NP_005553.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPALWLGCCL CFSLLLPAAR ATSRREVCDC NGKSRQCIFD RELHRQTGNG FRCLNCNDNT   60
DGIHCEKCKN GFYRHRERDR CLPCNCNSKG SLSARCDNSG RCSCKPGVTG ARCDRCLPGF   120
HMLTDAGCTQ DQRLLDSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGGN   180
PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQDVDGWKA VQRNGSPAKL QWSQRHQDVF   240
SSAQRLDPVY FVAPAKFLGN QQVSYGQSLS FDYRVDRGGR HPSAHDVILE GAGLRITAPL   300
MPLGKTLPCG LTKTYTFRLN EHPSNNWSPQ LSYFEYRRLL RNLTALRIRA TYGEYSTGYI   360
DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTCIPCNCQG   420
GGACDPDTGD CYSGDENPDI ECADCPIGFY NDPHDPRSCK PCPCHNGFSC SVMPETEEVV   480
CNNCPPGVTG ARCELCADGY FGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK   540
CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCNPMGS EPVGCRSDGT CVCKPGFGGP   600
NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL   660
QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLDDLKM TVERVRALGS QYQNRVRDTH   720
RLITQMQLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR   780
ETEDYSKQAL SLVRKALHEG VGSGSGSPDG AVVQGLVEKL EKTKSLAQQL TREATQAEIE   840
ADRSYQHSLR LLDSVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG   900
NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQEALSM GNATFYEVES ILKNLREFDL   960
QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE  1020
IEQEIGSLNL EANVTADCAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE  1080
AQKVDTRAKN AGVTIQDTLN TLDGLLHLMD QPLSVDEEGL VLLEQKLSRA KTQINSQLRP  1140
MMSELEERAR QQRGHLHLLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ         1193
```

Seq ID NO: C322 Protein Sequence
Protein Accession #: NP_066924.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG   60
```

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QIQCKVFDSL LNLSSTLQAT RALMVVGILL GVIAIFVATV GMKCMKCLED DEVQKMRMAV   120
IGGAIFLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGGA   180
LLCCSCPRKT TSYPTPRPYP KPAPSSGKDY V                                  211
```

Seq ID NO: C323 Protein Sequence
Protein Accession #: AAM77876

```
1          11         21         31         41         51
|          |          |          |          |          |
MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCKCSA SRIWCSDPSP GIVAFPRLEP   60
NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLTIVD SGLKFVAHKA FLKNSNLQHI   120
NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAKSSPD TQDLYCLNES   180
SKNIPLANLQ IPNCGLPSAN LAAPNLTVEE GKSITLSCSV AGDPVPNMYW DVGNLVSKHM   240
NETSHTQGSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH   300
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT   360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST   420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKGFVLF HKIPLDG      477
```

Seq ID NO: C324 Protein Sequence
Protein Accession #: NP_006171.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCKCSA SRIWCSDPSP GIVAFPRLEP   60
NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLTIVD SGLKFVAHKA FLKNSNLQHI   120
NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAKSSPD TQDLYCLNES   180
SKNIPLANLQ IPNCGLPSAN LAAPNLTVEE GKSITLSCSV AGDPVPNMYW DVGNLVSKHM   240
NETSHTQGSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH   300
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT   360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST   420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKGPASV ISNDDDSASP   480
LHHISNGSNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDTFV QHIKRHNIVL   540
KRELGEGAFG KVFLAECYNL CPEQDKILVA VKTLKDASDN ARKDFHREAE LLTNLQHEHI   600
VKFYGVCVEG DPLIMVFEYM KHGDLNKFLR AHGPDAVLMA EGNPPTELTQ SQMLHIAQQI   660
AAGMVYLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYYRVG GHTMLPIRWM   720
PPESIMYRKF TTESDVWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ   780
EVYELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG                      822
```

Seq ID NO: C325 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCKCSA SRIWCSDPSP GIVAFPRLEP   60
NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLTIVD SGLKFVAHKA FLKNSNLQHI   120
NFTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAKSSPD TQDLYCLNES   180
SKNIPLANLQ IPNCGLPSAN LAAPNLTVEE GKSITLSCSV AGDPVPNMYW DVGNLVSKHM   240
NETSHTQGSL RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDHH   300
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNNGDYT   360
LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST   420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLLKLARHS KFGMKGFVLF HKIPLDG      477
```

Seq ID NO: C326 Protein Sequence
Protein Accession #: NP_570843.1

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1          11         21         31         41         51
|          |          |          |          |          |
MPLKHYLLLL VGCQAWGAGL AYHGCPSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI   60
LNTHITELNE SPPLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL   120
FQGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFD HLVGLTKLNL   180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL   240
FHNNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRELWL   300
YDNHISSLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLDGNV   360
FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCELRL   420
YDNPWRCDSD ILPLRNWLLL NQPRLGTDTV PVCFSPANVR GQSLIIINVN VAVPSVHVPE   480
VPSYPETPWY PDTPSYPDTT SVSSTTELTS PVEDYTDLTT IQVTDDRSVW GMTQAQSGLA   540
IAAIVIGIVA LACSLAACVG CCCCKKRSQA VLMQMKAPNE C                       581
```

Seq ID NO: C327 Protein Sequence
Protein Accession #: NP_002649.1

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1          11         21         31         41         51
|          |          |          |          |          |
MRALLARLLL CVLVVSDSKG SNELHQVPSN CDCLNGGTCV SNKYFSNIHW CNCPKKFGGQ   60
HCEIDKSKTC YEGNGHFYRG KASTDTMGRP CLPWNSATVL QQTYHAHRSD ALQLGLGKHN   120
YCRNPDNRRR PWCYVQVGLK PLVQECMVHD CADGKKPSSP PEELKFQCGQ KTLRPRFKII   180
GGEFTTIENQ PWFAAIYRRH RGGSVTYVCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG   240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHHNDIALLK IRSKEGRCAQ PSRTIQTICL   300
PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVKLI SHRECQQPHY YGSEVTTKML   360
CAADPQWKTD SCQGDSGGPL VCSLQGRMTL TGIVSWGRGC ALKDKPGVYT RVSHFLPWIR   420
SHTKEENGLA L                                                        431
```

Seq ID NO: C328 Protein Sequence
Protein Accession #: XP_087254.1

```
          1          11         21         31         41         51
          |          |          |          |          |          |
MQFRECSING MKYQEINGRL VPEGPTPDSS EGNLSYLSSL SHLNNLSHLT TSSSFRTSPE   60
NETELIKEHD LFFKAVSLCH TVQISNVQTD CTGDGPWQSN LAPSQLEYYA SSPDEKALVE  120
AAARIGIVFI GNSEETMEVK TLGKLERYKL LHILEFDSDR RRMSVIVQAP SGEKLLFAKG  180
AESSILPKCI GGEIEKTRIH VDEFALKGLR TLCIAYRKFT SKEYEEIDKR IFEARTALQQ  240
REEKLAAVFQ FIEKDLILLG ATAVEDRLQD KVRETIEALR MAGIKVWVLT GDKHETAVSV  300
SLSCCHFHRT MNILELINQK SDSECAEQLR QLARRITEDH VIQHGLVVDG TSLSLALREH  360
EKLFMEVCRN CSAVLCCRMA PLQKAKVIRL IKISPEKPIT LAVGDGANDV SMIQEAHVGI  420
GIMGKEGRQA ARNSDYAIAR FKFLSKLLFV HGHFYYIRIA TLVQYFFYKN VCFITPQFLY  480
QFYCLFSQQT LYDSVYLTLY NICFTSLPIL IYSLLEQHVD PHVLQNKPTL YRDISKNRLL  540
SIKTFLYWTI LGFSHAFIFF FGSYLLIGKD TSLLGNGQMF GNWTFGTLVF TVMVITVTVK  600
MALETHFWTW INHLVTWGSI IFYFVFSLFY GGILWPFLGS QNMYFVFIQL LSSGSAWFAI  660
ILMVVTCLFL DIIKKVFDRH LHPTSTEKAQ LTETNAGIKC LDSMCCFPEG EAACASVGRM  720
LERVIGRCSP THISRSWSAS DPFYTNDRSI LTLSTMDSST C                      761

Seq ID NO: C329 Protein Sequence
Protein Accession #: XP_087461.1

          1          11         21         31         41         51
          |          |          |          |          |          |
MLPLLAALLA AACPLPPVRG GAADAPGLLG VPSNASVNAS SAASPSPRGC WPRRPPGPPS   60
ARARRRRRRR RRLCNISVQR QMLSSLLVRW GRPRGFQCDL LLFSTNAHGR AFPAAAPHRV  120
GPPLLIEHLG LAAGGAQQDL RLCVGCGWVR GRRTGRLRPA AAPSAAAATA GAPTALPAYP  180
AAEPPGPLWL QGEPLHFCCL DFSLEELQGE PGWRLNRKPI ESTLVACFMT LVIVVWSVAA  240
LIWPVPIIAG FLPNGMEQRR TTASTTAATP AAVPAGTTAA AAAAAAAAAA AVTSGVATK   299

Seq ID NO: C330 Protein Sequence
Protein Accession #: XP_051522.2

          1          11         21         31         41         51
          |          |          |          |          |          |
MDLHLFDYSE PGNFSDISWP CNSSDCIVVD TVMCPNMPNK SVLLYTLSFI YIFIFVIGMI   60
ANSVVVWVNI QAKTTGYDTH CYILNLAIAD LWVVLTIPVW VVSLVQHNQW PMGELTCKVT  120
HLIFSINLFG SIFFLTCMSV DRYLSITYFT NTPSSRKKMV RRVVCILVWL LAFCVSLPDT  180
YYLKTVTSAS NNETYCRSFY PEHSIKEWLI GMELVSVVLG FAVPFSIIAV FYFLLARAIS  240
ASSDQEKHSS RKIIFSYVVV FLVCWLPYHV AVLLDIFSIL HYIPFTCRLE HALFTALHVT  300
QCLSLVHCCV NPVLYSFINR NYRYELMKAF IFKYSAKTGL TKLIDASRVS ETEYSALEQS  360
TK                                                                 362

Seq ID NO: C331 Protein Sequence
Protein Accession #: NP_000341.1

          1          11         21         31         41         51
          |          |          |          |          |          |
MGFVRQIQLL LWKNWTLRKR QKIRFVVELV WPLSLFLVLI WLRNANPLYS HHECHFPNKA   60
MPSAGMLPWL QGIFCNVNNP CFQSPTPGES PGIVSNYNNS ILARVYRDFQ ELLMNAPESQ  120
HLGRIWTELH ILSQFMDTLR THPERIAGRG IRIRDILKDE ETLTLFLIKN IGLSDSVVYL  180
LINSQVRPEQ FAHGVPDLAL KDIACSEALL ERFIIFSQRR GAKTVRYALC SLSQGTLQWI  240
EDTLYANVDF FKLFRVLPTL LDSRSQGINL RSWGGILSDM SPRIQEFIHR PSMQDLLWVT  300
RPLMQNGGPE TFTKLMGILS DLLCGYPEGG GSRVLSFNWY EDNNYKAFLG IDSTRKDPIY  360
SYDRRTTSFC NALIQSLESN PLTKIAWRAA KPLLMGKILY TPDSPAARRI LKNANSTFEE  420
LEHVRKLVKA WEEVGPQIWY FFDNSTQMNM IRDTLGNPTV KDFLNRQLGE EGITAEAILN  480
FLYKGPRESQ ADDMANFDWR DIFNITDRTL RLVNQYLECL VLDKFESYND ETQLTQRALS  540
LLEENMFWAG VVFPDMYPWT SSLPPHVKYK IRMDIDVVEK TNKIKDRYWD SGPRADPVED  600
FRYIWGGFAY LQDMVEQGIT RSQVQAEAPV GIYLQQMPYP CFVDDSFMII LNRCFPIFMV  660
LAWIYSVSMT VKSIVLEKEL RLKETLKNQG VSNAVIWCTW FLDSFSIMSM SIFLLTIFIM  720
HGRILHYSDP FILFLFLLAF STATIMLCFL LSTFFSKASL AAACSGVIYF TLYLPHILCF  780
AWQDRMTAEL KKAVSLLSPV AFGFGTEYLV RFEEQGLGLQ WSNIGNSPTE GDEFSFLLSM  840
QMMLLDAACY GLLAWYLDQV FPGDYGTPLP WYFLLQESYW LSGEGCSTRE ERALEKTEPL  900
TEETEDPEHP EGIHDSFFER EHPGWVPGVC VKNLVKIFEP CGRPAVDRLN ITFYENQITA  960
FLGHNGAGKT TTLSILTGLL PPTSGTVLVG GRDIETSLDA VRQSLGMCPQ HNILFHHLTV 1020
AEHMLFYAQL KGKSQEEAQL EMEAMLEDTG LHHKRNEEAQ DLSGGMQRKL SVAIAFVGDA 1080
KVVILDEPTS GVDPYSRRSI WDLLLKYRSG RTIIMPTHHM DEADHQGDRI AIIAQGRLYC 1140
SGTPLFLKNC FGTGLYLTLV RKMKNIQSQR KGSEGTCSCS SKGFSTTCPA HVDDLTPEQV 1200
LDGDVNELMD VVLHHVPEAK LVECIGQELI FLLPNKNFKH RAYASLFREL EETLADLGLS 1260
SFGISDTPLE EIFLKVTEDS DSGPLFAGGA QQKRENVNPR HPCLGPREKA GQTPQDSNVC 1320
SPGAPAAHPE GQPPPEPECP GPQLNTGTQL VLQHVQALLV KRFQHTIRSH KDFLAQIVLP 1380
ATFVFLALML SIVILPFGEY PALTLHPWIY GQQYTFFSMD EPGSEQFTVL ADVLLNKPGF 1440
GNRCLKEGWL PEYPCGNSTP WKTPSVSPNI TQLFQKQKWT QVNPSPSCRC STREKLTMLP 1500
ECPEGAGGLP PPQRTQRSTE ILQDLTDRNI SDFLVKTYPA LIRSSLKSKF WVNEQRYGGI 1560
SIGGKLPVVP ITGEALVGFL SDLGRIMNVS GGPITREASK EIPDFLKHLE TEDNIKVWFN 1620
NKGWHALVSF LNVAHNAILR ASLPKDRSPE EYGITVISQP LNLTKEQLSE ITVLTTSVDA 1680
VVAICVIFSM SFVPASFVLY LIQERVNKSK HLQFISGVSP TTYWVTNFLW DIMNYSVSAG 1740
LVVGIFIGFQ KKAYTSPENL PALVALLLLY GWAVIPMMYP ASFLFDVPST AYVALSCANL 1800
FIGINSSAIT FILELFDNNR TLLRFNAVLR KLLIVFPHFC LGRGLIDLAL SQAVTDVVAR 1860
FGEEHSANPF HWDLIGKNLF AMVVEGVVYF LLTLLVQRHF FLSQWIAEPT KEPIVDEDDD 1920
VAEERQRIIT GGNKTDILRL HELTKIYLGT SSPAVDRLCV GVRPGECFGL LGVNGAGKTT 1980
TFKMLTGDTT VTSGDATVAG KSILTNISEV HQNMGYCPQF DAIDELLTGR EHLYLYARLR 2040
GVPAEEIEKV ANWSIKSLGL TVYADCLAGT YSGGNKRKLS TAIALIGCPP LVLLDEPTTG 2100
MDPQARRMLW NVIVSIIRKG RAVVLTSHSM EECEALCTRL AIMVKGAFRC MGTIQHLKSK 2160
FGDGYIVTMK IKSPKDDLLP DLNPVEQFFQ GNFPGSVQRE RHYNMLQFQV SSSSLARIFQ 2220
LLLSHKDSLL IEEYSVTQTT LDQVFVNFAK QQTESHDLPL HPRAAGASRQ AQD         2273
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Seq ID NO: C332 Protein Sequence
Protein Accession #: NP_006662.2

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1          11         21         31         41         51
|          |          |          |          |          |
MVPHAILARG RDVCRRNGLL ILSVLSVIVG CLLGFFLRTR RLSPQEISYF QFPGELLMRM   60
LKMMILPLVV SSLMSGLASL DAKTSSRLGV LTVAYYLWTT FMAVIVGIFM VSIIHPGSAA  120
QKETTEQSGK PIMSSADALL DLIRNMFPAN LVEATFKQYR TKTTPVVKSP KVAPEEAPPR  180
RILIYGVQEE NGSHVQNFAL DLTPPPEVVY KSEPGTSDGM NVLGIVFFSA TMGIMLGRMG  240
DSGAPLVSFC QCLNESVMKI VAVAVWYFPF GIVFLIAGKI LEMDDPRAVG KKLGFYSVTV  300
VCGLVLHGLF ILPLLYFFIT KKNPIVFIRG ILQALLIALA TSSSSATLPI TFKCLLENNH  360
IDRRIARFVL PVGATINMDG TALYEAVAAI FIAQVNNYEL DFGQIITISI TATAASIGAA  420
GIPQAGLVTM VIVLTSVGLP TDDITLIIAV DWALDRFRTM INVLGDALAA GIMAHICRKD  480
FARDTGTEKL LPCETKPVSL QEIVAAQQNG CVKSVAEASE LTLGPTCPHH VPVQVERDEE  540
LPAASLNHCT IQISELETNV                                              560
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Seq ID NO: C333 Protein Sequence
Protein Accession #: NP_005680.1

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1          11         21         31         41         51
|          |          |          |          |          |
MVTVGNYCEA EGPVGPAWMQ DGLSPCFFFT LVPSTRMALG TLALVLALPC RRRERPAGAD   60
SLSWGAGPRI SPYVLQLLLA TLQAALPLAG LAGRVGTARG APLPSYLLLA SVLESLAGAC  120
GLWLLVVERS QARQRLAMGI WIKFRHSPGL LLLWTVAFAA ENLALVSWNS PQWWWARADL  180
GQQVQFSLWV LRYVVSGGLF VLGLWAPGLR PQSYTLQVHE EDQDVERSQV RSAAQQSTWR  240
DFGRKLRLLS GYLWPRGSPA LQLVVLICLG LMGLERALNV LVPIFYRNIV NLLTEKAPWN  300
SLAWTVTSYV FLKFLQGGGT GSTGFVSNLR TFLWIRVQQF TSRRVELLIF SHLHELSLRW  360
HLGRRTGEVL RIADRGTSSV TGLLSYLVFN VIPTLADIII GIIYFSMFFN AWFGLIVFLC  420
MSLYLTLTIV VTEWRTKFRR AMNTQENATR ARAVDSLLNF ETVKYYNAES YEVERYREAI  480
IKYQGLEWKS SASLVLLNQT QNLVIGLGLL AGSLLCAYFV TEQKLQVGDY VLFGTYIIQL  540
YMPLNWFGTY YRMIQTNFID MENMFDLLKE ETEVKDLPGA GPLRFQKGRI EFENVHFSYA  600
DGRETLQDVS FTVMPGQTLA LVGPSGAGKS TILRLLFRFY DISSGCIRID GQDISQVTQA  660
SLRSHIGVVP QDTVLFNDTI ADNIRYGRVT AGNDEVEAAA QAAGIHDAIM AFPEGYRTQV  720
GERGLKLSGG EKQRVAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTIV  780
VAHRLSTVVN ADQILVIKDG CIVERGRHEA LLSRGGVYAD MWQLQQGQEE TSEDTKPQTM  840
ER                                                                 842
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Seq ID NO: C334 Protein Sequence
Protein Accession #: NP_000667.1

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1          11         21         31         41         51
|          |          |          |          |          |
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVGLFA   60
IPFAITISLG FCTDFYGCLF LACFVLVLTQ SSIFSLLAVA VDRYLAICVP LRYKSLVTGT  120
RARGVIAVLW VLAFGIGLTP FLGWNSKDSA TNNCTEPWDG TTNESCCLVK CLFENVVPMS  180
YMVYFNFFGC VLPPLLIMLV IYIKIFLVAC RQLQRTELMD HSRTTLQREI HAAKSLAMIV  240
GIFALCWLPV HAVNCVTLFQ PAQGKNKPKW AMNMAILLSH ANSVVNPIVY AYRNRDFRYT  300
FHKIISRYLL CQADVKSGNG QAGVQPALGV GL                                332
```

Seq ID NO: C335 Protein Sequence
Protein Accession #: NP_443164

```
1          11         21         31         41         51
|          |          |          |          |          |
MGLGARGAWA ALLLGTLQVL ALLGAAHESA AMAETLQHVP SDHTNETSNS TVKPPTSVAS   60
DSSNTTVTTM KPTAASNTTT PGMVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMTVTHNS  120
SVTSAASSVT ITTTMHSEAK KGSKFDTGSF VGGIVLTLGV LSILYIGCKM YYSRRGIRYR  180
TIDEHDAII                                                          189
```

Seq ID NO: C336 Protein Sequence
Protein Accession #: NP_004186.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAQHGAMGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTDARCC RVHTTRCCRD   60
YPGEECCSEW DCMCVQPEFH CGDPCCTTCR HHPCPPGQGV QSQGKFSFGF QCIDCASGTF  120
SGGHEGHCKP WTDCTQFGFL TVFPGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL  180
TSAQLGLHIW QLRSQCMWPR ETQLLLEVPP STEDARSCQF PEEERGERSA EEKGRLGDLW  240
V                                                                  241
```

Seq ID NO: C337 Protein Sequence
Protein Accession #: BAC03767.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGCDGRVSGL LRRNLQPTLT YWSVFFSFGL CIAFLGPTLL DLRCQTHSSL PQISWVFFSQ   60
QLCLLLGSAL GGVFKRTLAQ SLWALFTSSL AISLVFAVIP FCRDVKVLAS VMALAGLAMG  120
CIDTVANMQL VRMYQKDSAV FLQVLHFFVG FGALLSPLIA DPFLSEANCL PANSTANTTS  180
RGHLFHVSRV LGQHHVDAKP WSNQTFPGLT PKDGAGTRVS YAFWIMALID LPVPMAVLML  240
LSKERLLTCC PQRRPLLLSA DELALETQPP EKEDASSLPP KFQSHLGHED LFSCCQRKNL  300
RGAPYSFFAI HITGALVLFM TDGLTGAYSA FVYSYAVEKP LSVGHKVAGY LPSLFWGFIT  360
LGRLLSIPIS SRMKPATMVF INVVGVVVTF LVLLIFSYNV VFLFVGTASL GLFLSSTFPS  420
MLAYTEDSLQ YKGCATTVLV TGAGVGEMVL QMLVGSIFQA QGSYSFLVCG VIFGCLAFTF  480
```

YILLLFFHRM HPGLPSVPTQ DRSIGMENSE CYQR 514

Seq ID NO: C338 Protein Sequence
Protein Accession #: NP_002194.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGPERTGAAP LPLLLVLALS QGILNCCLAY NVGLPEAKIF SGPSSEQFGY AVQQFINPKG   60
NWLLVGSPWS GFPENRMGDV YKCPVDLSTA TCEKLNLQTS TSIPNVTEMK TNMSLGLILT  120
RNMGTGGFLT CGPLWAQQCG NQYYTTGVCS DISPDFQLSA SFSPATQPCP SLIDVVVVCD  180
ESNSIYPWDA VKNFLEKFVQ GLDIGPTKTQ VGLIQYANNP RVVFNLNTYK TKEEMIVATS  240
QTSQYGGDLT NTFGAIQYAR KYAYSAASGG RRSATKVMVV VTDGESHDGS MLKAVIDQCN  300
HDNILRFGIA VLGYLNRNAL DTKNLIKEIK AIASIPTERY FFNVSDEAAL LEKAGTLGEQ  360
IFSIEGTVQG GDNFQMEMSQ VGFSADYSSQ NDILMLGAVG AFGWSGTIVQ KTSHGHLIFP  420
KQAFDQILQD RNHSSYLGYS VAAISTGEST HFVAGAPRAN YTGQIVLYSV NENGNITVIQ  480
AHRGDQIGSY FGSVLCSVDV DKDTITDVLL VGAPMYMSDL KKEEGRVYLF TIKKGILGQH  540
QFLEGPEGIE NTRFGSAIAA LSDINMDGFN DVIVGSPLEN QNSGAVYIYN GHQGTIRTKY  600
SQKILGSDGA FRSHLQYFGR SLDGYGDLNG DSITDVSIGA FGQVVQLWSQ SIADVAIEAS  660
FTPEKITLVN KNAQIILKLC FSAKFRPTKQ NNQVAIVYNI TLDADGFSSR VTSRGLFKEN  720
NERCLQKNMV VNQAQSCPEH IIYIQEPSDV VNSLDLRVDI SLENPGTSPA LEAYSETAKV  780
FSIPFHKDCG EDGLCISDLV LDVRQIPAAQ EQPFIVSNQN KRLTFSVTLK NKRESAYNTG  840
IVVDFSENLF FASFSLPVDG TEVTCQVAAS QKSVACDVGY PALKREQQVT FTINFDFNLQ  900
NLQNQASLSF QALSESQEEN KADNLVNLKI PLLYDAEIHL TRSTNINFYE ISSDGNVPSI  960
VHSFEDVGPK FIFSLKVTTG SVPVSMATVI IHIPQYTKEK NPLMYLTGVQ TDKAGDISCN 1020
ADINPLKIGQ TSSSVSFKSE NFRHTKELNC RTASCSNVTC WLKDVHMKGE YFVNVTTRIW 1080
NGTFASSTFQ TVQLTAAAEI NTYNPEIYVI EDNTVTIPLM IMKPDEKAEV PTGVIIGSII 1140
AGILLLLALV AILWKLGFFK RKYEKMTKNP DEIDETTELS S                     1181
```

Seq ID NO: C339 Protein Sequence
Protein Accession #: NP_113648.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MYRPRARAAP EGRVRGCAVP STVLLLLAYL AYLALGTGVF WTLEGRAAQD SSRSFQRDKW   60
ELLQNFTCLD RPALDSLIRD VVQAYKNGAS LLSNTTSMGR WELVGSFFFS VSTITTIGYG  120
NLSPNTMAAR LFCIFFALVG IPLNLVVLNR LGHLMQQGVN HWASRLGGTW QDPDKARWLA  180
GSGALLSGLL LFLLLPPLLF SHMEGWSYTE GFYFAFITLS TVGFGDYVIG MNPSQRYPLW  240
YKNMVSLWIL FGMAWLALII KLILSQLETP GRVCSCCHHS SKEDFKSQSW RQGPDREPES  300
HSPQQGCYPE GPMGIIQHLE PSAHAAGCGK DS                               332
```

Seq ID NO: C340 Protein Sequence
Protein Accession #: NP_004145.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEWDNGTGQA LGLPPTTCVY RENFKQLLLP PVYSAVLAAG LPLNICVITQ ICTSRRALTR   60
TAVYTLNLAL ADLLYACSLP LLIYNYAQGD HWPFGDFACR LVRFLFYANL HGSILFLTCI  120
SFQRYLGICH PLAPWHKRGG RRAAWLVCVA VWLAVTTQCL PTAIFAATGI QRNRTVCYDL  180
SPPALATHYM PYGMALTVIG FLLPFAALLA CYCLLACRLC RQDGPAEPVA QERRGKAARM  240
AVVVAAAFAI SFLPFHITKT AYLAVRSTPG VPCTVLEAFA AAYKGTRPFA SANSVLDPIL  300
FYFTQKKFRR RPHELLQKLT AKWQRQGR                                     328
```

Seq ID NO: C341 Protein Sequence
Protein Accession #: NP_009128.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQRPGPRLWL VLQVMGSCAA ISSMDMERPG DGKCQPIEIP MCKDIGYNMT RMPNLMGHEN   60
QREAAIQLHE FAPLVEYGCH GHLRFFLCSL YAPMCTEQVS TPIPACRVMC EQARLKCSPI  120
MEQFNFKWPD SLDCRKLPNK NDPNYLCMEA PNNGSDEPTR GSGLFPPLFR PQRPHSAQEH  180
PLKDGGPGRG GCDNPGKFHH VEKSASCAPL CTPGVDVYWS REDKRFAVVW LAIWAVLCFF  240
SSAFTVLTFL IDPARFRYPE RPIIFLSMCY CVYSVGYLIR LFAGAESIAC DRDSGQLYVI  300
QEGLESTGCT LVFLVLYYFG MASSLWWVVL TLTWFLAAGK KWGHEAIEAN SSYFHLAAWA  360
IPAVKTILIL VMRRVAGDEL TGVCYVGSMD VNALTGFVLI PLACYLVIGT SFILSGFVAL  420
FHIRRVMKTG GENTDKLEKL MVRIGLFSVL YTVPATCVIA CYFYERLNMD YWKILAAQHK  480
CKMNNQTKTL DCLMAASIPA VEIFMVKIFM LLVVGITSGM WIWTSKTLQS WQQVCSRRLK  540
KKSRRKPASV ITSGGIYKKA QHPQKTHHGK YEIPAQSPTC V                     581
```

Seq ID NO: C342 Protein Sequence
Protein Accession #: NP_005752.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEVSRRKAPP RPPRPAAPLP LLAYLLALAA PGRGADEPVW RSEQAIGAIA ASQEDGVFVA   60
SGSCLDQLDY SLEHSLSRLY RDQAGNCTEP VSLAPPARPR PGSSFSKLLL PYREGAAGLG  120
GLLLTGWTFD RGACEVRPLG NLSRNSLRNG TEVVSCHPQG STAGVVYRAG RNNRWYLAVA  180
ATYVLPEPET ASRCNPAASD HDTAIALKDT EGRSLATQEL GRLKLCEGAG SLHFVDAFLW  240
NGSIYFPYYP YNYTSGAATG WPSMARIAQS TEVLFQGQAS LDCGHGHPDG RRLLLSSSLV  300
EALDVWAGVF SAAAGEGQER RSPTTTALCL FRMSEIQARA KRVSWDFKTA ESHCKEGDQP  360
ERVQPIASST LIHSDLTSVY GTVVMNRTVL FLGTGDGQLL KVILGENLTS NCPEVIYEIK  420
EETPVFYKLV PDPVKNIYIY LTAGKEVRRI RVANCNKHKS CSECLTATDP HCGWCHSLQR  480
CTFQGDCVHS ENLENWLDIS SGAKKCPKIQ IIRSSKEKTT VTMVGSFSPR HSKCMVKNVD  540
SSRELCQNKS QPNRTCTCSI PTRATYKDVS VVNVMFSFGS WNLSDRFNFT NCSSLKECPA  600
CVETGCAWCK SARRCIHPFT ACDPSDYERN QEQCPVAVEK TSGGGRPKEN KGNRTNQALQ  660
VFYIKSIEPQ KVSTLGKSNV IVTGANFTRA SNITMILKGT STCDKDVIQV SHVLNDTHMK  720
```

```
FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITMMGRNFD   780
VIDNLIISHE LKGNINVSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLQY   840
REDPRFTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LFHGENGQLN CSFENITRNQ   900
DLTTILCKIK GIKTASTIAN SSKKVRVKLG NLELYVEQES VPSTWYFLIV LPVLLVIVIF   960
AAVGVTRHKS KELSRKQSQQ LELLESELRK EIRDGFAELQ MDKLDVVDSF GTVPFLDYKH  1020
FALRTFFPES GGFTHIFTED MHNRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNFS  1080
VKDRCLFASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKLMLRRTE SVVEKLLTNW  1140
MSVCLSGFLR ETVGEPFYLL VTTLNQKINK GPVDVITCKA LYTLNEDWLL WQVPEFSTVA  1200
LNVVFEKIPE NESADVCRNI SVNVLDCDTI GQAKEKIFQA FLSKNGSPYG LQLNEIGLEL  1260
QMGTRQKELL DIDSSSVILE DGITKLNTIG HYEISNGSTI KVFKKIANFT SDVEYSDDHC  1320
HLILPDSEAF QDVQGKRHRG KHKFKVKEMY LTKLLSTKVA IHSVLEKLFR SIWSLPNSRA  1380
PFAIKYFFDF LDAQAENKKI TDPDVVHIWK TNSLPLRFWV NILKNPQFVF DIKKTPHIDG  1440
CLSVIAQAFM DAFSLTEQQL GKEAPTNKLL YAKDIPTYKE EVKSYYKAIR DLPPLSSSEM  1500
EEFLTQESKK HENEFNEEVA LTEIYKYIVK YFDEILNKLE RERGLEEAQK QLLHVKVLFD  1560
EKKKCKWM                                                           1568
```

Seq ID NO: C343 Protein Sequence
Protein Accession #: NP_002176.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTILGTTFGM VFSLLQVVSG ESGYAQNGDL EDAELDDYSF SCYSQLEVNG SQHSLTCAFE   60
DPDVNTTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK  120
IDLTTIVKPE APFDLSVIYR EGANDFVVTF NTSHLQKKYV KVLMHDVAYR QEKDENKWTH  180
VNLSSTKLTL LQRKLQPAAM YEIKVRSIPD HYFKGFWSEW SPSYYFRTPE INNSSGEMDP  240
ILLTISILSF FSVALLVILA CVLWKKRIKP IVWPSLPDHK KTLEHLCKKP RKNLNVSFNP  300
ESFLDCQIHR VDDIQARDEV EGFLQDTFPQ QLEESEKQRL GGDVQSPNCP SEDVVVTPES  360
FGRDSSLTCL AGNVSACDAP ILSSSRSLDC RESGKNGPHV YQDLLLSLGT TNSTLPPPFS  420
LQSGILTLNP VAQGQPILTS LGSNQEEAYV TMSSFYQNQ                         459
```

Seq ID NO: C344 Protein Sequence
Protein Accession #: NP_002713.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML   60
TRPRYGKRHK EDTLAFSEWG SPHAAVPREL SPLDL                              95
```

Seq ID NO: C345 Protein Sequence
Protein Accession #: NP_115934.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTWRHHVRLL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSHFGE   60
VTGSAEGWGP EEPLPYSRAF GEGASARPRC CRNGGTCVLG SFCVCPAHFT GRYCEHDQRR  120
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL  180
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPCGRPGLG HRL                    223
```

Seq ID NO: C346 Protein Sequence
Protein Accession #: NP_006524.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LQDYMAPDCR   60
FLTIHRGQVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD  120
VKTDKWDFYC Q                                                       131
```

Seq ID NO: C347 Protein Sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MTQVTEKSTE HPEKTTSTTE KTTRTPEKPT LYSEKTICTK GKNTPVPEKP TENLGNTTLT   60
TETIKAPVKS TENPEKTAAV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI  120
TSRTKLSSIT SEATGNESHP YLNKDGSQKG IHAGQMGEND SFPAWAIVIV VLVAVILLLV  180
FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSPR       235
```

Seq ID NO: C348 Protein Sequence
Protein Accession #: NP_543146.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MTQVTEKSTE HPEKTTSTTE KTTRTPEKPT LYSEKTICTK GKNTPVPEKP TENLGNTTLT   60
TETIKAPVKS TENPEKTAAV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI  120
TSRTKLSSIT SEATGNESHP YLNKDGSQKG IHAGQMGEND SFPAWAIVIV VLVAVILLLV  180
FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSPR       235
```

Seq ID NO: C349 Protein Sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
```

```
MWPRLAFCCW GLALVSGWAT FQQMSPSRNF SFRLFPETAP GAPGSIPAPP APGDEAAGSR   60
VERLGQAFRR RVRLLRELSE RLELVFLVDD SSSVGEVNFR SELMFVRKLL SDFPVVPTAT   120
RVAIVTFSSK NYVVPRVDYI STRRARQHKC ALLLQEIPAI SYRGGGTYTK GAFQQAAQIL   180
LHARENSTKV VFLITDGYSN GGDPRPIAAS LRDSGVEIFT FGIWQGNIRE LNDMASTPKE   240
EHCYLLHSFE EFEALARRAL HEDLPSGSFI QDDMVHCSYL CDEGKDCCDR MGSCKCGTHT   300
GHFECICEKG YYGKGLQYEC TACPSGTYKP EGSPGGISSC IPCPDENHTS PPGSTSPEDC   360
VCREGYRASG QTCELVHCPA LKPPENGYFI QNTCNNHFNA ACGVRCHPGF DLVGSSIILC   420
LPNGLWSGSE SYCRVRTCPH LRQPKHGHIS CSTREMLYKT TCLVACDEGY RLEGSDKLTC   480
QGNSQWDGPE PRCVERHCST FQMPKDVIIS PHNCGKQPAK FGTICYVSCR QGFILSGVKE   540
MLRCTTSGKW NVGVQAAVCK DVEAPQINCP KDIEAKTLEQ QDSANVTWQI PTAKDNSGEK   600
VSVHVHPAFT PPYLFPIGDV AIVYTATDLS GNQASCIFHI KVIDAEPPVI DWCRSPPPVQ   660
VSEKVHAASW DEPQFSDNSG AELVITRSHT QGDLFPQGET IVQYTATDPS GNNRTCDIHI   720
VIKGSPCEIP FTPVNGDFIC TPDNTGVNCT LTCLEGYDFT EGSTDKYYCA YEDGVWKPTY   780
TTEWPDCAKK RFANHGFKSF EMFYKAARCD DTDLMKKFSE AFETTLGKMV PSFCSDAEDI   840
DCRLEENLTK KYCLEYNYDY ENGFAIGPGG WGAANRLDYS YDDFLDTVQE TATSIGNAKS   900
SRIKRSAPLS DYKIKLIFNI TASVPLPDER NDTLEWENQQ RLLQTLETIT NKLKRTLNKD   960
PMYSFQLASE ILIADSNSLE TKKASPFCRP GSVLRGRMCV NCPLGTYYNL EHFTCESCRI   1020
GSYQDEEGQL ECKLCPSGMY TEYIHSRNIS DCKAQCKQGT YSYSGLETCE SCPLGTYQPK   1080
FGSRSCLSCP ENTSTVKRGA VNISACGVPC PEGKFSRSGL MPCHPCPRDY YQPNAGKAFC   1140
LACPFYGTTP FAGSRSITEC STSVLNITIF GGFGHLELLN CPSEVFHECF FNPCHNSGTC   1200
QQLGRGYVCL CPLGYTGLKC ETDIDECSPL PCLNNGVCKD LVGEFICECP SGYTGQRCEE   1260
NINECSSSPC LNKGICVDGV AGYRCTCVKG FVGLHCETEV NECQSNPCLN NAVCEDQVGG   1320
FLCKCPPGFL GTRCGKNVDE CLSQPCKNGA TCKDGANSFR CLCAAGFTGS HCELNINECQ   1380
SNPCRNQATC VDELNSYSCK CQPGFSGKRC ETEQSTGFNL DFEVSGIYGY VMLDGMLPSL   1440
HALTCTFWMK SSDDMNYGTP ISYAVDNGSD NTLLLTDYNG WVLYVNGREK ITNCPSVNDG   1500
RWHHIAITWT SANGIWKVYI DGKLSDGGAG LSVGLPIPGG GALVLGQEQD KKGEGFSPAE   1560
SFVGSISQLN LWDYVLSPQQ VKSLATSCPE ELSKGNVLAW PDFLSGIVGK VKIDSKSIFC   1620
SDCPRLGGSV PHLRTASEDL KPGSKVNLFC DPGFQLVGNP VQYCLNQGQW TQPLPHCERI   1680
SCGVPPPLEN GFHSADDFYA GSTVTYQCNN GYYLLGDSRM FCTDNGSWNG VSPSCLDVDE   1740
CAVGSDCSEH ASCLNVDGSY ICSCVPPYTG DGKNCAEPIK CKAPGNPENG HSSGEIYTVG   1800
AGVTFSCQEG YQLMGVTKIT CLESGEWNHL IPYCKAVSCG KPAIPENGCI EELAFTFGSK   1860
VTYRCNKGYT LAGDKESSCL ANSSWSHSPP VCEPVKCSSP ENINNGKYIL SGLTYLSTAS   1920
YSCDTGYSLQ GPSIIECTAS GIWDRAPPAC HLVFCGEPPA IKDAVITGNN FTFRNTVTYT   1980
CKEGYTLAGL DTIECLADGK WSRSDQQCLA VSCDEPPIVD HASPETAHRL FGDIAFYYCS   2040
DGYSLADNSQ LLCNAQGKWV PPEGQDMPRC IAHFCEKPPS VSYSILESVS KAKFAAGSVV   2100
SFKCMEGFVL NTSAKIECMR GGQWNPSPMS IQCIPVRCGE PPSIMNGYAS GSNYSFGAMV   2160
AYSCNKGFYI KGEKKSTCEA TGQWSSPIPT CHPVSCGEPP KVENGFLEHT TGRIFESEVR   2220
YQCNPGYKSV GSPVFVCQAN RHWHSESPLM CVPLDCGKPP PIQNGFMKGE NFEVGSKVQF   2280
FCNEGYELVG DSSWTCQKSG KWNKKSNPKC MPAKCPEPPL LENQLVLKEL TTEVGVVTFS   2340
CKEGHVLQGP SVLKCLPSQQ WNDSFPVCKI VLCTPPPLIS FGVPIPSSAL HFGSTVKYSC   2400
VGGFFLRGNS TTLCQPDGTW SSPLPECVPV ECPQPEEIPN GIIDVQGLAY LSTALYTCKP   2460
GFELVGNTTT LCGENGHWLG GKPTCKAIEC LKPKEILNGK FSYTDLHYGQ TVTYSCNRGF   2520
RLEGPSALTC LETGDWDVDA PSCNAIHCDS PQPIENGFVE GADYSYGAII IYSCFPGFQV   2580
AGHAMQICEE SGWSSSIPTC MPIDCGLPPH IDFGDCTKLK DDQGYFEQED DMMEVPYVTP   2640
HPPYHLGAVA KTWENTKESP ATHSSNFLYG TMVSYTCNPG YELLGNPVLI CQEDGTWNGS   2700
APSCISIECD LPTAPENGFL RFTETSMGSA VQYSCKPGHI LAGSDLRLCL ENRKWSGASP   2760
RCEAISCKKP NPVMNGSIKG SNYTYLSTLY YECDPGYVLN GTERRTCQDD KNWDEDEPIC   2820
IPVDCSSPPV SANGQVRGDE YTFQKEIEYT CNEGFLLEGA RSRVCLANGS WSGATPDCVP   2880
VRCATPPQLA NGVTEGLDYG FMKEVTFHCH EGYILHGAPK LTCQSDGNWD AEIPLCKPVN   2940
CGPPEDLAHG FPNGFSFIHG GHIQYQCFPG YKLHGNSSRR CLSNGSWSGS SPSCLPCRCS   3000
TPVIEYGTVN GTDFDCGKAA RIQCFKGFKL LGLSEITCEA DGQWSSGFPH CEHTSCGSLP   3060
MIPNAFISET SSWKENVITY SCRSGYVIQG SSDLICTEKG VWSQPYPVCE PLSCGSPPSV   3120
ANAVATGEAH TYESEVKLRC LEGYTMDTDT DTFTCQKDGR WFPERISCSP KKCPLPENIT   3180
HILVHGDDFS VNRQVSVSCA EGYTFEGVNI SVCQLDGTWE PPFSDESCSP VSCGKPESPE   3240
HGFVVGSKYT FESTIIYQCE PGYELEGNRE RVCQENRQWS GGVAICKETR CETPLEFLNG   3300
KADIENRTTG PNVVYSCNRG YSLEGPSEAH CTENGTWSHP VPLCKPNPCP VPFVIPENAL   3360
LSEKEFYVDQ NVSIKCREGF LLQGHGIITC NPDETWTQTS AKCEKISCGP PAHVENAIAR   3420
GVHYQYGDMI TYSCYSGYML EGFLRSVCLE NGTWTSPPIC RAVCRFPCQN GGICQRPNAC   3480
SCPEGWMGRL CEEPICILPC LNGGRCVAPY QCDCPPGWTG SRCHTAVCQS PCLNGGKCVR   3540
PNRCHCLSSW TGHNCSR                                                  3557
```

Seq ID NO: C350 Protein Sequence
Protein Accession #: FGENESH predicted

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1          11         21         31         41         51
|          |          |          |          |          |
MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLCQPAPR CGDKIYNPLE   60
QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLKVQGV NSQCHSSPIS   120
SKCERGRIC                                                           129
```

Seq ID NO: C351 Protein Sequence
Protein Accession #: AAH35671.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MVPGARGGGA LARAAGRGLL ALLLAVSAPL RLQAEELGDG CGHLVTYQDS GTMTSKNYPG   60
TYPNHTVCEK TITVPKGKRL ILRLGDLDIE SQTCASDYLL FTSSSDQYGP YCGSMTVPKE   120
LLLNTSEVTV RFESGSHISG RGFLLTYASS DHPDLITCLE RASHYLKTEY SKFCPAGCRD   180
VAGDISGNMV DGYRDTSLLC KAAIHAGIIA DELGGQISVL QRKGISRYEG ILANGVLSRD   240
GSLSDKRFLF TSNGCSRSLS FEPDGQIRAS SSWQSVNESG DQVHWSPGQA RLQDQGPSWA   300
SGDSSNNHKP REWLEIDLGE KKKITGIRTT GSTQSNFNFY VKSFVMNFKN NNSKWKTYKG   360
IVNNEEKVFQ GNSNFRDPVQ NNFIPPIVAR YVRVVPQTWH QRIALKVELI GCQITQGNDS   420
LVWRKISQST SVSTKKEDET ITRPIPSEET STGINITTVA IPLVLLVVLV FAGMGIFAAF   480
RKKKKKGSPY GSAEAQKTDC WKQIKYPFAR HQSAEFTISY DNEKEMTQKL DLITSDMAG    539
```

Seq ID NO: C352 Protein Sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MGFGAGQRLR PVPAPRSSAE EAARPGQLRL GIRRGEAELA KLAPSGVMVP GARGGGALAR   60
AAGRGLLALL LAVSAPLRLQ AEELGDGCGH LVTYQDSGTM TSKNYPGTYP NHTVCEKTIT  120
VPKGKRLILR LGDLDIESQT CASDYLLFTS SSDQYGPYCG SMTVPKELLL NTSEVTVRFE  180
SGSHISGRGF LLTYASSDHP DLITCLERAS HYLKTEYSKF CPAGCRDVAG DISGNMVDGY  240
RDTSLLCKAA IHAGIIADEL GGQISVLQRK GISRYEGILA NGVLSRDGSL SDKRFLFTSN  300
GCSRSLSFEP DGQIRASSSW QSVNESGDQV HWSPGQARLQ DQGPSWASGD SSNNHKPREW  360
LEIDLGEKKK ITGIRTTGST QSNFNFYVKS FVMNFKNNNS KWKTYKGIVN NEEKVFQGNS  420
NFRDPVQNNF IPPIVARYVR VVPQTWHQRI ALKVELIGCQ ITQGNDSLVW RKTSQSTSVS  480
TKKEDETITR PIPSEETSTG INITTVAIPL VLLVVLVFAG MGIFAAFRKK KKKGSPYGSA  540
EAQKTDCWKQ IKYPFARHQS AEFTISYDNE KEMTQKLDLI TSDMAG                  586
```

Seq ID NO: C353 Protein Sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MFQRQERFLD LSSAEAVAAW ILHQHPDIIN KGDGCGHLVT YQDSGTMTSK NYPGTYPNHT   60
VCEKTITVPK GKRLILRLGD LDIESQTCAS DYLLFTSSSD QYGMQKEEET EVLCLSVAGA  120
QRVDIPVQLL PSFLEGWKGH ADARGPYCGS MTVPKELLLN TSEVTVRFES GSHISGRGFL  180
LTYASSDHPD LITCLERASH YLKTEYSKFC PAGCRDVAGD ISGNMVDGYR DTSLLCKAAI  240
HAGIIADELG GQISVLQRKG ISRYEGILAN GVLSRDGSLS DKRFLFTSNG CSRSLSFEPD  300
GQIRASSSWQ SVNESGDQVH WSPGQARLQD QGPSWASGDS SNNHKPREWL EIDLGEKKKI  360
TGIRTTGSTQ SNFNFYVKSF VMNFKNNNSK WKTYKGIVNN EEKVFQGNSN FRDPVQNNFI  420
PPIVARYVRV VPQTWHQRIA LKVELIGCQI TQGNDSLVWR KTSQSTSVST KKEDETITRP  480
IPSEETSTDA MPVQIVGDHT QMISQRENLG PDEGKIPFKG TAESMVRVVF AVVVNDLGML  540
FLAHTPEEDI DHYCWKQIKY PFARHQSAEF TISYDNEKEM TQKLDLITSD MADYQQPLMI  600
GTGTVTRKGS TFRPMDTDAE EAGVSTDAGG HYDCPQRAGR HEYALPLAPP EPEYATPIVE  660
RHVLRAHTFS AQSGYRVPGP QPGHKHSLSS GGFSPVAGVG AQDGDYQRPH SAQPADRGYD  720
RPKAVSALAT ESGHPDSQKP PTHPGTSDSY SAPRDCLTPL NQTAMTALL              769
```

Seq ID NO: C354 Protein Sequence
Protein Accession #: NP_004607.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAGVSACIKY SMFTFNFLFW LCGILILALA IWVRVSNDSQ AIFGSEDVGS SSYVAVDILI   60
AVGAIIMILG FLGCCGAIKE SRCMLLLFFI GLLLILLLQV ATGILGAVFK SKSDRIVNET  120
LYENTKLLSA TGESEKQFQE AIIVFQEEFK CCGLVNGAAD WGNNFQHYPE LCACLDKQRP  180
CQSYNGKQVY KETCISFIKD FLAKNLIIVI GISFGLAVIE ILGLVFSMVL YCQIGNK     237
```

Seq ID NO: C355 Protein Sequence
Protein Accession #: NP_004608.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MCTGGCARCL GGTLIPLAFF GFLANILLFF PGGKVIDDND HLSQEIWFFG GILGSGVLMI   60
FPALVFLGLK NNDCCGCCGN EGCGKRFAMF TSTIFAVVGF LGAGYSFIIS AISINKGPKC  120
LMANSTWGYP FHDGDYLNDE ALWNKCREPL NVVPWNLTLF SILLVVGGIQ MVLCAIQVVN  180
GLLGTLCGDC QCCGCCGGDG PV                                           202
```

Seq ID NO: C356 Protein Sequence
Protein Accession #: NP_002372.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPRPAPARRL PGLLLLLWPL LLLPSAAPDP VARPGFRRLE TRGPGGSPGR RPSPAAPDGA   60
PASGTSEPGR ARGAGVCKSR PLDLVFIIDS SRSVRPLEFT KVKTFVSRII DTLDIGPADT  120
RVAVVNYAST VKIEFQLQAY TDKQSLKQAV GRITPLSTGT MSGLAIQTAM DEAFTVEAGA  180
REPSSNIPKV AIIVTDGRPQ DQVNEVAARA QASGIELYAV GVDRADMASL KMMASEPLEE  240
HVFYVETYGV IEKLSSRFQE TFCALDPCVL GTHQCQHVCI SDGEGKHHCE CSQGYTLNAD  300
KKTCSALDRC ALNTHGCEHI CVNDRSGSYH CECYEGYTLN EDRKTCSAQD KCALGTHGCQ  360
HICVNDRTGS HHCECYEGYT LNADKKTCSV RDKCALGSHG CQHICVSDGA ASYHCDCYPG  420
YTLNEDKKTC SATEEARRLV STEDACGCEA TLAFQDKVSS YLQRLNTKLD DILEKLKINE  480
YGQIHR                                                             486
```

Seq ID NO: C357 Protein Sequence
Protein Accession #: NP_057723.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MARGSLRRLL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH   60
SDFCLGCAAA PPAPFRLLWP ILGGALSLTF VLGLLSGFLV WRRCRRREKF TTPIEETGGE  120
GCPAVALIQ                                                          129
```

Seq ID NO: C358 Protein Sequence
Protein Accession #: NP_001810.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQPTLLLSLL GAVGLAAVNS MPVDNRNHNE GMVTRCIIEV LSNALSKSSA PPITPECRQV   60
LKTSRKDVKD KETTENENTK FEVRLLRDPA DASEAHESSS RGEAGAPGEE DIQGPTKADT  120
EKWAEGGGHS RERADEPQWS LYPSDSQVSE EVKTRHSEKS QREDEEEEEG ENYQKGERGE  180
DSSEEKHLEE PGETQNAFLN ERKQASAIKK EELVARSETH AAGHSQEKTH SREKSSQESG  240
EEAGSQENHP QESKGQPRSQ EESEEGEEDA TSEVDKRRTR PRHHHGRSRP DRSSQGGSLP  300
SEEKGHPQEE SEESNVSMAS LGEKRDHHST HYRASEEEPE YGEEIKGYPG VQAPEDLEWE  360
RYRGRGSEEY RAPRPQSEES WDEEDKRNYP SLELDKMAHG YGEESEEERG LEPGKGRHHR  420
GRGGEPRAYF MSDTREEKRF LGEGHHRVQE NQMDKARRHP QGAWKELDRN YLNYGEEGAP  480
GKWQQQGDLQ DTKENREEAR FQDKQYSSHH TAEKRKRLGE LFNPYYDPLQ WKSSHFERRD  540
NMNDNFLEGE EENELTLNEK NFFPEYNYDW WEKKPFSEDV NWGYEKRNLA RVPKLDLKRQ  600
YDRVAQLDQL LHYRKKSAEF PDFYDSEEPV STHQEAENEK DRADQTVLTE DEKKELENLA  660
AMDLELQKIA EKFSQRG                                                 677
```

Seq ID NO: C359 Protein Sequence
Protein Accession #: XP_093082.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MKLLCEGLKQ PNCVLQTLRW YRCLISSASC GALAAVLSTS QWLTELEFSE TKLEASALKL   60
LYGGLKDPNC KLQKLNLQFS LSVTAAKLPV GMVGNCSGFS GSLVQSHFGY CQDSSFKCDL  120
CKLLWPSTRV AAAKDCGSPK SFLSEGLNWA GRLEAVEEVL GLGVLVQPGD PASQGGGHCE  180
NYGSFRDLVD LEVKAEPSLR KGGMDLQRPT LQVVLLCKIF SLKLFLFIAL PNSPGQVSVV  240
QVTIPDGFVN VTVGSNVTLI CIYTTTVASR EQLSIQWSFF HKKEMEPISS PWEEGKWPDV  300
EAVKGTLDGQ QAELQIYFSQ GGQAVAICQF KDRITGSNDP GNASITISHM QPADSGIYIC  360
DVNNPPDFLG QNQGILNVSV LVKPSKPLCS VQGRPETGHT ISLSCLSALG TPSPVYYWHK  420
LEGRDIVPVK ENFNPTTGIL VIGNLTNFEQ GYYQCTAINR LGNSSCEIDL TSSHPEVGII  480
VGALIGSLVG AAIIISVVCF ARNKAKAKAK ERNSKTIAEL EPMTKINPRG ESEAMPREDA  540
TQLEVTLPSS IHETGPDTIQ EPDYEPKPTQ EPAPEPAPGS EPMAVPDLDI ELELEPETQS  600
ELEPEPEPEP ESEPGVVVEP LSEDEKGVVK A                                  631
```

Seq ID NO: C360 Protein Sequence
Protein Accession #: FGENESH predicted

```
1          11         21         31         41         51
|          |          |          |          |          |
MVFAFWKVFL ILSCLAGQVS VVQVTIPDGF VNVTVGSNVT LICIYTTTVA SREQLSIQWS   60
FFHKKEMEPI SSPWEEGKWP DVEAVKGTLD GQQAELQIYF SQGGQAVAIG QFKDRITGSN  120
DPGNASITIS HMQPADSGIY ICDVNNPPDF LGQNQGILNV SVLVKPSKPL CSVQGRPETG  180
HTISLSCLSA LGTPSPVYYW HKLEGRDIVP VKENFNPTTG ILVIGNLTNF EQGYYQCTAI  240
NRLGNSSCEI DLTSSHPEVG IIVGALIGSL VGAAIIISVV CFARNKAKAK AKERNSKTIA  300
ELEPMTKINP RGESEAMPRE DATQLEVTLP SSIHETGPDT IQEPDYEPKP TQEPAPEPAP  360
GSEPMAVPDL DIELELEPET QSELEPEPEP EPESEPGVVV EPLSEDEKGV VKA          413
```

Seq ID NO: C361 Protein Sequence
Protein Accession #: NP_003011.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MVSRMVSTML SGLLFWLASG WTPAFAYSPR TPDRVSEADI QRLLHGVMEQ LGIARPRVEY   60
PAHQAMNLVG PQSIEGGAHE GLQHLGPFGN IPNIVAELTG DNIPKDFSED QGYPDPPNPC  120
PVGKTDDGCL ENTPDTAEFS REFQLHQHLF DPEHDYPGLG KWNKKLLYEK MKGGERRKRR  180
SVNPYLQGQR LDNVVAKKSV PHFSDEDKDP E                                  211
```

Seq ID NO: C362 Protein Sequence
Protein Accession #: NP_076926.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MTTMQGMEQA MPGAGPGVPQ LGNMAVIHSH LWKGLQEKFL KGEPKVLGVV QILTALMSLS   60
MGITMMCMAS NTYGSNPISV YIGYTIWGSV MFIISGSLSI AAGIRTTKGL VRGSLGMNIT  120
SSVLAASGIL INTFSLAFYS FHHPYCNYYG NSNNCHGTMS ILMGLDGMVL LLSVLEFCIA  180
VSLSAFGCKV LCCTPGGVVL ILPSHSHMAE TASPTPLNEV                        220
```

Seq ID NO: C363 Protein Sequence
Protein Accession #: NP_002082.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTKMYPR GNHWAVGHLM GKKSTGESSS   60
VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQQPS WDSEDSSNFK  120
DVGSKGKVGR LSAPGSQREG RNPQLNQQ                                     148
```

Seq ID NO: C364 Protein Sequence
Protein Accession #: NP_036393.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA   60
EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELQVFW VDRAYALKML  120
FVKESHNMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY  180
ECQAQQTISL ASSDPQKTVT MILSAVHIQP FDIISDFVFS EEHKCPVDER EQLEETLPLI  240
LGLILGLVIM VTLAIYHVHH KMTANQVQIP RDRSQYKHMG                        280
```

Seq ID NO: C365 Protein Sequence
Protein Accession #: NP_003217.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLGLVLALLS SSSAEEYVGL SANQCAVPAK DRVDCGYPHV TPKECNNRGC CFDSRIPGVP   60
WCFKPLTRKT ECTF                                                     74
```

Seq ID NO: C366 Protein Sequence
Protein Accession #: NP_002984.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSLPSSRAAR VPGPSGSLCA LLALLLLLTP PGPLASAGPV SAVLTELRCT CLRVTLRVNP   60
KTIGKLQVFP AGPQCSKVEV VASLKNGKQV CLDPEAPFLK KVIQKILDSG NKKN        114
```

Seq ID NO: C367 Protein Sequence
Protein Accession #: NP_005233.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MRSPSAAWLL GAAILLAASL SCSGTIQGTN RSSKGRSLIG KVDGTSHVTG KGVTVETVFS   60
VDEFSASVLT GKLTTVFLPI VYTIVFVVGL PSNGMALWVF LFRTKKKHPA VIYMANLALA   120
DLLSVIWFPL KIAYHIHANN WIYGEALCNV LIGFFYGNMY CSILFMTCLS VQRYWVIVNP   180
MGHSRKKANI AIGISLAIWL LILLVTIPLY VVKQTIFIPA LNITTCHDVL PEQLLVGDMF   240
NYFLSLAIGV FLFPAFLTAS AYVLMIRMLR SSAMDENSEK KRKRAIKLIV TVLAMYLICF   300
TPSNLLLVVH YFLIKSQGQS HVYALYIVAL CLSTLNSCID PFVYYFVSHD FRDHAKNALL   360
CRSVRTVKQM QVSLTSKKHS RKSSSYSSSS TTVKTSY                            397
```

Seq ID NO: C368 Protein Sequence
Protein Accession #: NP_003460.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAEAKTHWLG AALSLIPLIF LISGAEAASF QRNQLLQKEP DLRLENVQKF PSPEMIRALE   60
YIENLRQQAH KEESSPDYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ   120
AENEPQSAPK ENKPYALNSE KNFPMDMSDD YETQQWPERK LKHMQFPPMY EENSRDNPFK   180
RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EEQKLYTDDE DDIYKANNIA   240
YEDVVGGEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSGQLGI QEEDLRKESK   300
DQLSDDVSKV IAYLKRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRNLQI   360
PPEDLIEMLK TGEKPNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKTPG   420
RAGTEALPDG LSVEDILNLL GMESAANQKT SYFPNPYNQE KVLPRLPYGA GRSRSNQLPK   480
AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPGQ GSSEDDLQEE   540
EQIEQAIKEH LNQGSSQETD KLAPVSKRFP VGPPKNDDTP NRQYWDEDLL MKVLEYLNQE   600
KAEKGREHIA KRAMENM                                                  617
```

Seq ID NO: C369 Protein Sequence
Protein Accession #: NP_112217.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPCAQRSWLA NLSVVAQLLN FGALCYGRQP QPGPVRFPDR RQEHFIKGLP EYHVVGPVRV   60
DASCHFLSYG LHYPITSSRR KRDLDGSEDW VYYRISHEEK DLFFNLTVNQ GFLSNSYIME   120
KRYGNLSHVK MMASSAPLCH LSGTVLQQGT RVGTAALSAC HGLTGFFQLP HGDFFIEPVK   180
KHPLVEGGYH PHIVYRRQKV PETKEPTCGL KDSVNISQKQ ELWREKWERH NLPSRSLSRR   240
SISKERWVET LVVADTKMIE YHGSENVESY ILTIMNMVTG LFHNPSIGNA IHIVVVRLIL   300
LEEEEQGLKI VHHAEKTLSS FCKWQKSINP KSDLNPVHHD VAVLLTRKDI CAGFNRPCET   360
LGLSHLSGMC QPHRSCNINE DSGLPLAFTI AHELGHSFGI QHDGKENDCE PVGRHPYIMS   420
RQLQYDPTPL TWSKCSEEYI TRFLDRGWGF CLDDIPKKKG LKSKVIAPGV IYDVHHQCQL   480
QYGPNATFCQ EVENVCQTLW CSVKGFCRSK LDAAADGTQC GEKKWCMAGK CITVGKKPES   540
IPGGWGRWSP WSHCSRTCGA GVQSAERLCN NPEPKFGGKY CTGERKRYRL CNVHPCRSEA   600
PTFRQMQCSE FDTVPYKNEL YHWFPIFNPA HPCELYCRPI DGQFSEKMLD AVIDGTPCFE   660
GGNSRNVCIN GICKMVGCDY EIDSNATEDR CGVCLGDGSS CQTVRKMFKQ KEGSGYVDIG   720
LIPKGARDIR VMEIEGAGNF LAIRSEDPEK YYLNGGFIIQ WNGNYKLAGT VFQYDRKGDL   780
EKLMATGPTN ESVWIQLLFQ VTNPGIKYEY TIQKDGLDND VEQMYFWQYG HWTECSVTCG   840
TGIRRQTAHC IKKGRGMVKA TFCDPETQPN GRQKKCHEKA CPPRWWAGEW EACSATCGPH   900
GEKKRTVLCI QTMVSDEQAL PPTDCQHLLK PKTLLSCNRD ILCPSDWTVG NWSECSVSCG   960
GGVRIRSVTC AKNHDEPCDV TRKPNSRALC GLQQCPSSRR VLKPNKGTIS NGKNPPTLKP   1020
VPPPTSRPRM LTTPTGPESM STSTPAISSP SPTTASKEGD LGGKQWQDSS TQPELSSRYL   1080
ISTGSTSQPI LTSQSLSIQP SEENVSSSDT GPTSEGGLVA TTTSGSGLSS SRNPITWPVT   1140
PFYNTLTKGP EMEIHSGSGE EREQPEDKDE SNPVIWTKIR VPGNDAPVES TEMPLAPPLT   1200
PDLSRESWWP PPSTVMEGLL PSQRPTTSET GTPRVEGMVT EKPANTLLPL GGDHQPEPSG   1260
KTANRNHLKL PNNMNQTKSS EPVLTEEDAT SLITEGFLLN ASNYKQLTNG HGSAHWIVGN   1320
WSECSTTCGL GAYWKRVECT TQMDSDCAAI QRPDPAKRCH LRPCAGWKVG NWSKCSRNCS   1380
GGFKIREIQC VDSRDHRNLR PFHCQFLAGI PPPLSMSCNP EPCEAWQVEP WSQCSRSCGG   1440
GVQERGVFCP GGLCDWTKRP TSTMSCNEHL CCHWATGNWD LCSTSCGGGF QKRIVQCVPS   1500
EGNKTEDQDQ CLCDHKPRPP EFKKCNQQAC KKSADLLCTK DKLSASFCQT LKAMKKCSVP   1560
TVRAECCFSC PQTHITHTQR QRRQRLLQKS KEL                                1593
```

Seq ID NO: C370 Protein Sequence
Protein Accession #: NP_001053.1

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1          11         21         31         41         51
```

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|          |          |          |          |          |
MRQSHQLPLV GLLLFSFIPS QLCEICEVSE ENYIRLKPLL NTMIQSNYNR GTSAVNVVLS   60
LKLVGIQIQT LMQKMIQQIK YNVKSRLSDV SSGELALIIL ALGVCRNAEE NLIYDYHLTD  120
KLENKFQAEI ENMEAHNGTP LTNYYQLSLD VLALCLFNGN YSTAEVVNHF TPENKNYYFG  180
SQFSVDTGAM AVLALTCVKK SLINGQIKAD EGSLKNISIY TKSLVEKILS EKKENGLIGN  240
TFSTGEAMQA LFVSSDYYNE NDWNCQQTLN TVLTEISQGA FSNPNAAAQV LPALMGKTFL  300
DINKDSSCVS ASGNFNISAD EPITVTPPDS QSYISVNYSV RINETYFTNV TVLNGSVFLS  360
VMEKAQKMND TIFGFTMEER SWGPYITCIQ GLCANNNDRT YWELLSGGEP LSQGAGSYVV  420
RNGENLEVRW SKY                                                     433
```

Seq ID NO: C371 Protein Sequence
Protein Accession #: NP_004582.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MCCTKSLLLA ALMSVLLLHL CGESEAASNF DCCLGYTDRI LHPKFIVGFT RQLANEGCDI   60
NAIIFHTKKK LSVCANPKQT WVKYIVRLLS KKVKNM                             96
```

Seq ID NO: C372 Protein Sequence
Protein Accession #: NP_037403.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAGSPLLWGP RAGGVGLLVL LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR   60
RSVPRGEAAG AVQELARALA HLLEAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD  120
PALGLDDDPD APAAQLARAL LRARLDPAAL AAQLVPAPVP AAALRPRPPV YDDGPAGPDA  180
EEAGDETPDV DPELLRYLLG RILAGSADSE GVAAPRRLRR AADHDVGSEL PPEGVLGALL  240
RVKRLETPAP QVPARRLLPP                                              260
```

Seq ID NO: C373 Protein Sequence
Protein Accession #: NP_002236.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLQSLAGSSC VRLVERHRSA WCFGFLVLGY LLYLVFGAVV FSSVELPYED LLRQELRKLK   60
RRFLEEHECL SEQQLEQFLG RVLEASNYGV SVLSNASGNW NWDFTSALFF ASTVLSTTGY  120
GHTVPLSDGG KAFCIIYSVI GIPFTLLFLT AVVQRITVHV TRRPVLYFHI RWGFSKQVVA  180
IVHAVLLGFV TVSCFFFIPA AVFSVLEDDW NFLESFYFCF ISLSTIGLGD YVPGEGYNQK  240
FRELYKIGIT CYLLLGLIAM LVVLETFCEL HELKKFRKMF YVKKDKDEDQ VHIIEHDQLS  300
FSSITDQAAG MKEDQKQNEP FVATQSSACV DGPANH                            336
```

Seq ID NO: C374 Protein Sequence
Protein Accession #: NP_005463.1

```
1          11         21         31         41         51
|          |          |          |          |          |
METTNGTETW YESLHAVLKA LNATLHSNLL CRPGPGLGPD NQTEERRASL PGRDDNSYMY   60
ILFVMFLFAV TVGSLILGYT RSRKVDKRSD PYHVYIKNRV SMI                     103
```

Seq ID NO: C375 Protein Sequence
Protein Accession #: NP_005236.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGRHLALLLL LLLLFQHFGD SDGSQRLEQT PLQFTHLEYN VTVQENSAAK TYVGHPVKMG   60
VYITHPAWEV RYKIVSGDSE NLFKAEEYIL GDFCFLRIRT KGGNTAILNR EVKDHYTLIV  120
KALEKNTNVE ARTKVRVQVL DTNDLRPLFS PTSYSVSLPE NTAIRTSIAR VSATDADIGT  180
NGEFYYSFKD RTDMFAIHPT SGVIVLTGRL DYLETKLYEM EILAADRGMK LYGSSGISSM  240
AKLTVHIEQA NECAPVITAV TLSPSELDRD PAYAIVTVDD CDQGANGDIA SLSIVAGDLL  300
QQFRTVRSFP GSKEYKVKAI GDIDWDSHPF GYNLTLQAKD KGTPPQFSSV KVIHVTSPQF  360
KAGPVKFEKD VYRAEISEFA PPNTPVVMVK AIPAYSHLRY VFKRTPGKAK FSLNYNTCLI  420
SILEPVKRQQ AAHFELEVTT SDRKASTKVL VKVLGANSNP PEFTQTAYKA AFDENVPIGT  480
TIMSLSAVDP DEGENGYVTY SIANLNHVPF AIDHFTGAVS TSENLDYELM PRVYTLRIRA  540
SDWGLPYRRE VEVLATITLN NLNDNTPLFE KINCEGTIPR DLGVGEQITT VSAIDADELQ  600
LVQYQIEAGN ELDLFSLNPN SGVLSLKRSL MDGLGAKVSF HSLRITATDG ENFATPLYIN  660
ITVAASHKLV NLQCEETGVA KMLAEKLLQA NKLHNQGEVE DIFFDSHSVN AHIPQFRSTL  720
PTGIQVKENQ PVGSSVIFMN STDLDTGFNG KLVYAVSGGN EDSCFMIDME TGMLKILSPL  780
DRETTDKYTL NITVYDLGIP QKAAWRLLHV VVVDANDNPP EFLQESYFVE VSEDKEVHSE  840
IIQVEATDKD LGPNGHVTYS ILTDTDTFSI DSVTGVVNIA RPLDRELQHE HSLKIEARDQ  900
AREEPQLFST VVVKVSLEDV NDNPPTFIPP NYRVKVREDL PEGTVIMWLE AHDPDLGQSG  960
QVRYSLLDHG EGNFDVDKLS GAVRIVQQLD FEKKQVYNLT VRAKDKGKPV SLSSTCYVEV 1020
EVVDVNENLH PPVFSSFVEK GTVKEDAPVG SLVMTVSAHD EDAGRDGEIR YSIRDGSGVG 1080
VFKIGEETGV IETSDRLDRE STSHYWLTVF ATDQGVVPLS SFIEIYIEVE DVNDNAPQTS 1140
EPVYYPEIME NSPKDVSVVQ IEAFDPDSSS NDKLMYKITS GNPQGFFSIH PKTGLITTTS 1200
RKLDREQQDE HILEVTVTDN GSPPKSTIAR VIVKILDEND NKPQFLQKFY KIRLPEREKP 1260
DRERNARREP LYRVIATDKD EGPNAEISYS IEDGNEHGKF FIEPKTGVVS SKRFSAAGEY 1320
DILSIKAVDN GRPQKSSTTR LHIEWISKPK QSLEPISFEE SFFTFTVMES DPVAHMIGVI 1380
SVEPPGIPLW FDITGGNYDS HFDVDKGTGT IIVAKPLDAE QKSNYNLTVE ATDGTTTILT 1440
QVFIKVIDTN DHRPQFSTSK YEVVIPEDTA PETEILQISA VDQDEKNKLI YTLQSSRDPL 1500
SLKKFRLDPA TGSLYTSEKL DHEAVSPAHL TVMVRDQDVP VKRNFARIVV NVSDTNDHAP 1560
WFTASSYKGR VYESAAVGSV VLQVTALDKD KGKNAEVLYS IESGNIGNIG NSFMIDPVLG 1620
SIKTAKELDR SNQAEYDLMV KATDKGSPPM SEITSVRIFV TIADNASPKF TSKEYSVELS 1680
ETVSICSFVG MVTAHSQSSV VYEIKDGNTG DAFDINPHSG TIITQKALDF ETLPIYTLII 1740
QGTNMAGLST NTTVLVHLQD ENDNAPVFMQ AEYTGLISES ASINSVVLTD RNVPLVIRAA 1800
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DADKDSNALL VYHIVEPSVH TYFAIDSSTG AIHTVLSLDY EETSIFHFTV QVHDMGTPRL   1860
FAEYAANVTV HVIDINDCPP VFAKPLYEAS LLLPTYKGVK VITVNATDAD SSAFSQLIYS   1920
ITEGNIGEKF SMDYKTGALT VQNTTQLRSR YELTVRASDG RFAGLTSVKI NVKESKESHL   1980
KFTQDVYSAV VKENSTEAET LAVITAIGSP INEPLFYHIL NPDRRFKISR TSGVLSTTGT   2040
PFDREQQEAF DVVVEVIEEH KPSAVAHVVV KVIVEDQNDN APVFVNLPYY AVVKVDTEVG   2100
HVIRYVTAVD RDSGRNGEVH YYLKEHHEHF QIGPLGEISL KKQFELDTLN KEYLVTVVAK   2160
DGGNPAFSAE VIVPITVMNK AMPVFEKPFY SAEIAESIQV HSPVVHVQAN SPEGLKVFYS   2220
ITDGDPFSQF TINFNTGVIN VIAPLDFEAH PAYKLSIRAT DSLTGAHAEV FVDIIVDDIN   2280
DNPPVFAQQS YAVTLSEASV IGTSVVQVRA TDSDSEPNRG ISYQMFGNHS KSHDHFHVDS   2340
STGLISLLRT LDYEQSRQHT IFVRAVDGGM PTLSSDVIVT VDVTDLNGNP PLFEQQIYEA   2400
RISEHAPHGH FVTCVKAYDA DSSDIDKLQY SILSGNDHKH FVIDSATGII TLSNLHRHAL   2460
KPFYSLNLSV SDGVFRSSTQ VHVTVIGGNL HSPAFLQNEY EVELAENAPL HTLVMEVKTT   2520
DGDSGIYGHV TYHIVNDFAK DRFYINERGQ IFTLEKLDRE TPAEKVISVR LMAKDAGGKV   2580
AFCTVNVILT DDNDNAPQFR ATKYEVNIGS SAAKGTSVVK SASDADEGSN ADITYAIEAD   2640
SESVKENLEI NKLSGVITTK ESLIGLENEF FTFFVRAVDN GSPSKESVVL VYVKILPPEM   2700
QLPKFSEPFY TFTVSEDVPV GTEIDLIRAE HSGTVLYSLV KGNTPESNRD ESFVIDRQSG   2760
RLKLEKSLDH ETTKWYQFSI LARCTQDDHE MVASVDVSIQ VKDANDNSPV FESSPYEAFI   2820
VENLPGGSRV IQIRASDADS GTNGQVMYSL DQSQSVEVIE SFAINMETGW ITTLKELDHE   2880
KRDNYQIKVV ASDHGEKIQL SSTAIVDVTV TDVNDSPPRF TAEIYKGTVS EDDPQGGVIA   2940
ILSTTDADSE EINRQVTYFI TGGDPLGQFA VETIQNEWKV YVKKPLDREK RDNYLLTITA   3000
TDGTFSSKAI VEVKVLDAND NSPVCEKTLY SDTIPEDVLP GKLIMQISAT DADIRSNAEI   3060
TYTLLGSGAE KFKLNPDTGE LKTSTPLDRE EQAVYHLLVR ATDGGGRFCQ ASIVVTLEDV   3120
NDNAPEFSAD PYAITVFENT EPGTLLTRVQ ATDADAGLNR KILYSLIDSA DGQFSINELS   3180
GIIQLEKPLD RELQAVYTLS LKAVDQGLPR RLTATGTVIV SVLDINDNPP VFEYREYGAT   3240
VSEDILVGTE VLQVYAASRD IEANAEITYS IISGNEHGKF SIDSKTGAVF IIENLDYESS   3300
HEYYLTVEAT DGGTPSLSDV ATVNVNVTDI NDNTPVFSQD TYTTVISEDA VLEQSVITVM   3360
ADDADGPSNS HIHYSIIDGN QGSSFTIDPV RGEVKVTKLL DRETISGYTL TVQASDNGSP   3420
PRVNTTTVNI DVSDVNDNAP VFSRGNYSVI IQENKPVGFS VLQLVVTDED SSHNGPPFFF   3480
TIVTGNDEKA FEVNPQGVLL TSSAIKRKEK DHYLLQVKVA DNGKPQLSSL TYIDIRVIEE   3540
SIYPPAILPL EIFITSSGEE YSGGVIGKIH ATDQDVYDTL TYSLDPQMDN LFSVSSTGGK   3600
LIAHKKLDIG QYLLNVSVTD GKFTTVADIT VHIRQVTQEM LNHTIAIRFA NLTPEEFVGD   3660
YWRNFQRALR NILGVRRNDI QIVSLQSSEP HPHLDVLLFV EKPGSAQIST KQLLHKINSS   3720
VTDIEEIIGV RILNVFQKLC AGLDCPWKFC DEKVSVDESV MSTHSTARLS FVTPRHHRAA   3780
VCLCKEGRCP PVHHGCEDDP CPEGSECVSD PWEEKHTCVC PSGRFGQCPG SSSMTLTGNS   3840
YVKYRLTENE NKLEMKLTMR LRTYSTHAVV MYARGTDYSI LEIHHGRLQY KFDCGSGPGI   3900
VSVQSIQVND GQWHAVALEV NGNYARLVLD QVHTASGTAP GTLKTLNLDN YVFFGGHIRQ   3960
QGTRHGRSPQ VGNGFRGCMD SIYLNGQELP LNSKPRSYAH IEESVDVSPG CFLTATEDCA   4020
SNPCQNGGVC NPSPAGGYYC KCSALYIGTH CEISVNPCSS NPCLYGGTCV VDNGGFVCQC   4080
RGLYTGQRCQ LSPYCKDEPC KNGGTCFDSL DGAVCQCDSG FRGERCQSDI DECSGNPCLH   4140
GALCENTHGS YHCNCSHEYR GRHCEDAAPN QYVSTPWNIG LAEGIGIVVF VACIFLLVVV   4200
FVLCRKMISR KKKHQAEPKD KHLGPATAFL QRPYFDSKLN KNIYSDIPPQ VPVRPISYTP   4260
SIPSDSRNNL DRNSFEGSAI PEHPEFSTFN PESVHGHRKA VAVCSVAPNL PPPPPSNSPS   4320
DSDSIQKPSW DFDYDTKVVD LDPCLSKKPL EEKPSQPYSA RESLSEVQSL SSFQSESCDD   4380
NGYHWDTSDW MPSVPLPDIQ EFPNYEVIDE QTPLYSADPN AIDTDYYPGG YDIESDFPPP   4440
PEDFPAADEL PPLPPEFSNQ FESIHPPRDM PAAGSLGSSS RNRQRFNLNQ YLPNFYPLDM   4500
SEPQTKGTGE NSTCREPHAP YPPGYQRHFE APAVESMPMS VYASTASCSD VSACCEVESE   4560
VMMSDYESGD DGHFEEVTIP PLDSQQHTEV                                    4590
```

Seq ID NO: C376 Protein Sequence
Protein Accession #: NP_055035.1

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1          11         21         31         41         51
|          |          |          |          |          |
MCYGKCARCI GHSLVGLALL CIAANILLYF PNGETKYASE NHLSRFVWFF SGIVGGGLLM   60
LLPAFVFIGL EQDDCCGCCG HENCGKRCAM LSSVLAALIG IAGSGYCVIV AALGLAEGPL   120
CLDSLGQWNY TFASTEGQYL LDTSTWSECT EPKHIVEWNV SLFSILLALG GIEFILCLIQ   180
VINGVLGGIC GFCCSHQQQY DC                                            202
```

Seq ID NO: C377 Protein Sequence
Protein Accession #: NP_003750.1

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1          11         21         31         41         51
|          |          |          |          |          |
MSTENVEGKP SNLGERGRAR SSTFLRVVQP MFNHSIFTSA VSPAAERIRF ILGEEDDSPA   60
PPQLFTELDE LLAVDGQEME WKETARWIKF EEKVEQGGER WSKPHVATLS LHSLFELRTC   120
MEKGSIMLDR EASSLPQLVE MIVDHQIETG LLKPELKDKV TYTLLRKHRH QTKKSNLRSL   180
ADIGKTVSSA SRMFTNPDNG SPAMTHRNLT SSSLNDISDK PEKDQLKNKF MKKLPRDAEA   240
SNVLVGEVDF LDTPFIAFVR LQQAVMLGAL TEVPVPTRFL FILLGPKGKA KSYHEIGRAI   300
ATLMSDEVFH DIAYKAKDRH DLIAGIDEFL DEVIVLPPGE WDPAIRIEPP KSLPSSDKRK   360
NMYSGGENVQ MNGDTPHDGG HGGGGHGDCE ELQRTGRFCG GLIKDIKRKA PFFASDFYDA   420
LNIQALSAIL FIYLATVTNA ITFGGLLGDA TDNMQGVLES FLGTAVSGAI FCLFAGQPLT   480
ILSSTGPVLV FERLLFNFSK DNNFDYLEPR LWIGLWSAFL CLILVATDAS FLVQYFTRFT   540
EEGFSSLISF IFIYDAFKKM IKLADYYPIN SNFKVGYNTL FSCTCVPPDP ANISISNDTT   600
LAPEYLPTMS STDMYHNTTF DWAFLSKKEC SKYGGNLVGN NCNFVPDITL MSFILFLGTY   660
TSSMALKKFK TSPYFPTTAR KLISDFAIIL SILIFCVIDA LVGVDTPKLI VPSEFKPTSP   720
NRGWFVPPFG ENPWWVCLAA AIPALLVTIL IFMDQQITAV IVNRKEHKLK KCAGYHLDLF   780
WVAILMVICS LMALPWYVAA TVISIAHIDS LKMETETSAP GEQPKFLGVR EQRVTGTLVF   840
ILTGLSVFMA PILKFIPMPV LYGVFLYMGV ASLNGVQFMD RLKLLLMPLK HQPDFIYLRH   900
VPLRRVHLFT FLQVLCLALL WILKSTVAAI IFPVMILALV AVRKGMDYLF SQHDLSFLDD   960
VIPEKDKKKK EDEKKKKKKK GSLDSDNDDS DCPYSEKVPS IKIPMDIMEQ QPFLSDSKPS   1020
DRERSPTFLE RHTSC                                                    1035
```

Seq ID NO: C378 Protein Sequence
Protein Accession #: NP_000949.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSTPGVNSSA SLSPDRLNSP VTIPAVMFIF GVVGNLVAIV VLCKSRKEQK ETTFYTLVCG   60
LAVTDLLGTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL PFSLSGLSII CAMSVERYLA   120
INHAYFYSHY VDKRLAGLTL FAVYASNVLF CALPNMGLGS SRLQYPDTWC FIDWTTNVTA   180
HAAYSYMYAG FSSFLILATV LCNVLVCGAL LRMHRQFMRR TSLGTEQHHA AAAASVASRG   240
HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICSIPLVV RVFVNQLYQP   300
SLEREVSKNP DLQAIRIASV NPILDPWIYI LLRKTVLSKA IEKIKCLFCR IGGSRRERSG   360
QHCSDSQRTS SAMSGHSRSF ISRELKEISS TSQTLLPDLS LPDLSENGLG GRNLLPGVPG   420
MGLAQEDTTS LRTLRISETS DSSQGQDSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET   480
LNLSEKCI                                                            488
```

Seq ID NO: C379 Protein Sequence
Protein Accession #: NP_002650.1

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1          11         21         31         41         51
|          |          |          |          |          |
MGHPPLLPLL LLLHTCVPAS WGLRCMQCKT NGDCRVEECA LGQDLCRTTI VRLWEEGEEL   60
ELVEKSCTHS EKTNRTLSYR TGLKITSLTE VVCGLDLCNQ GNSGRAVTYS RSRYLECISC   120
GSSDMSCERG RHQSLQCRSP EEQCLDVVTH WIQEGEEGRP KDDRHLRGCG YLPGCPGSNG   180
FHNNDTFHFL KCCNTTKCNE GPILELENLP QNGRQCYSCK GNSTHGCSSE ETFLIDCRGP   240
MNQCLVATGT HEPKNQSYMV RGCATASMCQ HAHLGDAFSM NHIDVSCCTK SGCNHPDLDV   300
QYRSGAAPQP GPAHLSLTIT LLMTARLWGG TLLWT                              335
```

Seq ID NO: C380 Protein Sequence
Protein Accession #: BAB55406.1

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1          11         21         31         41         51
|          |          |          |          |          |
MDFESGQVDP LASVILPPNL LENLSPEDSV LVRRAQFTFF NKTGLFQDVG PQRKTLVSYV   60
MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAFWDLN KNKSFGGWNT SGCVAHRDSD   120
ASETVCLCNH FTHFGVLMDL PRSASQLDAR NTKVLTFISY IGCGISAIFS AATLLTYVAF   180
EKLRRDYPSK ILMNLSTALL FLNLLFLLDG WITSFNVDGL CIAVAVLLHF FLLATFTWMG   240
LEAIHMYIAL VKVFNTYIRR YILKFCIIGW GLPALVVSVV LASRNNNEVY GKESYGKEKG   300
DEFCWIQDPV IFYVTCAGYF GVMFFLNIAM FIVVMVQICG RNGKRSNRTL REEVLRNLRS   360
VVSLTFLLGM TWGFAFFAWG PLNIPFMYLF SIFNSLQGLF IFIFHCAMKE NVQKQWRRHL   420
CCGRFRLADN SDWSKTATNI IKKSSDNLGK SLSSSSIGSN STYLTSKSKS SSTTYFKRNS   480
HTDNVSYEHS FNKSGSLRQC FHGQVLVKTG PC                                 512
```

Seq ID NO: C381 Protein Sequence
Protein Accession #: NP_000565.1

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1          11         21         31         41         51
|          |          |          |          |          |
MTVARPSVPA ALPLLGELPR LLLLVLLCLP AVWGDCGLPP DVPNAQPALE GRTSFPEDTV   60
ITYKCEESFV KIPGEKDSVI CLKGSQWSDI EEFCNRSCEV PTRLNSASLK QPYITQNYFP   120
VGTVVEYECR PGYRREPSLS PKLTCLQNLK WSTAVEFCKK KSCPNPGEIR NGQIDVPGGI   180
LFGATISFSC NTGYKLFGST SSFCLISGSS VQWSDPLPEC REIYCPAPPQ IDNGIIQGER   240
DHYGYRQSVT YACNKGFTMI GEHSIYCTVN NDEGEWSGPP PECRGKSLTS KVPPTVQKPT   300
TVNVPTTEVS PTSQKTTTKT TTPNAQATRS TPVSRTTKHF HETTPNKGSG TTSGTTRLLS   360
GHTCFTLTGL LGTLVTMGLL T                                             381
```

Seq ID NO: C382 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL   60
PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLM   120
LQNNQLRHVP TEALQNLRSL QSLRLDANHI SYVPPSCFSG LHSLRHLWLD DNALTEIPVQ   180
AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD   240
LNYNNLDEFP TAIRTLSNLK ELHFYDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEFPDL   300
TGTANLESLT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSFSVCQ KLQKIDLRHN   360
EIYEIKVDTF QQLLSLRSLN LAWNKIAIIH PNAFSTLPSL IKLDLSSNLL SSFPITGLHG   420
LTHLKLTGNH ALQSLISSEN FPELKVIEMP YAYQCCAFGV CENAYKISNQ WNKGDNSSMD   480
DLHKKDAGMF QAQDERDLED FLLDFEEDLK ALHSVQCSPS PGPFKPCEHL LDGWLIRIGV   540
WTIAVLALTC NALVTSTVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDAFTFGSF   600
ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSAKFET KAPFSSLKVI   660
ILLCALLALT MAAVPLLGGS KYGASPLCLP LPFGEPSTMG YMVALILLNS LCFLMMTIAY   720
TKLYCNLDKG DLENIWDCSM VKHIALLLFT NCILNCPVAF LSFSSLINLT FISPEVIKFI   780
LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS   840
TQALVTFTSS SITYDLPPSS VPSPAYPVTE SCHLSSVAFV PCL                     883
```

Seq ID NO: C383 Protein Sequence
Protein Accession #: NP_003658.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL   60
PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLM   120
LQNNQLRHVP TEALQNLRSL QSLRLDANHI SYVPPSCFSG LHSLRHLWLD DNALTEIPVQ   180
AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD   240
LNYNNLDEFP TAIRTLSNLK ELGFHSNNIR SIPEKAFVGN PSLITIHFYD NPIQFVGRSA   300
```

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FQHLPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS   360
YNLLEDLPSF SVCQKLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIIHPNAFST   420
LPSLIKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPELKV IEMPYAYQCC   480
AFGVCENAYK ISNQWNKGDN SSMDDLHKKD AGMFQAQDER DLEDFLLDFE EDLKALHSVQ   540
CSPSPGPFKP CEHLLDGWLI RIGVWTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA   600
AVNMLTGVSS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLLTLAAL   660
ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEP   720
STMGYMVALI LLNSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC   780
PVAFLSFSSL INLTFISPEV IKFILLVVVP LPACLNPLLY ILFNPHFKED LVSLRKQTYV   840
WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS   900
VAFVPCL                                                             907
```

Seq ID NO: C384 Protein Sequence
Protein Accession #: NP_003497.1

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1          11         21         31         41         51
|          |          |          |          |          |
MEMFTFLLTC IFLPLLRGHS LFTCEPITVP RCMKMAYNMT FFPNLMGHYD QSIAAVEMEH   60
FLPLANLECS PNIETFLCKA FVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTFGIRWPEE   120
LECDRLQYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGFW CPRHLKTSGG QGYKFLGIDQ   180
CAPPCPNMYF KSDELEFAKS FIGTVSIFCL CATLFTFLTF LIDVRRFRYP ERPIIYYSVC   240
YSIVSLMYFI GFLLGDSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFTMAGTVWW   300
VILTITWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCFVG   360
LYDLDASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEKL KKFMIRIGVF   420
SGLYLVPLVT LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMIKY   480
LMTLIVGISA VFWVGSKKTC TEWAGFFKRN RKRDPISESR RVLQESCEFF LKHNSKVKHK   540
KKHYKPSSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLTEIQ TSPETSMREV   600
KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD   660
TGLAQSNNLQ VPSSSEPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT                  706
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Seq ID NO: C385 Protein Sequence
Protein Accession #: NP_000573

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1          11         21         31         41         51
|          |          |          |          |          |
MRIAVICFCL LGITCAIPVK QADSGSSEEK QLYNKYPDAV ATWLNPDPSQ KQNLLAPQTL   60
PSKSNESHDH MDDMDDEDDD DHVDSQDSID SNDSDDVDDT DDSHQSDESH HSDESDELVT   120
DFPTDLPATE VFTPVVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYPDA TDEDITSHME   180
SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES   240
NEHSDVIDSQ ELSKVSREFH SHEFHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN   300
```

Seq ID NO: C386 Protein Sequence
Protein Accession #: NP_002812

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1          11         21         31         41         51
|          |          |          |          |          |
MGAARGSPAR PRRLPLLSVL LLPLLGGTQT AIVFIKQPSS QDALQGRRAL LRCEVEAPGP   60
VHVYWLLDGA PVQDTERRFA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN   120
IKWIEAGPVV LKHPASEAEI QPQTQVTLRC HIDGHPRPTY QWFRDGTPLS DGQSNHTVSS   180
KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SSQNFTLSIA DESFARVVLA PQDVVVARYE   240
EAMFHCQFSA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR   300
CIGQGQRGPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG   360
VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD   420
SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVYDGTWYR   480
CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QQCMEFDKEA TVPCSATGRE KPTIKWERAD   540
GSSLPEWVTD NAGTLHFARV TRDDAGNYTC IASNGPQGQI RAHVQLTVAV FITFKVEPER   600
TTVYQGHTAL LQCEAQGDPK PLIQWKGKDR ILDPTKLGPR MHIFQNGSLV IHDVAPEDSG   660
RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPGSPPPYK MIQTIGLSVG AAVAYIIAVL   720
GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN   780
KRHSTSDKMH FPRSSLQPIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ   840
LDFRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ   900
PLSTKQKVAL CTQVALGMEH LSNNRFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY   960
YHFRQAWVPL RWMSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLADLQ   1020
AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP              1070
```

Seq ID NO: C387 Protein Sequence
Protein Accession #: NP_002300.1

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1          11         21         31         41         51
|          |          |          |          |          |
MKVLAAGVVP LLLVLHWKHG AGSPLPITPV NATCAIRHPC HNNLMNQIRS QLAQLNGSAN   60
ALFILYYTAQ GEPFPNNLDK LCGPNVTDFP PFHANGTEKA KLVELYRIVV YLGTSLGNIT   120
RDQKILNPSA LSLHSKLNAT ADILRGLLSN VLCRLCSKYH VGHVDVTYGP DTSGKDVFQK   180
KKLGCQLLGK YKQIIAVLAQ AF                                            202
```

Seq ID NO: C388 Protein Sequence
Protein Accession #: XP_097508

```
1          11         21         31         41         51
|          |          |          |          |          |
MGRPRLTLVC HVSIIISARD LSMNNLTELQ PGLFHHLRFL EELRLSGNHL SHIPGQAFSG   60
LYSLKILMLQ NNQLGGIPAE ALWELPSLQS LRLDANLISL VPERSFEGLS SLRHLWLDDN   120
ALTEIPVRAL NNLPALQAMT LALNRISHIP DYAFQNLTSL VVLHLHNNRI QHLGTHSFEG   180
LHNLETLDLN YNKLQEFPVA IRTLGRLQEL GFHNNNIKAI PEKAFMGNPL LQTIHFYDNP   240
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IQFVGRSAFQ YLPKLHTLSL NGAMDIQEFP DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP   300
RLRVLELSHN QIEELPSLHR CQKLEEIGLQ HNRIWEIGAD TFSQLSSLQA LDLSWNAIRS   360
IHPEAFSTLH SLVKLDLTDN QLTTLPLAGL GGLMHLKLKG NLALSQAFSK DSFPKLRILE   420
VPYAYQCCPY GMCASFFKAS GQWEAEDLHL DDEESSKRPL GLLARQAENH YDQDLDELQL   480
EMEDSKPHPS VQCSPTPGPF KPCEYLFESW GIRLAVWAIV LLSVLCNGLV LLTVFAGGPV   540
PLPPVKFVVG AIAGANTLTG ISCGLLASVD ALTFGQFSEY GARWETGLGC RATGFLAVLG   600
SEASVLLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG   660
ASPLCLPYAP PEGQPAALGF TVALVMMNSF CFLVVAGAYI KLYCDLPRGD FEAVWDCAMV   720
RHVAWLIFAD GLLYCPVAFL SFASMLGLFP VTPEAVKSVL LVVLPLPACL NPLLYLLFNP   780
HFRDDLRRLR PRAGDSGPLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE   840
TYGFPSVTLI SCQQPGAPRL EGSHCVEPEG NHFGNPQPSM DGELLLRAEG STPAGGGLSG   900
GGGFQPSGLA FASHV                                                   915
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Seq ID NO: C389 Protein Sequence
Protein Accession #: NP_570901

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1          11         21         31         41         51
|          |          |          |          |          |
MASLVSLELG LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLLNT LADRVHCTNG   60
PCGKCLSVED ALGLGEPEGS GLPPGPVLEA RYVARLSAAA VLYLSNPEGT CEDTRAGLWA   120
SHADHLLALL ESPKALTPGL SWLLQRMQAR AAGQTPKTAC VDIPQLLEEA VGAGAPGSAG   180
GVLAALLDHV RSGSCFHALP SPQYFVDFVF QQHSSEVPMT LAELSALMQR LGVGREAHSD   240
HSHRHRGASS RDPVPLISSS NSSSVWDTVC LSARDVMAAY GLSEQAGVTP EAWAQLSPAL   300
LQQQLSGACT SQSRPPVQDQ LSQSERYLYG SLATLLICLC AVFGLLLLTC TGCRGVAHYI   360
LQTFLSLAVG ALTGDAVLHL TPKVLGLHTH SEEGLSPQPT WRLLAMLAGL YAFFLFENLF   420
NLLLPRDPED LEDGPCGHSS HSHGGHSHGV SLQLAPSELR QPKPPHEGSR ADLVAEESPE   480
LLNPEPRRLS PELRLLPYMI TLGDAVHNFA DGLAVGAAFA SSWKTGLATS LAVFCHELPH   540
ELGDFAALLH AGLSVRQALL LNLASALTAF AGLYVALAVG VSEESEAWIL AVATGLFLYV   600
ALCDMLPAML KVRDPRPWLL FLLHNVGLLG GWTVLLLLSL YEDDITF                 648
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Seq ID NO: C390 Protein Sequence
Protein Accession #: NP_061844

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1          11         21         31         41         51
|          |          |          |          |          |
MANASEPGGS GGGEAAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPYYLLLDL   60
CLADGLRALA CLPAVMLAAR RAAAAAGAPP GALGCKLLAF LAALFCFHAA FLLLGVGVTR   120
YLAIAHHRFY AERLAGWPCA AMLVCAAWAL ALAAAFPPVL DGGGDDEDAP CALEQRPDGA   180
PGALGFLLLL AVVVGATHLV YLRLLFFIHD RRKMRPARLV PAVSHDWTFH GPGATGQAAA   240
NWTAGFGRGP TPPALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LLFLLLWGPY   300
VVASYLRVLV RPGAVPQAYL TASVWLTFAQ AGINPVVCFL FNRELRDCFR AQFPCCQSPR   360
TTQATHPCDL KGIGL                                                   375
```

Seq ID NO: C391 Protein Sequence
Protein Accession #: NP_005622

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1          11         21         31         41         51
|          |          |          |          |          |
MAAARPARGP ELPLLGLLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP   60
LSHCGRAAPC EPLRYNVCLG SVLPYGATST LLAGDSDSQE EAHGKLVLWS GLRNAPRCWA   120
VIQPLLCAVY MPKCENDRVE LPSRTLCQAT RGPCAIVERE RGWPDFLRCT PDRFPEGCTN   180
EVQNIKFNSS GQCEVPLVRT DNPKSWYEDV EGCGIQCQNP LFTEAEHQDM HSYIAAFGAV   240
TGLCTLFTLA TFVADWRNSN RYPAVILFYV NACFFVGSIG WLAQFMDGAR REIVCRADGT   300
MRLGEPTSNE TLSCVIIFVI VYYALMAGVV WFVVLTYAWH TSFKALGTTY QPLSGKTSYF   360
HLLTWSLPFV LTVAILAVAQ VDGDSVSGIC FVGYKNYRYR AGFVLAPIGL VLIVGGYFLI   420
RGVMTLFSIK SNHPGLLSEK AASKINETML RLGIFGFLAF GFVLITFSCH FYDFFNQAEW   480
ERSFRDYVLC QANVTIGLPT KQPIPDCEIK NRPSLLVEKI NLFAMFGTGI AMSTWVWTKA   540
TLLIWRRTWC RLTGQSDDEP KRIKKSKMIA KAFSKRHELL QNPGQELSFS MHTVSHDGPV   600
AGLAFDLNEP SADVSSAWAQ HVTKMVARRG AILPQDISVT PVATPVPPEE QANLWLVEAE   660
ISPELQKRLG RKKKRRKRKK EVCPLAPPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG   720
AGDSCRQGAW TLVSNPFCPE PSPPQDPFLP SAPAPVAWAH GRRQGLGPIH SRTNLMDTEL   780
MDADSDF                                                            788
```

Seq ID NO: C392 Protein Sequence
Protein Accession #: BAC04382

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1          11         21         31         41         51
|          |          |          |          |          |
MGARSGARGA LLLALLLCWD PRLSQAGRKR SGEVLPDSFP SAPAEPLPYF LQEPQDAYIV   60
KNKPVELRCR AFPATQIYFK CNGEWVSQND HVTQEGLDEA TLGARGGLRV REVQIEVSRQ   120
QVEELFGLED YWCQCVAWSS AGTTKSRRAY VRIAYLRKNF DQEPLGKEVP LDHEVLLQCR   180
PPEGVPVAEV EWLKNEDVID PTQDTNFLLT IDHNLIIRQA RLSDTANYTC VAKNIVAKRR   240
STTATVIVYV NGGWSSWAEW SPCSNRCGRG WQKRTRTCTN PAPLNGGAFC EGQAFQKTAC   300
TTICPVDGAW TEWSKWSACS TECAHWRSRE CMAPPPQNGG RDCSGTLLDS KNCTDGLCMQ   360
NKKTLSDPNS HLLEASGDAA LYAGLVVAIF VVVAILMAVG VVVYRRNCRD FDTDITDSSA   420
ALTGGFHPVN FKTARPSNPQ LLHPSVPPDL TASAGIYRGP VYALQDSTDK IPMTNSPLLD   480
PLPSLKVEVY SSSTTGSGPG LADGADLLGV LPPGTYPSDF ARDTHFLHLR SASLGSQQLL   540
GLPRDPGSSV SGTFGCLGGR LSIPGTGVSL LVPNGAIPQG KFYEMYLLIN KAESTLPLSE   600
GTQTVLSPSV TCGPTGLLLC RPVILTMPHC AEVSARDWIF QLKTQAHQGH WEEVVTLDEE   660
TLNTPCYCQL EPRACHILLD QLGTYVFTGE SYSRSAVKRL QLAVFAPALC TSLEYSLRVY   720
CLEDTPVALK EVLELERTLG GYLVEEPKPL MFKDSYHNLR LSLHDLPHAH WRSKLLAKYQ   780
EIPFYHIWSG SQKALHCTFT LERHSLASTE LTCKICVRQV EGEGQIFQLH TTLAETPAGS   840
LDTLCSAPGS TVTTQLGPYA FKIPLSIRQK ICNSLDAPNS RGNDWRMLAQ KLSMDRYLNY   900
FATKASPTGV ILDLWEALQQ DDGDLNSLAS ALEEMGKSEM LVAVATDGDC              950
```

Seq ID NO: C393 Protein Sequence
Protein Accession #: NP_004616

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1          11         21         31         41         51
|          |          |          |          |          |
MNRKARRCLG HLFLSLGMVY LRIGGFSSVV ALGASIICNK IPGLAPRQRA ICQSRPDAII   60
VIGEGSQMGL DECQFQFRNG RWNCSALGER TVFGKELKVG SREAAFTYAI IAAGVAHAIT  120
AACTQGNLSD CGCDKEKQGQ YHRDEGWKWG GCSADIRYGI GFAKVFVDAR EIKQNARTLM  180
NLHNNEAGRK ILEENMKLEC KCHGVSGSCT TKTCWTTLPQ FRELGYVLKD KYNEAVHVEP  240
VRASRNKRPT FLKIKKPLSY RKPMDTDLVY IEKSPNYCEE DPVTGSVGTQ GRACNKTAPQ  300
ASGCDLMCCG RGYNTHQYAR VWQCNCKFHW CCYVKCNTCS ERTEMYTCK              349
```

Seq ID NO: C394 Protein Sequence
Protein Accession #: NP_003777

```
1          11         21         31         41         51
|          |          |          |          |          |
MDALCGSGEL GSKFWDSNLS VHTENPDLTP CFQNSLLAWV PCIYLWVALP CYLLYLRHHC   60
RGYIILSHLS KLKMVLGVLL WCVSWADLFY SFHGLVHGRA PAPVFFVTPL VVGVTMLLAT  120
LLIQYERLQG VQSSGVLIIF WFLCVVCAIV PFRSKILLAK AEGEISDPFR FTTFYIHFAL  180
VLSALILACF REKPPFFSAK NVDPNPYPET SAGFLSRLFF WWFTKMAIYG YRHPLEEKDL  240
WSLKEEDRSQ MVVQQLLEAW RKQEKQTARH KASAAPGKNA SGEDEVLLGA RPRPRKPSFL  300
KALLATFGSS FLISACFKLI QDLLSFINPQ LLSILIRFIS NPMAPSWWGF LVAGLMFLCS  360
MMQSLILQHY YHYIFVTGVK FRTGIMGVIY RKALVITNSV KRASTVGEIV NLMSVDAQRF  420
MDLAPFLNLL WSAPLQIILA IYFLWQNLGP SVLAGVAFMV LLIPLNGAVA VKMRAFQVKQ  480
MKLKDSRIKL MSEILNGIKV LKLYAWEPSF LKQVEGIRQG ELQLLRTAAY LHTTTTFTWM  540
CSPFLVTLIT LWVYVYVDPN NVLDAEKAFV SVSLFNILRL PLNMLPQLIS NLTQASVSLK  600
RIQQFLSQEE LDPQSVERKT ISPGYAITIH SGTFTWAQDL PPTLHSLDIQ VPKGALVAVV  660
GPVGCGKSSL VSALLGEMEK LEGKVHMKGS VAYVPQQAWI QNCTLQENVL FGKALNPKRY  720
QQTLEACALL ADLEMLPGGD QTEIGEKGIN LSGGQRQRVS LARAVYSDAD IFLLDDPLSA  780
VDSHVAKHIF DHVIGPEGVL AGKTRVLVTH GISFLPQTDF IIVLADGQVS EMGPYPALLQ  840
RNGSFANFLC NYAPDEDQGH LEDSWTALEG AEDKEALLIE DTLSNHTDLT DNDPVTYVVQ  900
KQFMRQLSAL SSDGEGQGRP VPRRHLGPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW  960
DYAKAVGLCT TLAICLLYVG QSAAAIGANV WLSAWTNDAM ADSRQNNTSL RLGVYAALGI 1020
LQGFLVMLAA MAMAAGGIQA ARVLHQALLH NKIRSPQSFF DTTPSGRILN CFSKDIYVVD 1080
EVLAPVILML LNSFFNAIST LVVIMASTPL FTVVILPLAV LYTLVQRFYA ATSRQLKRLE 1140
SVSRSPIYSH FSETVTGASV IRAYNRSRDF EIISDTKVDA NQRSCYPYII SNRWLSIGVE 1200
FVGNCVVLFA ALFAVIGRSS LNPGLVGLSV SYSLQVTFAL NWMIRMMSDL ESNIVAVERV 1260
KEYSKTETEA PWVVEGSRPP EGWPPRGEVE FRNYSVRYRP GLDLVLRDLS LHVHGGEKVG 1320
IVGRTGAGKS SMTLCLFRIL EAAKGEIRID GLNVADIGLH DLRSQLTIIP QDPILFSGTL 1380
RMNLDPFGSY SEEDIWWALE LSHLHTFVSS QPAGLDFQCS EGGENLSVGQ RQLVCLARAL 1440
LRKSRILVLD EATAAIDLET DNLIQATIRT QFDTCTVLTI AHRLNTIMDY TRVLVLDKGV 1500
VAEFDSPANL IAARGIFYGM ARDAGLA                                     1527
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Seq ID NO: C395 Protein Sequence
Protein Accession #: NP_004617

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1          11         21         31         41         51
|          |          |          |          |          |
MRARPQVCEA LLFALALQTG VCYGIKWLAL SKTPSALALN QTQHCKQLEG LVSAQVQLCR   60
SNLELMHTVV HAAREVMKAC RRAFADMRWN CSSIELAPNY LLDLERGTRE SAFVYALSAA  120
AISHAIARAC TSGDLPGCSC GPVPGEPPGP GNRWGGCADN LSYGLLMGAK FSDAPMKVKK  180
TGSQANKLMR LHNSEVGRQA LRASLEMKCK CHGVSGSCSI RTCWKGLQEL QDVAADLKTR  240
YLSATKVVHR PMGTRKHLVP KDLDIRPVKD SELVYLQSSP DFCMKNEKVG SHGTQDRQCN  300
KTSNGSDSCD LMCCGRGYNP YTDRVVERCH CKYHWCCYVT CRRCERTVER YVCK        354
```

Seq ID NO: C396 Protein Sequence
Protein Accession #: NP_114072

```
1          11         21         31         41         51
|          |          |          |          |          |
MEWGYLLEVT SLLAALALLQ RSSGAAAASA KELACQEITV PLCKGIGYNY TYMPNQFNHD   60
TQDEAGLEVH QFWPLVEIQC SPDLKFFLCS MYTPICLEDY KKPLPPCRSV CERAKAGCAP  120
LMRQYGFAWP DRMRCDRLPE QGNPDTLCMD YNRTDLTTAA PSPPRRLPPP PPGEQPPSGS  180
GHGRPPGARP PHRGGGRGGG GGDAAAPPAR GGGGGGKARP PGGGAAPCEP GCQCRAPMVS  240
VSSERHPLYN RVKTGQIANC ALPCHNPFFS QDERAFTVFW IGLWSVLCFV STFATVSTFL  300
IDMERFKYPE RPIIFLSACY LFVSVGYLVR LVAGHEKVAC SGGAPGAGGA GGAGGAAAGA  360
GAAGAGAGGP GGRGEYEELG AVEQHVRYET TGPALCTVVF LLVYFFGMAS SIWWVILSLT  420
WFLAAGMKWG NEAIAGYSQY FHLAAWLVPS VKSIAVLALS SVDGDPVAGI CYVGNQSLDN  480
LRGFVLAPLV IYLFIGTMFL LAGFVSLFRI RSVIKQQDGP TKTHKLEKLM IRLGLFTVLY  540
TVPAAVVVAC LFYEQHNRPR WEATHNCPCL RDLQPDQARR PDYAVFMLKY FMCLVVGITS  600
GVWVWSGKTL ESWRSLCTRC CWASKGAAVG GGAGATAAGG GGGPGGGGGG GPGGGGGPGG  660
GGGSLYSDVS TGLTWRSGTA SSVSYPKQMP LSQV                             694
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Seq ID NO: C397 Protein Sequence
Protein Accession #: XP_050625

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1          11         21         31         41         51
|          |          |          |          |          |
MLQGPGSLLL LFLASHCCLG SARGLFLFGQ PDFSYKRSNC KPIPANLQLC HGIEYQNMRL   60
PNLLGHETMK EVLEQAGAWI PLVMKQCHPD TKKFLCSLFA PVCLDDLDET IQPCHSLCVQ  120
VKDRCAPVMS AFGFPWPDML ECDRFPQDND LCIPLASSDH LLPATEEAPK VCEACKNKND  180
DDNDIMETLC KNDFALKIKV KEITYINRDT KIILETKSKT IYKLNGVSER DLKKSVLWLK  240
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DSLQCTCEEM NDINAPYLVM GQKQGGELVI TSVKRWQKGQ REFKRISRSI RKLQC        295

Seq ID NO: C398 Protein Sequence
Protein Accession #: NP_001297.1

1          11         21         31         41         51
|          |          |          |          |          |
MSMGLEITGT ALAVLGWLGT IVCCALPMWR VSAFIGSNII TSQNIWEGLW MNCVVQSTGQ    60
MQCKVYDSLL ALPQDLQAAR ALIVVAILLA AFGLLVALVG AQCTNCVQDD TAKAKITIVA    120
GVLFLLAALL TLVPVSWSAN TIIRDFYNPV VPEAQKREMG AGLYVGWAAA ALQLLGGALL    180
CCSCPPREKK YTATKVVYSA PRSTGPGASL GTGYDRKDYV                          220

Seq ID NO: C399 Protein Sequence
Protein Accession #: NP_036581.1

1          11         21         31         41         51
|          |          |          |          |          |
MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE    60
LQHTQELFPQ WHLPIKIAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM    120
VSITLLALVY LPGVIAAIVQ LHNGTKYKKF PHWLDKWMLT RKQFGLLSFF FAVLHAIYSL    180
SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS    240
VSDSLTWREF HYIQSKLGIV SLLLGTIHAL IFAWNKWIDI KQFVWYTPPT FMIAVFLPIV    300
VLIFKSILFL PCLRKKILKI RHGWEDVTKI NKTEICSQL                           339

Seq ID NO: C400 Protein Sequence
Protein Accession #: NP_001766.1

1          11         21         31         41         51
|          |          |          |          |          |
MANCEFSPVS GDKPCCRLSR RAQLCLGVSI LVLILVVVLA VVVPRWRQTW SGPGTTKRFP    60
ETVLARCVKY TEIHPEMRHV DCQSVWDAFK GAFISKHPCN ITEEDYQPLM KLGTQTVPCN    120
KILLWSRIKD LAHQFTQVQR DMFTLEDTLL GYLADDLTWC GEFNTSKINY QSCPDWRKDC    180
SNNPVSVFWK TVSRRFAEAA CDVVHVMLNG SRSKIFDKNS TFGSVEVHNL QPEKVQTLEA    240
WVIHGGREDS RDLCQDPTIK ELESIISKRN IQFSCKNIYR PDKFLQCVKN PEDSSCTSEI    300

Seq ID NO: C401 Protein Sequence
Protein Accession #: XP_120513.2

1          11         21         31         41         51
|          |          |          |          |          |
MVSCTFSGPL RETNENVKKF YALRAFMFRM SSEAAMLGES RTPKPRKHRA TTRAKIFKRF    60
FSEGSESNSR LVEELAVIHT YSDDPAPTTS PSSVQPREFG VMQGAPRARF GSRTPPAAAE    120
ASSPHLGIGE AACQSGARAA APRAGARRCQ PQRQAAAAAA TAQTHTLPHA RTRADPAGRR    180
RRHPRSPAPG GEGTCSEGPA PRRRMEEEMQ PAEEGPSVPK IYKQRSPYSV LKTFPSKRPA    240
LAKRYERPTL VELPHGHLRT PAQPPPASPA ASSSSSFAAV VRLGAPPRPP RRGFRARGTI    300
PPLLPAPGVA GTLLPPPTSS SPPSPRPRPW HAAAPRGGTS HTHMWRSQST LPGSDTMVSV    360
FGLMAQRRWQ HRSLKQFEWG ILGSWGTWPC GQDWLEKEGQ VAVLLPRSEG NTAPKKSRMI    420
LDAFAQQCSR VLSLLNCGGK LLDSNHSQSM ISCVKQEGSS YNERQEHCHI GKGVHSQTSD    480
NVDIEMQYMQ RKQQTSAFLR VFTDSLQNYL LSGSFPTPNP SSASEYGHLA DVDPLSTSPV    540
HTLENISLDS TASLCKSRHL SREPPVKSDF PNPLQQALAG GASRPFSGAQ QSIAYRVNSE    600
LEDGIRSPVP LSCEALEMDL TSLGSKQLLN NYPVYITSKQ WDEAVNSSKK DGRRLLRYLI    660
RFVFTTDELK YSCGLGKRKR SVQSGETGPE RRPLDPVKVT CLRGTASFRS VSPSVISFHR    720
IGCGSPRTSV QPSVF                                                     735

Seq ID NO: C402 Protein Sequence
Protein Accession #: BAA92562.1

1          11         21         31         41         51
|          |          |          |          |          |
METTVLSGIN FEYKGMTGWE VAGDHIYTAA GASDNDFMIL TLVVPGFRPP QSVMADTENK    60
EVARITFVFE TLCSVNCELY FMVGVNSRTN TPVETWKGSK GKQSYTYIIE ENTTTSFTWA    120
FQRTTFHEAS RKYTNDVAKI YSINVTNVMN GVASYCRPCA LEASDVGSSC TSCPAGYYID    180
RDSGTCHSCP PNTILKAHQP YGVQACVPCG PGTKNNKIHS LCYNDCTFSR NTPTRTFNYN    240
FSALANTVTL AGGPSFTSKG LKYFHHFTLS LCGNQGRKMS VCTDNVTDLR IPEGESGFSK    300
SITAYVCQAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELFHLESLGI    360
PDVIFFYRSN DVTQSCSSGR STTIRVRCSP QKTVPGSLLL PGTCSDGTCD GCNFHFLWES    420
AAACPLCSVA DYHAIVSSCV AGIQKTTYVW REPKLCSGGI SLPEQRVTIC KTIDFWLKVG    480
ISAGTCTAIL LTVLTCYFWK KNQKLEYKYS KLVMNATLKD CDLPAADSCA IMEGEDVEDD    540
LIFTSKKSLF GKIKSFTSKQ PAPVTISLSE DS                                  572

Seq ID NO: C403 Protein Sequence
Protein Accession #: NP_055139.1

1          11         21         31         41         51
|          |          |          |          |          |
MALQGISVVE LSGLAPGRXC AMVLADFGAR VVRVDRPGSR YDVSRLGRGK RSLVLDLKQP    60
REPRAAASVQ AVGCAAGALP PRCHGETPAG PRDSAAGKSK AYLCQAEWIW PVQESFCRLA    120
GHDINYLALS GVLSKIGRSG ENPYAPLNLV ADFAGGGLMC ALGIIMALFD RTRTDKGQVI    180
DANMVEGTAY LSSFLWKTQK SSLWEAPRGQ NMLDGGAPFY TTYRTADGEF MAVGAIEPQF    240
YELLIKGLGL KSDELPNQMS TDDWPEMKKK FADVFAKKTK AEWCQIFDGT DACVTPVLTF    300
EEVVHHDHNK ERGSFITSEE QDVSPRLAPL LLNTPAIPSS KGDPFIGEHT EEILEEFGFS    360
REEIYQLNSD KIIESNKVKA SL                                             382

Seq ID NO: C404 Protein Sequence
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Protein Accession #: XP_091332.1

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1          11         21         31         41         51
|          |          |          |          |          |
MQRWTLWAAA FLTLHSAQAF PQTDISISPA LPELPLPSLC PLFWMEFKGH CYRFFPLNKT   60
WAEADLYCSE FSVGRKSAKL ASIHSWEENV FVYDLVNSCV PGIPADVWTG LHDHRQEGQF  120
EWTDGSSYDY SYWDGSQPDD GVHADPEEED CVQIWYRPTS EQLQAPEPQL PLSISEATDV  180
YLPEDFPAEP KLMDQSWVSR KSLKPSKSHL MEPPTPVAKH QKAKTRHRSL RGVWWPSGKA  240
GSWKERMNAD YGRRKRSAPR QEGRLRCRER RLRAASGQGR PEGQRKQRQQ ERQERGWEEL  300
GGVSPMRGAQ AWQHGLGAGS QRGAAPECGE NHQAPELGST WRGQRLQPQT AALCHFALRK  360
LPGNAHGLAA AFVQPALQVQ EEKNNRTRFS GAYFTMSDPT CDQDSKEQSL RRHGREAEKD  420
GPYRLVKKKR GPVACPSSFE LQSGGEVCLD FPVELRAGTW IAREPP                 466
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Seq ID NO: C405 Protein Sequence
Protein Accession #: XP_054869.2

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1          11         21         31         41         51
|          |          |          |          |          |
MHTCCPPVTL EQDLHRKMHS WMLQTLAFAV TSLVLSCAET IDYYGEICDN ACPCEEKDGI   60
LTVSCENRGI ISLSEISPPR FPIYHLLLSG NLLNRLYPNE FVNYTGASIL HLGSNVIQDI  120
ETGAFHGLRG LRRLHLNNNK LELLRDDTFL GLENLEYLQV DYNYISVIEP NAFGKLHLLQ  180
VLILNDNLLS SLPNNLFRFV PLTHLDLRGN RLKLLPYVGL LQHMDKVVEL QLEENPWNCS  240
CELISLKDWL DSISYSALVG DVVCETPFRL HGRDLDEVSK QELCPRRLIS DYEMRPQTPL  300
STTGYLHTTP ASVNSVATSS SAVYKPPLKP PKGTRQPNKP RVRPTSRQPS KDLGYSNYGP  360
SIAYQTKSPV PLECPTACSC NLQISDLGLN VNCQERKIES IAELQPKPYN PKKMYLTENY  420
IAVVRRTDFL EATGLDLLHL GNNRISMIQD RAFGDLTNLR RLYLNGNRIE RLSPELFYGL  480
QSLQYLFLQY NLIREIQSGT FDPVPNLQLL FLNNNLLQAM PSGVFSGLTL LRLNLRSNHF  540
TSLPVSGVLD QLKSLIQIDL HDNPWDCTCD IVGMKLWVEQ LKVGVLVDEV ICKAPKKFAE  600
TDMRSIKSEL LCPDYSDVVV STPTPSSIQV PARTSAVTPA VRLNSTGAPA SLGAGGGASS  660
VPLSVLILSL LLVFIMSVFV AAGLFVLVMK RRKKNQSDHT STNNSDVSSF NMQYSVYGGG  720
GGTGGHPHAH VHHRGPALPK VKTPAGHVYE YIPHPLGHMC KNPIYRSREG NSVEDYKDLH  780
ELKVTYSSNH HLQQQQQPPP PPQQPQQQPP PQLQLQPGEE ERRESHHLRS PAYSVSTIEP  840
REDLLSPVQD ADRFYRGILE PDKHCSTTPA GNSLPEYPKF PCSPAAYTFS PNYDLRRPHQ  900
YLHPGAGDSR LREPVLYSPP SAVFVEPNRN EYLELKAKLN VEPDYLEVLE KQTTFSQF    958
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Seq ID NO: C406 Protein Sequence
Protein Accession #: NP_000784.2

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1          11         21         31         41         51
|          |          |          |          |          |
MGILSVDLLI TLQILPVFFS NCLFLALYDS VILLKHVVLL LSRSKSTRGE WRRMLTSEGL   60
RCVWKSFLLD AYKQVKLGED APNSSVVHVS STEGGDNSGN GTQEKIAEGA TCHLLDFASP  120
ERPLVVNFGS ATUPPFTSQL PAFRKLVEEF SSVADFLLVY IDEAHPSDGW AIPGDSSLSF  180
EVKKHQNQED RCAAAQQLLE RFSLPPQCRV VADRMDNNAN IAYGVAFERV CIVQRQKIAY  240
LGGKGPFSYN LQEVRHWLEK NFSKRUKKTR LAG                               273
```

Seq ID NO: C407 Protein Sequence
Protein Accession #: NP_006540.2

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1          11         21         31         41         51
|          |          |          |          |          |
MSSCVSSQPS SNRAAPQDEL GGRGSSSSES QKPCEALRGL SSLSIHLGME SFIVVTECEP   60
GCAVDLGLAR DRPLEADGQE VPLDSSGSQA RPHLSGRKLS LQERSQGGLA AGGSLDMNGR  120
CICPSLPYSP VSSPQSSPRL PRRPTVESHH VSITGMQDCV QLNQYTLKDE IGKGSYGVVK  180
LAYNENDNTY YAMKVLSKKK LIRQAGFPRR PPPRGTRPAP GGCIQPRGPI EQVYQEIAIL  240
KKLDHPNVVK LVEVLDDPNE DHLYMVFELV NQGPVMEVPT LKPLSEDQAR FYFQDLIKGI  300
EYLHYQKIIH RDIKPSNLLV GEDGHIKIAD FGVSNEFKGS DALLSNTVGT PAFMAPESLS  360
ETRKIFSGKA LDVWAMGVTL YCFVFGQCPF MDERIMCLHS KIKSQALEFP DQPDIAEDLK  420
DLITRMLDKN PESRIVVPEI KLHPWVTRHG AEPLPSEDEN CTLVEVTEEE VENSVKHIPS  480
LATVILVKTM IRKRSFGNPF EGSRREERSL SAPGNLLTKK PTRECESLSE LKEARQRRQP  540
PGHRPAPRGG GGSALVRGSP CVESCWAPAP GSPARMHPLR PEEAMEPE               588
```

Seq ID NO: C408 Protein Sequence
Protein Accession #: NP_061116.2

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1          11         21         31         41         51
|          |          |          |          |          |
MGLSLPKEKG LILCLWSKFC RWFQRRESWA QSRDEQNLLQ QKRIWESPLL LAAKDNDVQA   60
LNKLLKYEDC KVHQRGAMGE TALHIAALYD NLEAAMVLME AAPELVFEPM TSELYEGQTA  120
LHIAVVNQNM NLVRALLARR ASVSARATGT AFRRSPCNLI YFGEHPLSFA ACVNSEEIVR  180
LLIEHGADIR AQDSLGNTVL HILILQPNKT FACQMYNLLL SYDRHGDHLQ PLDLVPNHQG  240
LTPFKLAGVE GNTVMFQHLM QKRKHTQWTY GPLTSTLYDL TEIDSSGDEQ SLLELIITTK  300
KREARQILDQ TPVKELVSLK WKRYGRPYFC MLGAIYLLYI ICFTMCCIYR PLKPRTNNRT  360
SPRDNTLLQQ KLLQEAYMTP KDDIRLVGEL VTVIGAIIIL LVEVPDIFRM GVTRFFGQTI  420
LGGPFHVLII TYAFMVLVTM VMRLISASGE VVPMSFALVL GWCNVMYFAR GFQMLGPFTI  480
MIQKMIFGDL MRFCWLMAVV ILGFASAFYI IFQTEDPEEL GHFYDYPMAL FSTFELFLTI  540
IDGPANYNVD LPFMYSITYA AFAIIATLLM LNLLIAMMGD THWRVAHERD ELWRAQIVAT  600
TVMLERKLPR CLWPRSGICG REYGLGDRWF LRVEDRQDLN RQRIQRYAQA FHTRGSEDLD  660
KDSVEKLELG CPFSPHLSLP MPSVSRSTSR SSANWERLRQ GTLRRDLRGI INRGLEDGES  720
WEYQI                                                              725
```

Seq ID NO: C409 Protein Sequence
Protein Accession #: NP_068710.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQKVTLGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW   60
RSSGEQAGRG WGSPPLTTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS         113
```

Seq ID NO: C410 Protein Sequence
Protein Accession #: NP_005962.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MQKVTLGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK   60
CKCKFGQKSG HHPGETPPLI TPGSAQS                                       87
```

Seq ID NO: C411 Protein Sequence
Protein Accession #: NP_004952.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MLSKVLPVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE   60
TGSRVGKLPE ASRILNTILS NYDHKLRPGI GEKPTVVTVE IAVNSLGPLS ILDMEYTIDI   120
IFSQTWYDER LCYNDTFESL VLNGNVVSQL WIPDTFFRNS KRTHEHEITM PNQMVRIYKD   180
GKVLYTIRMT IDAGCSLHML RFPMDSHSCP LSFSSPSYPE NEMIYKWENF KLEINEKNSW   240
KLFQFDFTGV SNKTEIITTP VGDFMVMTIF FNVSRRFGYV AFQNYVPSSV TTMLSWVSFW   300
IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIAICFVF CFCALLEFAV   360
LNFLIYNQTK AHASPKLRHP RINSRAHART RARSRACARQ HQEAFVCQIV TTEGSDGEER   420
PSCSAQQPPS PGSPEGPRSL CSKLACCEWC KRFKKYFCMV PDCEGSTWQQ GRLCIHVYRL   480
DNYSRVVFPV TFFFFNVLYW LVCLNL                                        506
```

Seq ID NO: C412 Protein Sequence
Protein Accession #: NP_068819.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEYTIDIIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ   60
MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWENFKLE   120
INEKNSWKLF QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTTM   180
LSWVSFWIKT ESAPARTSLG ITSVLTMTTL GTFSRKNFPR VSYITALDFY IAICFVFCFC   240
ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE   300
GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPDC EGSTWQQARL   360
CIHVYRLDNY SRVVFPVTFF FFNVLYWLVC LNL                                393
```

Seq ID NO: C413 Protein Sequence
Protein Accession #: NP_068822.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEYTIDIIFS QTWNSKRTHE HEITMPNQMV RIYKDGKVLY TIRMTIDAGC SLHMLRFPMD   60
SHSCPLSFSS FSYPENEMIY KWENFKLEIN EKNSWKLFQF DFTGVSNKTE IITTPVGDFM   120
VMTIFFNVSR RFGYVAFQNY VPSSVTTMLS WVSFWIKTES APARTSLGIT SVLTMTTLGT   180
FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFLI YNQTKAHASP KLRHPRINSR   240
AHARTRARSR ACARQHQEAP VCQIVTTEGS DGEERPSCSA QQPPSPGSPE GPRSLCSKLA   300
CCEWCKRFKK YFCMVPDCEG STWQQGRLCI HVYRLDNYSR VVFPVTFFFF NVLYWLVCLN   360
L                                                                   361
```

Seq ID NO: C414 Protein Sequence
Protein Accession #: NP_068830.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEYTIDIIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ   60
MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWENFKLE   120
INEKNSWKLF QFDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTTM   180
LSWVSFWIKT ESAPARTSLG ITSVLTMTTL GTFSRKNFPR VSYITALDFY IAICFVFCFC   240
ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE   300
GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPDC EGSTWQQGRL   360
CIHVYRLDNY SRVVFPVTFF FFNVLYWLVC LNL                                393
```

Seq ID NO: C415 Protein Sequence
Protein Accession #: NP_068591.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPAVSGPGPL FCLLLLLLDP HSPETGCPPL RRFEYKLSFK GPRLALPGAG IPFWSHHGDA   60
ILGLEEVRLT PSMRNRSGAV WSRASVPFSA WEVEVQMRVT GLGRRGAHGM AVWYTRGRGH   120
VGSVLGGLAS WDGIGIFFDS PAEDTQDSPA IRVLASDGHI PSEQPGDGAS QGLGSCHWDF   180
RNRPHPFRAR ITYWGQRLRM SLNSGLTPSD PGEFCVDVGP LLLVPGGFFG VSAATGTLAD   240
DHDVLSFLTF SLSEPSPEVP PQPFLEMQQL RLARQLEGLW ARLGLGTRED VTPKSDSEAQ   300
GEGERLFDLE ETLGRHRRIL QALRGLSKQL AQAERQWKKQ LGPPGQARPD GGWALDASCQ   360
IPSTPGRGGH LSMSLNKDSA KVGALLHGQW TLLQALQEMR DAAVRMAAEA QVSYLPVGIE   420
HHFLELDHIL GLLQEELRGP AKAAAKAPRP PGQPPRASSC LQPGIFLFYL LIQTVGFFGY   480
VHFRQELNKS LQECLSTGSL PLGPAPHTPR ALGILRRQPL PASMPA                   526
```

Seq ID NO: C416 Protein Sequence
Protein Accession #: XP_117036.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MERRTRGALG SRRPPPPLPA LRHLCTGLQA AGMAWPGTLW RHTCQGRAXA AEGPWGLFRP   60
HRCPREAGQA PVGPSPETQG VAHVCSRARV SVDEREPGGG AYAMHVTPRW KGCHRHSGRT   120
VRGSVSWKRP EQAAPETGRG PAVARGSGDG NECGWG                          156
```

Seq ID NO: C417 Protein Sequence
Protein Accession #: XP_167803.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGKGQRKTA TNKPGGLPGA PGVGIGGHCL YVLECKCFIK NKTKTHHHKK KNFAAKRNEE   60
KLKKKKKQEK KNHTKFPHHT YPLSQQDPLF AKSYFCGNGP CFLWQGLF               108
```

Seq ID NO: C418 Protein Sequence
Protein Accession #: NP_079056.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYYWLNT VALSGEECWE TLIGQDIYRL   60
LLMDFVFSLV NSFLGEFLRR IIGMQLITSL GLQEFDIARN VLELIYAQTL VWIGIFFCPL   120
LPFIQMIMLF IMFYSKNISL MMNFQPPSKA WRASQMMTFF IFLLFFPSFT GVLCTLAITI   180
WRLKPSADCG PFRGLPLFIH SIYSWIDTLS TRPGYLWVVW IYRNLIGSVH FFFILTLIVL   240
IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP SSLVLERREV   300
EQQGFLHLGE HDGSLDLRSR RSVQEGNPRA                                    330
```

Seq ID NO: C419 Protein Sequence
Protein Accession #: Eos sequence

```
1          11         21         31         41         51
|          |          |          |          |          |
MLSDDHVNEI IIQVENVSSG VQSHPSSNQI FQEKVLLDSS INMVLSISDI DVIDSQTVSK   60
RNDQKGNQVL RFSTSLNESM SQTLHSLECM GIDTPGSSHE TVQGQKLIAS LIPMTSRDRI   120
KAIRNQPRTM EEKRNLRKIV DKEKSKQTHR ILQLNCCIQC LNSISRAYRR SKNSLSEILN   180
SISLWQKTLK IIGGKFGTSV LSYFNFLRWL LKFNIFSFIL NFSFIIIPQF TVAKKNTLQF   240
TGLEFFTGVG YFRDTVMYYG FYTNSTIQHG NSGASYNMQL AYIFTIGACL TTCFFSLLFS   300
MAKYFRNNFI NPHIYSGGIT KLIFCWDFTV THEKAVKLKQ KNLSTEIREN LSELRQENSK   360
LTFNQLLTRF SAYMVAWVVS TGVAIACCAA VYYLAEYNLE FLKTHSNPGA VLLLPFVVSC   420
INLAVPCIYS MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYYWLNT VALSGEECWE   480
TLIGQDIYRL LLMDFVFSLV NSFLGEFLRR IIGMQLITSL GLQEFDIARN VLELIYAQTL   540
VWIGIFFCPL LPFIQMIMLF IMFYSKNISL MMNFQPPSKA WRASQMMTFF IFLLFFPSFT   600
GVLCTLAITI WRLKPSADCG PFRGLPLFIH SIYSWIDTLS TRPGYLWVVW IYRNLIGSVH   660
FFFILTLIVL IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP   720
SSLVLERREV EQQGFLHLGE HDGSLDLRSR RSVQEGNPRA                          760
```

Seq ID NO: C420 Protein Sequence
Protein Accession #: NP_002241.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGGDLVLGLG ALRRRKRLLE QEKSLAGWAL VLAGTGIGLM VLHAEMLWFG GCSWALYLFL   60
VKCTISISTF LLLCLIVAFH AKEVQLFMTD NGLRDWRVAL TGRQAAQIVL ELVVCGLHPA   120
PVRGPPCVQD LGAPLTSPQP WPGFLGQGEA LLSLAMLLRL YLVPRAVLLR SGVLLNASYR   180
SIGALNQVRF RHWFVAKLYM NTHPGRLLLG LTLGLWLTTA WVLSVAERQA VNATGHLSDT   240
LWLIPITFLT IGYGDVVPGT MWGKIVCLCT GVMGVCCTAL LVAVVARKLE FNKAEKHVHN   300
FMMDIQYTKE MKESAARVLQ EAWMFYKHTR RKESHAARRH QRKLLAAINA FRQVRLKHRK   360
LREQVNSMVD ISKMHMILYD LQQNLSSSHR ALEKQIDTLA GKLDALTELL STALGPRQLP   420
EPSQQSK                                                             427
```

Seq ID NO: C421 Protein Sequence
Protein Accession #: NP_079533.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGGKQRDEDD EAYGKPVKYD PSFRGPIKNR SCTDVICCVL FLLFILGYIV VGIVAWLYGD   60
PRQVLYPRNS TGAYCGMGEN KDKPYLLYFN IFSCILSSNI ISVAENGLQC PTPQVCVSSC   120
PEDPWTVGKN EFSQTVGEVF YTKNRNFCLP GVPWNMTVIT SLQQELCPSF LLPSAPALGR   180
CFPWTNITPP ALPGITNDTT IQQGISGLID SLNARDISVK IFEDFAQSWY WILVALGVAL   240
VLSLLFILLL RLVAGPLVLV LILGVLGVLA YGIYYCWEEY RVLRDKGASI SQLGFTTNLS   300
AYQSVQETWL AALIVLAVLE AILLLVLIFL RQRIRIAIAL LKEASKAVGQ MMSTMFYPLV   360
TFVLLLICIA YWAMTALYPL PTQPATLGYV LWASNISSPG CEKVPINTSC NPTAHLVNSS   420
CPGLMCVFQG YSSKGLIQRS VFNLQIYGVL GLFWTLNWVL ALGQCVLAGA FASFYWAFHK   480
PQDIPTFPLI SAFIRTLRYH TGSLAFGALI LTLVQIARVI LEYIDHKLRG VQNPVARCIM   540
CCFKCCLWCL EKFIKFLNRN AYIMIAIYGK NFCVSAKNAF MLLMRNIVRV VVLDKVTDLL   600
LFFGKLLVVG GVGVLSFFFF SGRIPGLGKD FKSPHLNYYW LPIMTSILGA YVIASGFFSV   660
FGMCVDTLFL CFLEDLERNN GSLDRPYYMS KSLLKILGKK NEAPPDNKKR KK           712
```

Seq ID NO: C422 Protein Sequence
Protein Accession #: NP_057264.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGSNSGQAGR HIYKSLADDG PFDSVEPPKR PTSRLIMHSM AMFGREFCYA VEAAYVTPVL   60
```

```
LSVGLPSSLY SIVWFLSPIL GFLLQPVVGS ASDHCRSRWG RRRPYILTLG VMMLVGMALY   120
LNGATVVAAL IANPRRKLVW AISVTMIGVV LFDFAADFID GPIKAYLFDV CSHQDKEKGL   180
HYHALFTGFG GALGYLLGAI DWAHLELGRL LGTEFQVMFF FSALVLTLCF TVHLCSISEA   240
PLTEVAKGIP PQQTPQDPPL SSDGMYEYGS IEKVKNGYVN PELAMQGAKN KNHAEQTRRA   300
MTLKSLLRAL VNMPPHYRYL CISHLIGWTA FLSNMLFFTD FMGQIVYRGD PYSAHNSTEF   360
LIYERGVEVG CWGFCINSVF SSLYSYFQKV LVSYIGLKGL YFTGYLLFGL GTGFIGLFPN   420
VYSTLVLCSL FGVMSSTLYT VPFNLITEYH REEEKERQQA PGGDFDNSVR GKGMDCATLT   480
CMVQLAQILV GGGLGFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD               530
```

Seq ID NO: C423 Protein Sequence
Protein Accession #: NP_003264.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEGPGGVGGR GTRGFAAKGV WRGRAEEGPV LGAAERGFMV STGSRRRVFE GPGGGGLRWT   60
PGKGTGRQRG AWGPRAEDGV RRRTLGMPRG SRRDVRAPCG PAGSWGARGG RRRDGPSRRR   120
RGSATAAARH HVPPAPGGPF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT   180
AGAQGAGPAR GRSGEGSEWA RRGKGRPGPY QSPLGPAVAE GQELKDKSRL RYPINGFQAL   240
VLTALLVGLG MSAGLPLGAL PEMLLPLAFV ATLTAFIFSL FLYMKAQVAP VSALAPGGNS   300
GNPIYDFFLG RELNPRICFF DFKYFCELRP GLIGWVLINL ALLMKEAELR GSPSLAMWLV   360
NGFQLLYVGD ALWHEEAVLT TMDITHDGFG FMLAFGDMAW VPFTYSLQAQ FLLHHPQPLG   420
LPMASVICLI NATGYYIFRG ANSQKNTFRK NPSDPRVAGL ETISTATGRK LLVSGWWGMV   480
RHPNYLGDLI MALAWSLPCG VSHLLPYFYL LYFTALLVHR EARDERSACR STAWPGRSTA   540
GVCLTASCPT STEAAPPPQV GHVPTHPPAH PGPGASTHLG LKGLHPTQP               589
```

Seq ID NO: C424 Protein Sequence
Protein Accession #: NP_056535.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MGRLLRAARL PPLLSPLLLL LVGGAFLGAC VAGSDEPGPE GLTSTSLLDL LLPTGLEPLD   60
SEEPSETMGL GAGLGAPGSG FPSEENEESR ILQPPQYFWE EEEELNDSSL DLGPTADYVF   120
PDLTEKAGSI EDTSQAQELP NLPSPLPKMN LVEPPWHMPP REEEEEEEEE EEREKEEVEK   180
QEEEEEEELL PVNGSQEEAK PQVRDFSLTS SSQTPGATKS RHEDSGDQAS SGVEVESSMG   240
PSLLLPSVTP TTVTPGDQDS TSQEAEATVL PAAGLGVEFE APQEASEEAT AGAAGLSGQH   300
EEVPALPSFP QTTAPSGAEH PDEDPLGSRT SASSPLAPGD MELTPSSATL GQEDLNQQLL   360
EGQAAEAQSR IPWDSTQVIC KDWSNLAGKN YIILNMTENI DCEVFRQHRG PQLLALVEEV   420
LPRHGSGHHG AWHISLSKPS EKEQHLLMTL VGEQGVVPTQ DVLSMLGDIR RSLEEIGIQN   480
YSTTSSCQAR ASQVRSDYGT LFVVLVVIGA ICIIIIALGL LYNCWQRRLP KLKHVSHGEE   540
LRFVENGCHD NPTLDVASDS QSEMQEKHPS LNGGGALNGP GSWGALMGGK RDPEDSDVFE   600
EDTHL                                                               605
```

Seq ID NO: C425 Protein Sequence
Protein Accession #: NP_001188.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MSEVRPLSRD ILMETLLYEQ LLEPPTMEVL GMTDSEEDLD PMEDFDSLEC MEGSDALALR   60
LACIGDEMDV SLRAPRLAQL SEVAMHSLGL AFIYDQTEDI RDVLRSFMDG FTTLKENIMR   120
FWRSPNPGSW VSCEQVLLAL LLLLALLLPL LSGGLHLLLK                         160
```

Seq ID NO: C426 Protein Sequence
Protein Accession #: AAF76225.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MATPLPPPSP RHLRLLRLLL SGLVLGAALR GAAAGHPDVA ACPGSLDCAL KRRARCPPGA   60
HACGPCLQPF QEDQQGLCVP RMRRPPGGGR PQPRLEDEID PLAQELARKE SGQSTPPLPK   120
DRQRLPEPAT LGFSARGQGL ELGLPSTPGT PTPTPHTSLG SPVSSDPVHM SPLEPRGGQG   180
DGLALVLILA FCVAGAAALS VASLCWCRLQ REIRLTQKAD YATAKAPGSP AAPRISPGDQ   240
RLAQSAEMYH YQHQRQQMLC LERHKEPPKE LDTASSDEEN EDGDFTVYEC PGLAPTGEME   300
VRNPLFDHAA LSAPLPAPSS PPALP                                         325
```

Seq ID NO: C427 Protein Sequence
Protein Accession #: NP_004436.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MVCSLWVLLL VSSVLALEEV LLDTTGETSE IGWLTYPPGG WDEVSVLDDQ RRLTRTFEAC   60
HVAGAPPGTG QDNWLQTHFV ERRGAQRAHI RLHFSVRACS SLGVSGGTCR ETFTLYYRQA   120
EEPDSPDSVS SWHLKRWTKV DTIAADESFP SSSSSSSSSS SAAWAVGPHG AGQRAGLQLN   180
VKERSFGPLT QRGFYVAFQD TGACLALVAV RLFSYTCPAV LRSFASFPET QASGAGGASL   240
VAAVGTCVAH AEPEEDGVGG QAGGSPPRLH CNGEGKWMVA VGGCRCQPGY QPARGDKACQ   300
ACPRGLYKSS AGNAPCSPCP ARSHAPNPAA PVCPCLEGFY RASSDPPEAP CTGPPSAPQE   360
LWFEVQGSAL MLHWRLPREL GGRGDLLFNV VCKECEGRQE PASGGGGTCH RCRDEVHFDP   420
RQRGLTESRV LVGGLRAHVP YILEVQAVNG VSELSPDPPQ AAAINVSTSH EVPSAVPVVH   480
QVSRASNSIT VSWPQPDQTN GNILDYQLRY YDQAEDESHS FTLTSETNTA TVTQLSPGHI   540
YGFQVRARTA AGHGPYGGKV YFQTLPQGEL SSQLPERLSL VIGSILGALA FLLLAAITVL   600
AVVFQRKRRG TGYTEQLQQY SSPGLGVKYY IDPSTYEDPC QAIRELAREV DPAYIKIEEV   660
IGTGSFGEVR QGRLQPRGRR EQTVAIQALW AGGAESLQMT FLGRAAVLGQ FQHPNILRLE   720
GVVTKSRPLM VLTEFMELGP LDSFLRQREG QFSSLQLVAM QRGVAAAMQY LSSFAFVHRS   780
LSAHSVLVNS HLVCKVARLG HSPQGPSCLL RWAAPEVIAH GKHTTSSDVW SFGILMWEVM   840
SYGERPYWDM SEQEVLNAIE QEFRLPPPPG CPPGLHLLML DTWQKDRARR PHFDQLVAAF   900
DKMIRKPDTL QAGGDPGERP SQALLTPVAL DFPCLDSPQA WLSAIGLECY QDNFSKFGLC   960
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TFSDVAQLSL EDLPALGITL AGHQKKLLHH IQLLQQHLRQ QGSVEV                    1006
```

Seq ID NO: C428 Protein Sequence
Protein Accession #: XP_043340.2

```
1          11         21         31         41         51
|          |          |          |          |          |
MPFDFRRFDI YRKVPKDLTQ PTYTGAIISI CCCLFILFLF LSELTGFITT EVVNELYVDD   60
PDKDSGGKID VSLNISLPNL HCELVGLDIQ DEMGRHEVGH IDNSMKIPLN NGAGCRFEGQ  120
FSINKVPGNF HVSTHSATAQ PQNPDMTHVI HKLSFGDTLQ VQNIHGAFNA LGGADRLTSN  180
PLASHDYILK IVPTVYEDKS GKQRYSYQYT VANKEYVAYS HTGRIIPAIW FRYDLSPITV  240
KYTERRQPLY RFITTICAII GGTFTVAGIL DSCIFTASEA WKKIQLGKMH              290
```

Seq ID NO: C429 Protein Sequence
Protein Accession #: NP_002142.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MAQKEGGRTV PCCSRPKVAA LTAGTLLLLT AIGAASWAIV AVLLRSDQEP LYPVQVSSAD   60
ARLMVFDKTE GTWRLLCSSR SNARVAGLSC EEMGFLRALT HSELDVRTAG ANGTSGFFCV  120
DEGRLPHTQR LLEVISVCDC PRGRFLAAIC QDCGRRKLPV DRIVGGRDTS LGRWPWQVSL  180
RYDGAHLCGG SLLSGDWVLT AAHCFPERNR VLSRWRVFAG AVAQASPHGL QLGVQAVVYH  240
GGYLPFRDPN SEENSNDIAL VHLSSPLPLT EYIQPVCLPA AGQALVDGKI CTVTGWGNTQ  300
YYGQQAGVLQ EARVPIISND VCNGADFYGN QIKPKMFCAG YPEGGIDACQ GDSGGPFVCE  360
DSISRTPRWR LCGIVSWGTG CALAQKPGVY TKVSDFREWI FQAIKTHSEA SGMVTQL      417
```

Seq ID NO: C430 Protein Sequence
Protein Accession #: BAA92562.1

```
1          11         21         31         41         51
|          |          |          |          |          |
METTVLSGIN FEYKGMTGWE VAGDHIYTAA GASDNDFMIL TLVVPGFRPP QSVMADTENK   60
EVARITFVFE TLCSVNCELY FMVGVNSRTN TPVETWKGSK GKQSYTYIIE ENTTTSFTWA  120
FQRTTFHEAS RKYTNDVAKI YSINVTNVMN GVASYCRPCA LEASDVGSSC TSCPAGYYID  180
RDSGTCHSCP PNTILKAHQP YGVQACVPCG PGTKNNKIHS LCYNDCTFSR NTPTRTFNYN  240
FSALANTVTL AGGPSFTSKG LKYFHHFTLS LCGNQGRKMS VCTDNVTDLR IPEGESGFSK  300
SITAYVCQAV IIPPEVTGYK AGVSSQPVSL ADRLIGVTTD MTLDGITSPA ELFHLESLGI  360
PDVIFFYRSN DVTQSCSSGR STTIRVRCSP QKTVPGSLLL PGTCSDGTCD GCNFHFLWES  420
AAACPLCSVA DYHAIVSSCV AGIQKTTYVW REPKLCSGGI SLPEQRVTIC KTIDFWLKVG  480
ISAGTCTAIL LTVLTCYFWK KNQKLEYKYS KLVMNATLKD CDLPAADSCA IMEGEDVEDD  540
LIFTSKKSLF GKIKSFTSKQ PAPVTISLSE DS                                572
```

Seq ID NO: C431 Protein Sequence
Protein Accession #: NP_004855.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRASF PGPSELHSED SRFRELRKRY   60
EDLLTRLRAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLPEASRL  120
HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSSARPQL  180
ELHLRPQAAR GRRRARARNG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC  240
IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTDT GVSLQTYDDL  300
LAKDCHCI                                                           308
```

Seq ID NO: C433 Protein Sequence
Protein Accession #: NP_443090.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MEDPSGAREP RARPRERDPG RRPHPDQGRT HDRPRDRPGD PRRKRSSDGN RRRDGDRDPK   60
RDQERDGNRD RNRDRERERE RERDPDRGPR RDTHRDAGPR AGEHGVWEKP RQSRTRDGAR  120
GLTWDAAAPP GPAPWEAPEP PQPQRKGDPG RRRPESEPPS ERYLPSTPRP GREEVEYYQS  180
EAEGLLECHK CKYLCTGRAC CQMLEVLLNL LILACSSVSY SSTGGYTGIT SLGGIYYYQF  240
GGAYSGFDGA DGEKAQQLDV QFYQLKLPMV TVAMACSGAL TALCCLFVAM GVLRVPWHCP  300
LLLVTEGLLD MLIAGGYIPA LYFYFHYLSA AYGSPVCKER QALYQSKGYS GFGCSPHGAD  360
IGAGIFAALG IVVFALGAVL AIKGYRKVRK LKEKPAEMFE F                      401
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Seq ID NO: C435 Protein Sequence
Protein Accession #: Eos sequence

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1          11         21         31         41         51
|          |          |          |          |          |
MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPWNPGH DQDHHVHIGQ   60
GKTLLLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFQGNF  120
TIILYGRADE GIQPDPYYGL KYIGVGKGGA LELHGQKKLS WTFLNKTLHP GGMAEGGYFF  180
ERSWGHRGVI VHVIDPKSGT VIHSDRFDTY RSKKESERLV QYLNAVPDGR ILSVAVNDEG  240
SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVKGNPSS SVEDHIEYHG HRGSAAARVF  300
KLFQTEHGEY FNVSLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID  360
IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVRPK LTVTIDTNVN  420
STILNLEDNV QSWKPGDTLV IASTDYSMYQ AEEFQVLPCR SCAPNQVKVA GKPMYLHIGE  480
EIDGVDMRAE VGLLSRNIIV MGEMEDKCYP YRNHICNFFD FDTFGGHIKF ALGFKAAHLE  540
GTELKHMGQQ LVGQYPIHFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI  600
KDVVGYNSLG HCFFTEDGPE ERNTFDHCLG LLVKSGTLLP SDRDSKMCKM ITEDSYPGYI  660
PKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP  720
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LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRPFLSII SARYSPHQDA DPLKPREPAI   780
IRHFIAYKNQ DHGAWLRGGD VWLDSCHFRG EAQEGFLLTG MKAGGILLGG DEAASGMAQG   840
FSPPCRCLLK LVTTGSPFAH VSLAHS                                       866
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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method for determining the presence or absence of a pathological cell in a patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell.

2. The method of Claim 1, wherein:

a) said pathology is described in Table 1, including a cancer; and/or

b) said biological sample comprises isolated nucleic acids.

3. The method of Claim 1, wherein said biological sample is tissue from an organ which is affected by said pathology of Table 1, including a cancer.

4. The method of Claim 2, wherein said nucleic acids are mRNA

5. The method of Claim 2:

a) further comprising a step of amplifying nucleic acids before said step of detecting said nucleic acid; or

b) where said detecting is of a protein encoded by said nucleic acid.

6. The method of Claim 1, wherein said nucleic acid comprises a sequence as described in Tables 2A-80.

7. The method of Claim 2, wherein:

a) said detecting step is carried out by:

i) using a labeled nucleic acid probe;

ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80; or

iii) detecting a polypeptide encoded by said nucleic acid; or

b) said patient is:

i) undergoing a therapeutic regimen to treat said pathology of Table 1; or

ii) is suspected of having said pathology or cancer.

8. An isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80.

9. The nucleic acid molecule of Claim 8, which is labeled.

10. An expression vector comprising the nucleic acid of Claim 8.

11. A host cell comprising the expression vector of Claim 10.

12. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a sequence as described in Tables 2A-80.

13. An antibody that specifically binds a polypeptide of Claim 12.

14. The antibody of Claim 13:

a) conjugated to an effector component;

b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a cytotoxic chemical;

c) which is an antibody fragment; or

d) which is a humanized antibody.

15. A method for specifically targeting a compound to a pathological cell in a patient, said method comprising administering to said patient an antibody of Claim 13, thereby providing said targetting.

16. A method for determining the presence or absence of a pathological cell in a patient, said method comprising contacting a biological sample with an antibody of Claim 13.

17. The method of Claim 16, wherein:

a) said antibody is conjugated to:

i) an effector component; or

ii) a fluorescent label; or

b) said biological sample is a blood, serum, urine, or stool sample.

18. A method for identifying a compound that modulates a pathology-associated polypeptide, said method comprising the steps of:

a) contacting said compound with a pathology-associated polypeptide, said polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and

b) determining the functional effect of said compound upon said polypeptide.

19. A drug screening assay comprising the steps of:

a) administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and

b) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of said polynucleotide in a control cell or mammal, wherein a test compound that modulates said level of expression of the polynucleotide is a candidate for the treatment of said pathology.